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OM protein - protein search, using sw model

Run on: September 21, 2005, 14:52:13 ; Search time 81.9233 Seconds
(without alignments)
618.452 Million cell updates/sec

Title: US-10-807-204-1

Perfect score: 753

Sequence: 1 MGLSGLPLVFPFILLGDIQ.....GNNNFQTEAICLVTCCKYH 131

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 50 summaries

Database : A_Geneseq_16Dec04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	753	100.0	131	7 ADA19800	Ada19800 Engineere
2	753	100.0	131	7 ADA19811	Ada19811 Engineere
3	731	97.1	131	7 ADA19814	Ada19814 Human Dyl
4	625	83.0	106	7 ADA19801	Ada19801 Mature fo
5	551	73.2	98	7 ADA19808	Ada19808 Engineere
6	492	65.3	136	7 ADA19815	Ada19815 Mouse Dyl
7	467	62.0	133	2 AAW75219	Aaw75219 Human sec
8	467	62.0	133	5 AAE26982	Aae26982 Human gen
9	467	62.0	133	5 AAE27120	Aae27120 Human gen
10	467	62.0	133	6 ABU64993	Abu64993 Human sec
11	467	62.0	133	7 ADA19812	Ada19812 Human EPP
12	467	62.0	133	8 ADG89802	Adg89802 Human pro
13	467	62.0	164	3 AAY70010	Aay70010 Human Pro
14	467	62.0	179	8 ABW85103	Abw85103 Human dia
15	404	53.7	86	5 ABF69809	Abf69809 Human pol
16	404	53.7	86	5 ABJ26667	Abj26667 Human pro
17	404	53.7	101	4 ABBI2236	Abbi2236 Human epp
18	401.5	53.3	117	5 AAE27094	Aae27094 Human sec
19	401.5	53.3	117	5 AAE27165	Aae27165 Human gen
20	401.5	53.3	117	6 ABU65038	Abu65038 Human sec
21	401.5	53.3	117	8 ADG98847	Adg98847 Human sec
22	400	53.1	102	5 AAE27095	Aae27095 Human sec
23	400	53.1	102	5 AAE28009	Aae28009 Human gen
24	400	53.1	102	6 ABU65039	Abu65039 Human sec
25	400	53.1	102	8 ADG98848	Adg98848 Human sec

ALIGNMENTS

RESULT 1

ADA19800

ID ADA19800 standard; protein; 131 AA.

XX ADA19800;

XX 20-NOV-2003 (first entry)

XX Engineered human DJ11 protein SEQ ID NO:1.

XX DJ11; Kunitz-type protease inhibitor domain; antiinflammatory;

KW antiallergic; thrombolytic; anticoagulant; cardiant; vasotropic;

KW antibacterial; immunosuppressive; antirheumatic; antithrictic;

KW nephrotropic; antipsoriatic; vulnery; protease inhibitor; gene therapy;

KW acute pancreatitis; pulmonary injury; allergy-induced protease release;

KW deep vein thrombosis; myocardial infarction; shock; septic shock;

KW hyperfibrinolytic haemorrhage; inflammatory disorder; emphysema;

KW idiopathic pulmonary fibrosis; rheumatoid arthritis; glomerulonephritis;

KW chronic inflammatory bowel disease; psoriasis.

XX Synthetic.

XX Homo sapiens.

XX Key Location/Qualifiers

FT Misc-difference 1..131

FT Peptide /note= "eppin-like precursor"

FT Protein /label= signal

FT Disulfide-bond 26..131

FT Disulfide-bond 33..61

FT Disulfide-bond 40..65

FT Disulfide-bond 48..60

FT Disulfide-bond 54..69

FT Domain /note = predicted disulfide bond

FT Disulfide-bond 77..127

FT Disulfide-bond 77..127

FT Disulfide-bond 85..110

FT Disulfide-bond 85..110

FT Disulfide-bond 85..110

FT Disulfide-bond 85..110

FT Disulfide-bond 85..110

FT Disulfide-bond 85..110

FT Disulfide-bond 85..110

FT Disulfide-bond 85..110

FT Disulfide-bond 85..110

FT Disulfide-bond 85..110

FT Disulfide-bond 85..110

FT Disulfide-bond 85..110

FT Disulfide-bond 85..110

FT Disulfide-bond 85..110

FT Disulfide-bond 85..110

FT Disulfide-bond 85..110

FT Disulfide-bond 85..110

FT Disulfide-bond 85..110

FT FT Disulfide-bond 102. .123 /note = predicted disulfide bond
 FT FT Disulfide-bond 102. .123 /note = predicted disulfide bond
 XX XX
 PN WO2003070770-A2.
 XX XX
 PD 28-AUG-2003.
 XX XX
 XX 18-FEB-2003; 2003WO-EP001629.
 XX XX
 PF 21-FEB-2002; 2002US-0358683P.
 XX XX
 XX (GENE-) GENEPROT INC.
 XX XX
 XX Bougueleret L, Bairoch A, Niknejad A;
 XX WPI; 2003-663849/62.
 DR N-PSDB; ADA19810.
 XX XX
 XX New engineered human Kunitz-type protease inhibitor for diagnosing,
 PT preventing or treating conditions associated with excessive proteinase
 PT activity, e.g. inflammation, pulmonary injuries, myocardial infarction or
 PT hemorrhage.
 XX XX
 PS Claim 5; Page 69-70; 87pp; English.
 XX XX
 CC The present invention describes an isolated, purified or recombinant DJ11
 CC polypeptide comprising a Kunitz-type protease inhibitor domain or its
 CC biologically active portion. The polypeptide comprises at least 98 %
 CC identity to residues 77-127 of a 131 amino acid sequence (S1, see
 CC ADA19800), or to residues 52-102 of a 106 amino acid sequence (S2, see
 CC ADA19801). DJ11 has antiinflammatory, antiallergic, thrombolytic,
 CC anticoagulant, cardiant, vasotropic, antibacterial, immunosuppressive,
 CC antirheumatic, antiarthritic, nephrotropic, antipsoriatic and vulnary
 CC activities, and can be used as a protease inhibitor and in gene therapy.
 CC Composition and methods from the present invention can be used in
 CC diagnosing, preventing or treating conditions associated with excessive
 CC proteinase activity, such as acute pancreatitis, pulmonary injury,
 CC allergy-induced protease release, deep vein thrombosis, myocardial
 CC infarction, shock (including septic shock), hyperfibrinolytic
 CC haemorrhage, and especially, inflammatory disorders (e.g. emphysema,
 CC idiopathic pulmonary fibrosis, rheumatoid arthritis, glomerulonephritis,
 CC chronic inflammatory bowel disease or psoriasis). The DJ11 proteins may
 CC be used in preserving platelet function, organ preservation or in wound
 CC healing. The polynucleotide sequence encoding DJ11 may be used as
 CC hybridisation probes, in chromosome and gene mapping, in the generation
 CC of antisense RNA and DNA, and as targets for pharmaceutical intervention.
 CC The present sequence represents an engineered human DJ11 protein from the
 CC present invention.
 XX XX
 SQ Sequence 131 AA;
 Query Match 100.0%; Score 753; DB 7; Length 131;
 Best Local Similarity 100.0%; Pred. No. 1.2e-56;
 Matches 131; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MGLSGLLPILVFPFILLGDIQEPGHAGILGKPCPKIKVECEVEIDQCTKPRDCPENMKC 60
 Db 1 MGLSGLLPILVFPFILLGDIQEPGHAGILGKPCPKIKVECEVEIDQCTKPRDCPENMKC 60
 QY 61 CPFSGGKKCLDFRDXICSMPOEAGPCLASIPHWYNNKTKICSEFIYGGCGGNNNFQTE 120
 Db 61 CPFSGGKKCLDFRDXICSMPOEAGPCLASIPHWYNNKTKICSEFIYGGCGGNNNFQTE 120
 QY 121 AICLVTCCKYH 131
 Db 121 AICLVTCCKYH 131
 RESULT 2
 ADA19811
 ID ADA19811 standard; protein; 131 AA.
 XX XX

AC ADA19811;
 XX 20-NOV-2003 (first entry)
 DT Engineered human DJ11 protein SEQ ID NO:12.
 XX XX
 DE DJ11; Kunitz-type protease inhibitor domain; antiinflammatory;
 KW antiallergic; thrombolytic; anticoagulant; cardiant; vasotropic;
 KW antibacterial; immunosuppressive; antirheumatic; antiarthritic;
 KW nephrotropic; antipsoriatic; vulnary; protease inhibitor; gene therapy;
 KW acute pancreatitis; pulmonary injury; allergy-induced protease release;
 KW deep vein thrombosis; myocardial infarction; shock; septic shock;
 KW hyperfibrinolytic haemorrhage; inflammatory disorder; emphysema;
 KW idiopathic pulmonary fibrosis; rheumatoid arthritis; glomerulonephritis;
 KW chronic inflammatory bowel disease; psoriasis.
 XX Synthetic.
 OS Homo sapiens.
 OS XX
 XX WO2003070770-A2.
 XX XX
 PD 28-AUG-2003.
 XX XX
 XX 18-FEB-2003; 2003WO-EP001629.
 XX XX
 XX 21-FEB-2002; 2002US-0358683P.
 PR (GENE-) GENEPROT INC.
 XX Bougueleret L, Bairoch A, Niknejad A;
 XX WPI; 2003-663849/62.
 XX New engineered human Kunitz-type protease inhibitor for diagnosing,
 PT preventing or treating conditions associated with excessive proteinase
 PT activity, e.g. inflammation, pulmonary injuries, myocardial infarction or
 PT hemorrhage.
 XX XX
 PS Disclosure; Page 84; 87pp; English.
 XX XX
 CC The present invention describes an isolated, purified or recombinant DJ11
 CC polypeptide comprising a Kunitz-type protease inhibitor domain or its
 CC biologically active portion. The polypeptide comprises at least 98 %
 CC identity to residues 77-127 of a 131 amino acid sequence (S1, see
 CC ADA19800), or to residues 52-102 of a 106 amino acid sequence (S2, see
 CC ADA19801). DJ11 has antiinflammatory, antiallergic, thrombolytic,
 CC anticoagulant, cardiant, vasotropic, antibacterial, immunosuppressive,
 CC antirheumatic, antiarthritic, nephrotropic, antipsoriatic and vulnary
 CC activities, and can be used as a protease inhibitor and in gene therapy.
 CC Composition and methods from the present invention can be used in
 CC diagnosing, preventing or treating conditions associated with excessive
 CC proteinase activity, such as acute pancreatitis, pulmonary injury,
 CC allergy-induced protease release, deep vein thrombosis, myocardial
 CC infarction, shock (including septic shock), hyperfibrinolytic
 CC haemorrhage, and especially, inflammatory disorders (e.g. emphysema,
 CC idiopathic pulmonary fibrosis, rheumatoid arthritis, glomerulonephritis,
 CC chronic inflammatory bowel disease or psoriasis). The DJ11 proteins may
 CC be used in preserving platelet function, organ preservation or in wound
 CC healing. The polynucleotide sequence encoding DJ11 may be used as
 CC hybridisation probes, in chromosome and gene mapping, in the generation
 CC of antisense RNA and DNA, and as targets for pharmaceutical intervention.
 CC The present sequence represents an engineered human DJ11 protein from the
 CC present invention.
 XX XX
 SQ Sequence 131 AA;
 Query Match 100.0%; Score 753; DB 7; Length 131;
 Best Local Similarity 100.0%; Pred. No. 1.2e-56;
 Matches 131; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MGLSGLLPILVFPFILLGDIQEPGHAGILGKPCPKIKVECEVEIDQCTKPRDCPENMKC 60
 Db 1 MGLSGLLPILVFPFILLGDIQEPGHAGILGKPCPKIKVECEVEIDQCTKPRDCPENMKC 60

CC of antisense RNA and DNA, and as targets for pharmaceutical intervention.
CC The present sequence represents a human DJ11 protein given in comparison
CC with DJ11 proteins in the exemplification of the present invention.
XX
SQ Sequence 131 AA;

Query Match 97.1%; Score 731; DB 7; Length 131;
Best Local Similarity 98.5%; Pred. No. 8.9e-55;
Matches 129; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 MGLSGLLPILVPFILLGDIQEPGHAEGILGKPCPKIKVECEVEIDQCTKPRDCPENMKC 60
DB 1 MGLSGLLPILVPFILLGDIQEPGHAEGILGKPCPKIKVECEVEIDQCTKPRDCPENMKC 60
QY 61 CPFGCGKKCLDFRKDICSMPQAGPCLASIPHHWYNNKTKICSEFIYGGCGGNNNFQTE 120
DB 61 CPFGCGKKCLDFRKDICSMPQAGPCLASIPHHWYNNKTKICSEFIYGGCGGNNNFQTE 120
QY 121 AICLVTCCKYH 131
DB 121 AICLVTCCKYH 131

RESULT 4
ADA19801
ID ADA19801 standard; protein; 106 AA.
XX
AC ADA19801;
XX
DT 20-NOV-2003 (first entry)
XX
DE Mature form of engineered human DJ11 protein SEQ ID NO:2.
XX
KW DJ11; Kunitz-type protease inhibitor domain; antiinflammatory;
KW anti-allergic; thrombolytic; anticoagulant; cardiant; vasotropic;
KW antibacterial; immunosuppressive; antirheumatic; antiarthritic;
KW nephrotropic; antipsoriatic; vulnary; protease inhibitor; gene therapy;
KW acute pancreatitis; pulmonary injury; allergy-induced protease release;
KW deep vein thrombosis; myocardial infarction; shock; septic shock;
KW hyperfibrinolytic haemorrhage; inflammatory disorder; emphysema;
KW idiopathic pulmonary fibrosis; rheumatoid arthritis; glomerulonephritis;
KW chronic inflammatory bowel disease; psoriasis.
XX
OS Synthetic.
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Disulfide-bond 8..36 /note = predicted disulfide bond
FT Disulfide-bond 15..40 /note = predicted disulfide bond
FT Disulfide-bond 23..35 /note = predicted disulfide bond
FT Disulfide-bond 29..44 /note = predicted disulfide bond
FT Domain 52..102 /note = Kunitz domain predicted by pfsan
FT Disulfide-bond 52..102 /note = predicted disulfide bond
FT Disulfide-bond 61..85 /note = predicted disulfide bond
FT Disulfide-bond 77..98 /note = predicted disulfide bond
XX WO2003070770-A2.
PN 28-AUG-2003.
XX
PF 18-FEB-2003; 2003WO-EP001629.
XX
PR 21-FEB-2002; 2002US-0358683P.
XX
PA (GENE-) GENEPROT INC.
PI Bougueleret L, Bairoch A, Niknejad A;
XX
DR WPI; 2003-663849/62.
XX
PT New engineered human Kunitz-type protease inhibitor for diagnosing,
PT preventing or treating conditions associated with excessive proteinase
PT activity, e.g. inflammation, pulmonary injuries, myocardial infarction or
PT hemorrhage.
XX
PS Disclosure; Fig 1; 87pp; English.

The present invention describes an isolated, purified or recombinant DJ11 polypeptide comprising a Kunitz-type protease inhibitor domain or its biologically active portion. The polypeptide comprises at least 98 % identity to residues 77-127 of a 131 amino acid sequence (S1, see ADA19800), or to residues 52-102 of a 106 amino acid sequence (S2, see ADA19801). DJ11 has antiinflammatory, antiallergic, thrombolytic, anticoagulant, cardiant, vasotropic, antibacterial, immunosuppressive, antirheumatic, antiarthritic, nephrotropic, antipsoriatic and vulnary activities, and can be used as a protease inhibitor and in gene therapy. Composition and methods from the present invention can be used in diagnosing, preventing or treating conditions associated with excessive proteinase activity, such as acute pancreatitis, pulmonary injury, allergy-induced protease release, deep vein thrombosis, myocardial infarction, shock (including septic shock), hyperfibrinolytic haemorrhage, and especially, inflammatory disorders (e.g. emphysema, idiopathic pulmonary fibrosis, rheumatoid arthritis, glomerulonephritis, chronic inflammatory bowel disease or psoriasis). The DJ11 proteins may be used in preserving platelet function, organ preservation or in wound healing. The polynucleotide sequence encoding DJ11 may be used as hybridisation probes, in chromosome and gene mapping, in the generation

61 CPFGCGKKCLDFRKDICSMPQAGPCLASIPHHWYNNKTKICSEFIYGGCGGNNNFQTE 120
61 CPFGCGKKCLDFRKDICSMPQAGPCLASIPHHWYNNKTKICSEFIYGGCGGNNNFQTE 120
121 AICLVTCCKYH 131
121 AICLVTCCKYH 131

ADA19814
ID ADA19814 standard; protein; 131 AA.
XX
AC ADA19814;
XX
DT 20-NOV-2003 (first entry)
XX
DE Human DJ11 protein SEQ ID NO:15.
XX
KW DJ11; Kunitz-type protease inhibitor domain; antiinflammatory;
KW anti-allergic; thrombolytic; anticoagulant; cardiant; vasotropic;
KW antibacterial; immunosuppressive; antirheumatic; antiarthritic;
KW nephrotropic; antipsoriatic; vulnary; protease inhibitor; gene therapy;
KW acute pancreatitis; pulmonary injury; allergy-induced protease release;
KW deep vein thrombosis; myocardial infarction; shock; septic shock;
KW hyperfibrinolytic haemorrhage; inflammatory disorder; emphysema;
KW idiopathic pulmonary fibrosis; rheumatoid arthritis; glomerulonephritis;
KW chronic inflammatory bowel disease; psoriasis.
XX
OS Homo sapiens.
XX
PN WO2003070770-A2.
XX
PD 28-AUG-2003.
XX
PF 18-FEB-2003; 2003WO-EP001629.
XX
PR 21-FEB-2002; 2002US-0358683P.
XX
XX (GENE-) GENEPROT INC.
XX
XX Bougueleret L, Bairoch A, Niknejad A;
XX
XX WPI; 2003-663849/62.
XX
XX New engineered human Kunitz-type protease inhibitor for diagnosing,
XX preventing or treating conditions associated with excessive proteinase
XX activity, e.g. inflammation, pulmonary injuries, myocardial infarction or
XX hemorrhage.
XX
XX Disclosure; Fig 1; 87pp; English.

XX PI Bougueleret L, Bairoch A, Niknejad A;
XX DR WPI; 2003-663849/62.
XX PF New engineered human Kunitz-type protease inhibitor for diagnosing,
XX PT preventing or treating conditions associated with excessive proteinase
XX PT activity, e.g. inflammation, pulmonary injuries, myocardial infarction or
XX PT hemorrhage.
XX PS Claim 5; Page 71; 87pp; English.
XX CC The present invention describes an isolated, purified or recombinant DJ11
XX CC polypeptide comprising a Kunitz-type protease inhibitor domain or its
XX CC biologically active portion. The polypeptide comprises at least 98 %
XX CC identity to residues 77-127 of a 131 amino acid sequence (S1, see
XX CC ADA19800), or to residues 52-102 of a 106 amino acid sequence (S2, see
XX CC ADA19801). DJ11 has antiinflammatory, antiallergic, thrombolytic,
XX CC anticoagulant, cardiact, vasotropic, antibacterial, immunosuppressive,
XX CC antirheumatic, antiarthritic, nephrotropic, antipsoriatic and vulnary
XX CC activities, and can be used as a protease inhibitor and in gene therapy.
XX CC Composition and methods from the present invention can be used in
XX CC diagnosing, preventing or treating conditions associated with excessive
XX CC proteinase activity, such as acute pancreatitis, pulmonary injury,
XX CC allergy-induced protease release, deep vein thrombosis, myocardial
XX CC infarction, shock (including septic shock), hyperfibrinolytic
XX CC haemorrhage, and especially, inflammatory disorders (e.g. emphysema,
XX CC idiopathic pulmonary fibrosis, rheumatoid arthritis, glomerulonephritis,
XX CC chronic inflammatory bowel disease or psoriasis). The DJ11 proteins may
XX CC be used in preserving platelet function, organ preservation or in wound
XX CC healing. The polynucleotide sequence encoding DJ11 may be used as
XX CC hybridisation probes, in chromosome and gene mapping, in the generation
XX CC of antisense RNA and DNA, and as targets for pharmaceutical intervention.
XX CC The present sequence represents the mature form of an engineered human
XX CC DJ11 protein from the present invention.
XX SQ Sequence 106 AA;
Query Match 83.0%; Score 625; DB 7; Length 106;
Best Local Similarity 100.0%; Pred. No. 8.2e-46; Indels 0; Gaps 0;
Matches 106; Conservative 0; Mismatches 0;
Qy 26 EGILGKCPKIKVEVEEIDQCTKPRDCPENMKCCPFCGCKCLDFRDKICSMFQAGP 85
Db 1 EGILGKCPKIKVEVEEIDQCTKPRDCPENMKCCPFCGCKCLDFRDKICSMFQAGP 60
Qy 86 CLASIPHWYNNKTKICSEFYGGCGQNNNNFQTEAICLVTCCKYH 131
Db 61 CLASIPHWYNNKTKICSEFYGGCGQNNNNFQTEAICLVTCCKYH 106
RESULT 5
ADA19808
ID ADA19808 standard; protein; 98 AA.
AC ADA19808;
XX XX
XX DT 20-NOV-2003 (first entry)
XX DE Engineered human DJ11 partial amino acid sequence SEQ ID NO:9.
XX KW DJ11; Kunitz-type protease inhibitor domain; antiinflammatory;
XX KW antiallergic; thrombolytic; cardiact; vasotropic;
XX KW antibacterial; immunosuppressive; antirheumatic; antiarthritic;
XX KW nephrotropic; antipsoriatic; vulnary; protease inhibitor; gene therapy;
XX KW acute pancreatitis; pulmonary injury; allergy-induced protease release;
XX KW deep vein thrombosis; myocardial infarction; shock; septic shock;
XX KW hyperfibrinolytic haemorrhage; inflammatory disorder; emphysema;
XX KW idiopathic pulmonary fibrosis; rheumatoid arthritis; glomerulonephritis;
XX KW chronic inflammatory bowel disease; psoriasis.
OS Synthetic.
OS Homo sapiens.

XX WO2003070770-A2.
XX FN 28-AUG-2003.
XX PD 18-FEB-2003; 2003WO-EP001629.
XX PF 21-FEB-2002; 2002US-0358683P.
XX PR (GENE-) GENEPROT INC.
XX PA Bougueleret L, Bairoch A, Niknejad A;
XX PI WPI; 2003-663849/62.
XX DR New engineered human Kunitz-type protease inhibitor for diagnosing,
XX PT preventing or treating conditions associated with excessive proteinase
XX PT activity, e.g. inflammation, pulmonary injuries, myocardial infarction or
XX PT hemorrhage.
XX PS Disclosure; Page 82; 87pp; English.
XX CC The present invention describes an isolated, purified or recombinant DJ11
XX CC polypeptide comprising a Kunitz-type protease inhibitor domain or its
XX CC biologically active portion. The polypeptide comprises at least 98 %
XX CC identity to residues 77-127 of a 131 amino acid sequence (S1, see
XX CC ADA19800), or to residues 52-102 of a 106 amino acid sequence (S2, see
XX CC ADA19801). DJ11 has antiinflammatory, antiallergic, thrombolytic,
XX CC anticoagulant, cardiact, vasotropic, antibacterial, immunosuppressive,
XX CC antirheumatic, antiarthritic, nephrotropic, antipsoriatic and vulnary
XX CC activities, and can be used as a protease inhibitor and in gene therapy.
XX CC Composition and methods from the present invention can be used in
XX CC diagnosing, preventing or treating conditions associated with excessive
XX CC proteinase activity, such as acute pancreatitis, pulmonary injury,
XX CC allergy-induced protease release, deep vein thrombosis, myocardial
XX CC infarction, shock (including septic shock), hyperfibrinolytic
XX CC haemorrhage, and especially, inflammatory disorders (e.g. emphysema,
XX CC idiopathic pulmonary fibrosis, rheumatoid arthritis, glomerulonephritis,
XX CC chronic inflammatory bowel disease or psoriasis). The DJ11 proteins may
XX CC be used in preserving platelet function, organ preservation or in wound
XX CC healing. The polynucleotide sequence encoding DJ11 may be used as
XX CC hybridisation probes, in chromosome and gene mapping, in the generation
XX CC of antisense RNA and DNA, and as targets for pharmaceutical intervention.
XX CC The present sequence represents a partial engineered human DJ11 protein
XX CC amino acid sequence from the present invention.
XX SQ Sequence 98 AA;
Query Match 73.2%; Score 551; DB 7; Length 98;
Best Local Similarity 99.0%; Pred. No. 1.6e-39;
Matches 97; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1 MGLSGLLPILVPFILLGDIQEPGHAEIGLKPCPKIKVEVEEIDQCTKPRDCPENMKC 60
Db 1 MGLSGLLPILVPFILLGDIQEPGHAEIGLKPCPKIKVEVEEIDQCTKPRDCPENMKC 60
Qy 61 CPFCGCKCLDFRDKICSMFQAGPCLASIPHWYNNK 98
Db 61 CPFCGCKCLDFRDKICSMFQAGPCLASIPHWYNNK 98
RESULT 6
ADA19815
ID ADA19815 standard; protein; 136 AA.
AC ADA19815;
XX XX
XX DT 20-NOV-2003 (first entry)
XX DE Mouse DJ11 protein SEQ ID NO:16.
XX KW DJ11; Kunitz-type protease inhibitor domain; antiinflammatory;
XX KW antiallergic; thrombolytic; anticoagulant; cardiact; vasotropic;

antibacterial; immunosuppressive; antirheumatic; antiarthritic; nephrotropic; antipsoriatic; vulnary; protease inhibitor; gene therapy; acute pancreatitis; pulmonary injury; allergy-induced protease release; deep vein thrombosis; myocardial infarction; shock; septic shock; hyperfibrinolytic haemorrhage; inflammatory disorder; emphysema; idiopathic pulmonary fibrosis; rheumatoid arthritis; glomerulonephritis; chronic inflammatory bowel disease; psoriasis.

Mus musculus.

WO2003070770-A2.

28-AUG-2003.

18-FEB-2003; 2003WO-EP001629.

21-FEB-2002; 2002US-0358683P.

(GENE-) GENEPROT INC.

Bougueleret L, Bairoch A, Niknejad A;

WPI; 2003-663849/62.

New engineered human Kunitz-type protease inhibitor for diagnosing, preventing or treating conditions associated with excessive proteinase activity, e.g. inflammation, pulmonary injuries, myocardial infarction or hemorrhage.

Disclosure: Fig 1; 87pp; English.

The present invention describes an isolated, purified or recombinant Djl1 polypeptide comprising a Kunitz-type protease inhibitor domain or its biologically active portion. The polypeptide comprises at least 98 % identity to residues 77-127 of a 131 amino acid sequence (S1, see ADA19800), or to residues 52-102 of a 106 amino acid sequence (S2, see ADA19801). Djl1 has antiinflammatory, antiallergic, thrombolytic, anticoagulant, cardiant, vasotropic, antibacterial, immunosuppressive, antirheumatic, antiarthritic, nephrotropic, antipsoriatic and vulnary activities, and can be used as a protease inhibitor and in gene therapy. Composition and methods from the present invention can be used in diagnosing, preventing or treating conditions associated with excessive proteinase activity, such as acute pancreatitis, pulmonary injury, allergy-induced protease release, deep vein thrombosis, myocardial infarction, shock (including septic shock), hyperfibrinolytic haemorrhage, and especially, inflammatory disorders (e.g. emphysema, idiopathic pulmonary fibrosis, rheumatoid arthritis, glomerulonephritis, chronic inflammatory bowel disease or psoriasis). The Djl1 proteins may be used in preserving platelet function, organ preservation or in wound healing. The polynucleotide sequence encoding Djl1 may be used as hybridisation probes, in chromosome and gene mapping, in the generation of antisense RNA and DNA, and as targets for pharmaceutical intervention. The present sequence represents a mouse Djl1 protein given in comparison with Djl1 proteins in the exemplification of the present invention.

Sequence 136 AA;

Query Match 65.3%; Score 492; DB 7; Length 136;
Best Local Similarity 62.8%; Pred. No. 2,3e-34;
Matches 81; Conservative 20; Mismatches 28; Indels 0; Gaps 0;

QY 1 MGLSGLPTLVFILLGDTQEPHARGILGKPCIKVCEVEEIDQCTKPRDCPENMKC 60
DB 1 MRLMGLLPFLVPFILLWSIQFELAEGRFIRTCPRVRVKCEVERNECTRHRQCPKKRC 60

QY 61 CFFSCGKKCLDFRKCISMPQAGPCLASIPHWYNNKTKICSEFYGCQGNNNFQTE 120
DB 61 CLFSCGKKCDLRQDVCSLPQDPGCLAYLPRWYTNQETDLCTEFYGCQGNPNFPSE 120

QY 121 AICLVTCCK 129
DB 121 GICTVVCCK 129

RESULT 7
AAW75219
ID AAW75219 standard; protein; 133 AA.
XX
AC AAW75219;
XX
DT 29-JAN-1999 (first entry)
XX
DE Human secreted protein encoded by gene 24 clone HTEBY11.
XX
KW Human; secreted protein; fusion protein; gene therapy; protein therapy;
diagnosis; tissue; cancer; tumour; neurodegenerative disorder; leukaemia;
developmental abnormality; foetal deficiency; blood; allergy; renal;
immune system; asthma; lymphocytic disease; brain; hepatitis; lymphoma;
inflammation; ischaemic shock; Alzheimer's disease; restenosis; AIDS;
cognitive disorder; schizophrenia; prostate; obesity; osteoclast; thymus;
osteoporosis; arthritis; testis; lung; thyroiditis; thyroid; digestion;
endocrine; metabolism; regulation; malabsorption; gastritis; neoplasm.
XX
OS Homo sapiens.
XX
PN WO9840483-A2.
XX
PD 17-SEP-1998.
XX
PF 12-MAR-1998; 98WO-US004858.
XX
PR 14-MAR-1997; 97US-0040710P.
PR 14-MAR-1997; 97US-0040762P.
PR 30-MAY-1997; 97US-0048100P.
PR 30-MAY-1997; 97US-0048189P.
PR 30-MAY-1997; 97US-0048357P.
PR 30-MAY-1997; 97US-0050934P.
PR 06-JUN-1997; 97US-0048970P.
PR 05-SEP-1997; 97US-0057765P.
PR 19-DEC-1997; 97US-0068366P.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Ruben SM, Rosen CA, Li Y, Zeng Z, Kyaw H, Fischer CL, Li H;
PI Soppet DR, Gentz RL, Wei YF, Moore PA, Young PE, Greene JM;
PI Ferrie AM;
XX
DR WPI; 1998-520811/44.
DR N-PSDB; AAV34309.
XX
XX Isolated human poly:nucleotide(s) encoding secretory peptide(s) - used to
develop products for the diagnosis and treatment of e.g. inflammation,
cancers, CNS disorders or immune system disorders.
XX
PS Claim 1; Page 167-168; 201pp; English.
XX
CC This sequence represents a secreted human protein encoded by the gene
clone detailed in the descriptor line. The gene can be used to generate
fusion proteins by linking to the gene to a human immunoglobulin FC
portion (e.g. AAV34277) for increasing the stability of the fused protein
as compared to the human protein only. The invention relates to 28 novel
genes and their fragments (nucleic acid sequences: AAV34286-V34325; amino
acid sequences AAW75196-W75235) which are useful for preventing, treating
or ameliorating medical conditions e.g. by protein or gene therapy. Also,
new polypeptides in a sample or by determining the amount of the
pathological conditions can be diagnosed by determining the presence of mutations
in the new polynucleotides. Specific uses are described for each of the
28 polynucleotides, based on which tissues they are most highly expressed
in (see AAV34286 for described uses)
XX
SQ Sequence 133 AA;
Query Match 62.0%; Score 467; DB 2; Length 133;
Best Local Similarity 60.9%; Pred. No. 3,1e-32;
Matches 78; Conservative 18; Mismatches 32; Indels 0; Gaps 0;

PA (YOUNG/) YOUNG P E.
PA (GREE/) GREENE J M.
PA (FERR/) FERRIE A M.
XX
PI Ruben SM, Rosen CA, Li Y, Zeng Z, Kyaw H, Fischer CL, Li H;
PI Soppet DR, Gentz RL, Wei Y, Moore PA, Young PE, Greene JM;
PI Ferrie AM;
XX
XX WPI: 2003-310989/30.
DR N-PSDB; ABX96989.
XX
XX New human secreted polypeptides and polynucleotides for diagnosing,
PT prognosing, preventing and treating immune, hyperproliferative, liver,
PT kidney, reproductive disorders and for identifying modulators of
PT therapeutic use.
XX
XX Claim 11; Page 185; 209pp; English.
XX
XX The invention relates to an isolated polypeptide comprising an amino acid
CC sequence at least 95% identical to sequence of 28 human secreted
CC proteins, their fragment, polypeptide domain, epitope, secreted form,
CC variant, allelic variant, or species homologue, or the encoded sequence
CC included in ATCC 97921 and 97922. Also included are the encoding nucleic
CC acids, recombinant vectors, host cells, antibodies, and genes. The
CC proteins and nucleic acids are useful for diagnosing, preventing,
CC treating, prognosing or ameliorating a medical condition e.g.
CC immunodeficiencies (e.g. X-linked agammaglobulinaemia, B cell
CC immunodeficiencies, severe combined immunodeficiencies), autoimmune
CC disorders (e.g. systemic erythematous, rheumatoid arthritis, multiple
CC sclerosis, autoimmune thyroiditis, autoimmune haemolytic anaemia,
CC Goodpasture's syndrome, Grave's disease, diabetes mellitus, dermatitis),
CC haematopoietic disorders, inflammatory conditions (e.g. septic shock,
CC sepsis, reperfusion injury, inflammatory bowel disease, Crohn's disease),
CC respiratory disorders (e.g. asthma and allergy), gastrointestinal
CC disorders, cancers (e.g. gastric, ovarian, lung, bladder, liver and
CC breast), central nervous system (CNS) disorders (e.g. ischaemic brain
CC injury and/or stroke, traumatic brain injury), neurodegenerative
CC disorders (e.g. Parkinson's disease and Alzheimer's disease, AIDS-related
CC dementia, and prion disease), cardiovascular disorders (e.g.
CC atherosclerosis, myocarditis, cardiovascular disease, and cardiopulmonary
CC bypass complications), inflammation (e.g. hepatitis, gout, trauma,
CC pancreatitis, sarcoidosis, dermatitis, allogeneic transplant rejection),
CC blood-related disorders (thrombosis, arterial thrombosis),
CC hyperproliferative disorders, renal disorders (e.g. acute
CC glomerulonephritis), endocrine disorders (e.g. Addison's disease,
CC hyperthyroidism, hypoparathyroidism), liver diseases and disorders,
CC reproductive system disorders (e.g. endometriosis), infectious diseases,
CC and pancreatic disorders. Many other diseases and disorders are listed in
CC the specification. They also useful as a vaccine adjuvant. Further they
CC are useful to enhance or inhibit complement mediated cell lysis, for
CC stimulating wound and tissue repair, angiogenesis, and the repair of
CC vascular or lymphatic diseases or disorders. They are also useful to
CC prevent hair loss, to modulate mammalian characteristics such as body
CC height, weight, hair colour, and to increase or decrease storage
CC capabilities, fat content, lipid, protein, carbohydrate, vitamins,
CC minerals, cofactors or other nutritional components. The proteins are
CC also useful for identifying binding partners. The present sequence
CC represents a secreted protein of the invention
XX
SQ Sequence 133 AA;
Query Match 62.0%; Score 467; DB 6; Length 133;
Best Local Similarity 60.9%; Pred. No. 3.1e-32;
Matches 78; Conservative 18; Mismatches 32; Indels 0; Gaps 0;
Qy 1 MGLSGLLPILVPFILLGDIOBFGHAEGILGKPCPKIKVCEVEBIDQCTPRDCPENMKC 60
Db 1 MGSSGLLSLLVLFVLLANVQPGGLTDLMPFRRCFKIRECECFQERDVCTKDRQCDKNKC 60
Qy 61 CPFSGCKKCLDFRDKICSMPOEAGPCLASIPHWYNNKTKICSPFIYGGCGGNNNNQTE 120
Db 61 CVFSGCKKCLDLKQDVCEMPKETGCLAYFLHWWYDKNDTCSMFVYGGCGGNNNNFQSK 120

Qy 121 AICLVTK 128
Db 121 ANCLNTCK 128
RESULT 11
ADA19812
ID ADA19812 standard; protein; 133 AA.
XX
AC ADA19812;
XX
DT 20-NOV-2003 (first entry)
XX
DE Human EPPIN protein SEQ ID NO:13.
XX
KW DJ11; Kunitz-type protease inhibitor domain; antiinflammatory;
KW antiallergic; thrombolytic; anticoagulant; cardiac; vasotrophic;
KW antibacterial; immunosuppressive; antirheumatic; antiarthritic;
KW nephrotropic; antipsoriatic; vulnary; protease inhibitor; gene therapy;
KW acute pancreatitis; pulmonary injury; allergy-induced protease release;
KW deep vein thrombosis; myocardial infarction; shock; septic shock;
KW hyperfibrinolytic haemorrhage; inflammatory disorder; emphysema;
KW idiopathic pulmonary fibrosis; rheumatoid arthritis; glomerulonephritis;
KW chronic inflammatory bowel disease; psoriasis; EPPIN.
XX
OS Homo sapiens.
XX
XX WO2003070770-A2.
XX
PD 28-AUG-2003.
XX
PF 18-FEB-2003; 2003WO-EP001629.
XX
XX 21-FEB-2002; 2002US-0358683P.
PR
XX (GENE-) GENEPROT INC.
XX
PI Bougueleret L, Bairoch A, Niknejad A;
XX
XX WPI: 2003-663849/62.
DR
XX
XX New engineered human Kunitz-type protease inhibitor for diagnosing,
PT preventing or treating conditions associated with excessive proteinase
PT activity, e.g. inflammation, pulmonary injuries, myocardial infarction or
PT hemorrhage.
XX
XX Disclosure; Fig 1; 87pp; English.
XX
XX The present invention describes an isolated, purified or recombinant DJ11
CC polypeptide comprising a Kunitz-type protease inhibitor domain or its
CC biologically active portion. The polypeptide comprises at least 98 %
CC identity to residues 77-127 of a 131 amino acid sequence (S1, see
CC ADA19800), or to residues 52-102 of a 106 amino acid sequence (S2, see
CC ADA19801). DJ11 has antiinflammatory, antiallergic, thrombolytic,
CC anticoagulant, cardiac, vasotrophic, antibacterial, immunosuppressive,
CC antirheumatic, antiarthritic, nephrotropic, antipsoriatic and vulnary
CC activities, and can be used as a protease inhibitor and in gene therapy.
CC Composition and methods from the present invention can be used in
CC diagnosing, preventing or treating conditions associated with excessive
CC proteinase activity, such as acute pancreatitis, pulmonary injury,
CC allergy-induced protease release, deep vein thrombosis, myocardial
CC infarction, shock (including septic shock), hyperfibrinolytic
CC haemorrhage, and especially inflammatory disorders (e.g. emphysema,
CC idiopathic pulmonary fibrosis, rheumatoid arthritis, glomerulonephritis,
CC chronic inflammatory bowel disease or psoriasis). The DJ11 proteins may
CC be used in preserving platelet function, organ preservation or in wound
CC healing. The polynucleotide sequence encoding DJ11 may be used as
CC hybridisation probes, in chromosome and gene mapping, in the generation
CC of antisense RNA and DNA, and as targets for pharmaceutical intervention.
CC The present sequence represents a human EPPIN protein given in comparison
XX with DJ11 proteins in the exemplification of the present invention.
XX Sequence 133 AA;

Query Match 62.0%; Score 467; DB 7; Length 133;
Best Local Similarity 60.9%; Pred. No. 3.1e-32;
Matches 78; Conservative 18; Mismatches 32; Indels 0; Gaps 0;

QY 1 MGLSGLLPILVPFILLGDIQBPQHAEGILGPKPKIKVECEVEEIDQCTKPRDCPENMKC 60
DB 1 MGSSGLLSLLVFLVLANVQFGLTDLWLPFRCPKIRECECFQERDVCTKDRQCQDNKKC 60

QY 61 CFFSCGKKCLDFRDKICSMPOEAGPCLASIPHHWYNNKTKICSEFIYGGCCGNNNNFQTE 120
DB 61 CVFSCGKKCLDLKQDVCMPKGTGCLAYFLHWWYDKDNTCSMFYGGCCGNNNNFQSK 120

QY 121 AICLVTKC 128
DB 121 ANCLVTCK 128

RESULT 12
ADG89802
ID ADG89802 standard; protein; 133 AA.
XX ADG89802;
AC XX
XX
DT 11-MAR-2004 (first entry)
XX
XX Human protein from secreted protein gene 24 #1.
DE
XX Secreted protein; gene therapy; neural disorder; immune system disorders;
KW muscular disorder; reproductive disorder; gastrointestinal disorder;
KW pulmonary disorder; cardiovascular disorder; renal disorder;
KW proliferative disorder; cancer; systemic lupus erythematosus;
KW rheumatoid arthritis; multiple sclerosis; thyroiditis; anaemia;
KW Grave's disease; diabetes; hepatitis; asthma; allergy; nephritis;
KW Parkinson's disease; Alzheimer's disease; atherosclerosis;
KW myocardial infarction; AIDS; infection; human.
XX
OS Homo sapiens.
XX
XX US2003225009-A1.
XX
XX 04-DEC-2003.
XX
XX 30-JAN-2002; 2002US-00058993.
XX
XX 14-MAR-1997; 97US-0040710P.
XX 14-MAR-1997; 97US-0040762P.
XX 30-MAY-1997; 97US-0048100P.
XX 30-MAY-1997; 97US-0048189P.
XX 30-MAY-1997; 97US-0048357P.
XX 30-MAY-1997; 97US-0050934P.
XX 06-JUN-1997; 97US-0048970P.
XX 05-SEP-1997; 97US-0057765P.
XX 19-DEC-1997; 97US-0068368P.
XX 12-MAR-1998; 98WO-US004858.
XX 11-SEP-1998; 98US-00152060.
XX 02-FEB-2001; 2001US-0265583P.
XX 11-MAY-2001; 2001US-00852659.
XX 11-MAY-2001; 2001US-00852797.
XX 11-MAY-2001; 2001US-00853161.
XX
XX (ROSE/) ROSEN C A.
XX (RUBE/) RUBEN S M.
XX (LIYY/) LI Y.
XX (ZENG/) ZENG Z.
XX (KYAW/) KYAW H.
XX (FISC/) FISCHER C L.
XX (LIHH/) LI H.
XX (SOPP/) SOPPET D R.
XX (GENT/) GENTZ R L.
XX (WEIY/) WEI Y.
XX (MOOR/) MOORE P A.
XX (YOUN/) YOUNG P E.

PA (GREE/) GREENE J M.
PA (FERR/) FERRIE A M.
XX (HAST/) HASTINGS G A.
PI ROSEN CA, RUBEN SM, Li Y, Zeng Z, Kyaw H, Fischer CL, Li H;
PI SOPPET DR, Gentz RL, Wei Y, Moore PA, Young PE, Greene JM;
XX Ferrie AM, Hastings GA;
DR WPI; 2004-042167/04.
XX N-PSDB; ADG89761.
XX
XX New polypeptides and nucleic acid molecules for diagnosing, preventing or
XX treating diseases associated with aberrant expression or activity of the
XX polypeptide, e.g. cancer, asthma, AIDS, Parkinson's disease or diabetes.
XX
XX Claim 11; SEQ ID NO 75; 320pp; English.
XX
XX The invention relates to an isolated nucleic acid molecule encoding a
XX secreted protein that is at least 95% identical to a polynucleotide
XX fragment of any of the nucleotide sequences listed in table 1A of the
XX specification, which is hybridisable to the nucleotide sequences, a
XX polynucleotide encoding a polypeptide (or a polypeptide fragment, domain
XX or epitope of any of the amino acid sequences) listed in table 1A of the
XX specification, a polynucleotide which is an (allelic) variant of the
XX nucleotide sequences listed in the specification, a polynucleotide which
XX encodes a species homologue of the above amino acid sequences, a
XX polynucleotide capable of hybridising under stringent conditions to any
XX of the above polynucleotides, where the polynucleotide does not hybridise
XX under stringent conditions to a nucleic acid molecule having a nucleotide
XX sequence of only A or T residues. Also included are a recombinant vector
XX comprising the above nucleic acid molecule, making a recombinant host
XX cell comprising the above nucleic acid molecule, an isolated polypeptide
XX comprising a sequence that is at least 95% identical to the polypeptide
XX (or its fragment, domain, epitope, secreted form, (allelic) variant or
XX homologue) encoded by the above nucleic acid molecule, an isolated
XX antibody that binds specifically to the above polypeptide, a recombinant
XX host cell produced by the above method and that expresses the above
XX polypeptide, making an isolated polypeptide, preventing, treating or
XX ameliorating a medical condition, diagnosing a pathological condition or
XX a susceptibility to a pathological condition in a subject, identifying a
XX binding partner to the above polypeptide, the gene corresponding to the
XX cDNA sequence given in the specification, and identifying an activity in
XX a biological assay. The nucleic acid molecule and polypeptide are useful
XX in diagnosing, preventing, prognosing or treating diseases or disorders
XX associated with aberrant expression and/or activity of the above
XX polypeptide, such as neural disorders, immune system disorders, muscular
XX disorders, reproductive disorders, gastrointestinal disorders, pulmonary
XX disorders, cardiovascular disorders, renal disorders, proliferative
XX disorders, and/or cancers. In particular, these diseases are systemic
XX lupus erythematosus, rheumatoid arthritis, multiple sclerosis,
XX thyroiditis, anaemia, Grave's disease, diabetes, hepatitis, asthma,
XX allergies, nephritis, Parkinson's disease, Alzheimer's disease,
XX atherosclerosis, myocardial infarction, AIDS and infections. The methods
XX may be used for identifying agonists and antagonists of the
XX polynucleotide and polypeptide. The present sequence is a protein from
XX one of the 28 disclosed secreted protein genes.

Sequence 133 AA;

Query Match 62.0%; Score 467; DB 8; Length 133;
Best Local Similarity 60.9%; Pred. No. 3.1e-32;
Matches 78; Conservative 18; Mismatches 32; Indels 0; Gaps 0;

QY 1 MGLSGLLPILVPFILLGDIQBPQHAEGILGPKPKIKVECEVEEIDQCTKPRDCPENMKC 60
DB 1 MGSSGLLSLLVFLVLANVQFGLTDLWLPFRCPKIRECECFQERDVCTKDRQCQDNKKC 60

QY 61 CFFSCGKKCLDFRDKICSMPOEAGPCLASIPHHWYNNKTKICSEFIYGGCCGNNNNFQTE 120
DB 61 CVFSCGKKCLDLKQDVCMPKGTGCLAYFLHWWYDKDNTCSMFYGGCCGNNNNFQSK 120

QY 121 AICLVTKC 128
DB 121 ANCLVTCK 128

Query Match 62.0%; Score 467; DB 8; Length 179;
Best Local Similarity 60.9%; Pred. No. 4.1e-32;
Matches 78; Conservative 18; Mismatches 33; Indels 0; Gaps 0;

Qy 1 MGLSGLLPILVPFILLGDIQEPGHAEGILGKPCPKIKVECEVEIDQTKPRDCPENMKC 60
Db 1 MGSGLLSLVFLVLLANVQPGFLTDWLPFRCPKIRECECFQBRDVCCTKQRCQDNKKC 60

Qy 61 CPFGCGKCLDPKRDICSMPOEAGPCLASIPHWYNTKTKICSFIYGGCCGNNNFOTE 120
Db 61 CVFSGCKCLDLKQDVCEMPKBTGFCLAYFLHWYDKDKNTCSMFVYGGCCGNNNFQSK 120

Qy 121 AICLVTK 128
Db 121 ANCLNTCK 128

RESULT 15
ID ABP69809 standard; protein; 86 AA.
AC ABP69809;
DT 20-JAN-2003 (first entry)
DE Human polypeptide SEQ ID NO 1856.
XX Human; genome mapping; gene therapy; food supplement; virus; fungus;
KW cell-proliferative disorder; neurodegenerative disease; bacterial;
KW Parkinson's disease; Alzheimer's disease; autoimmune disease;
KW multiple sclerosis; diabetes; genetic disorder; wound; burn; infection;
KW arthritis; cytostatic; immunomodulator; neurotropic; neuroprotective;
KW antiparkinsonian; antidiabetic; immunosuppressive; dermatological;
KW haemostatic; vulnery; fungicide; antibacterial; virucide; protozoacide;
KW antiarthritic.
XX
OS Homo sapiens.
XX
FN WO200270539-A2.
XX
PD 12-SEP-2002.
XX
PF 05-MAR-2002; 2002WO-US005095.
XX
PR 05-MAR-2001; 2001US-00799451.
XX
PA (HYSE-) HYSEQ INC.
XX
PI Tang YT, Zhou P, Goodrich RW, Asundi V, Zhang J, Zhao QA, Ren F;
PI Xue AJ, Yang Y, Ma Y, Yamazaki V, Chen R, Wang Z, Ghosh M;
PI Wehrman T, Wang J, Wang D, Drmanac RT;
XX
XX WPI; 2002-759812/82.
DR N-PSDB; AB212026.
XX
XX New polynucleotides comprising sequences assembled from expressed
PT sequence tags (ESTs), useful for treating cell-proliferative,
PT neurodegenerative, autoimmune, genetic, myeloid or lymphoid, or platelet
PT or coagulation disorders.
XX
XX Claim 9; SEQ ID NO 1856; 1012pp + Sequence Listing; English.
PS
XX The invention relates to an isolated polynucleotide (1) comprising a
CC nucleotide sequence selected from any of 948 sequences (AB21119-
CC AB212066) or their mature protein coding portion, active domain coding
CC protein or complementary sequences. The polynucleotides are useful for
CC identifying expressed genes or for physical mapping of human genome. The
CC encoded polypeptides (ABP68902-ABP69849) are useful as molecular weight
CC markers, as a food supplement, for generating antibodies, in medical
CC imaging, screening and diagnostic assays and for treating cell-
CC proliferative disorders (cancer), neurodegenerative diseases (Parkinson's
CC or Alzheimer's disease), autoimmune diseases (multiple sclerosis,

CC diabetes, lupus) genetic disorders, myeloid or lymphoid disorders,
CC platelet or coagulation disorders, wound, burns, incision, ulcers, liver
CC or lung fibrosis, infections (bacterial, viral, fungal, parasitic),
CC arthritis, etc. Note: The sequence data for this patent did not form part
CC of the printed specification, but was obtained in electronic format
CC directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 86 AA;

Query Match 53.7%; Score 404; DB 5; Length 86;
Best Local Similarity 98.6%; Pred. No. 4.9e-27;
Matches 73; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MGLSGLLPILVPFILLGDIQEPGHAEGILGKPCPKIKVECEVEIDQTKPRDCPENMKC 60
Db 1 MGLSGLLPILVPFILLGDIQEPGHAEGILGKPCPKIKVECEVEIDQTKPRDCPENMKC 60

Qy 61 CPFGCGKCLDLDFRK 74
Db 61 CFFSRGKKCLDLFRK 74

RESULT 16
ID ABJ26667 standard; protein; 86 AA.
AC ABJ26667;
XX
XX 01-MAY-2003 (first entry)
DT Human protein modification + maintenance molecule protein SEQ ID NO 21.
DE Cytostatic; antiarteriosclerotic; anti-HIV; antiallergic; anticonvulsant;
KW cerebroprotective; antiparkinsonian; neurotropic; antiinflammatory;
KW antiulcer; hepatotropic; gynaecological; antibacterial; virucide;
KW protozoacide; antiparasitic; cell proliferative disease; PMOD;
KW protein modification and maintenance molecule; immunogenic fragment;
KW cancer; autoimmune; inflammatory disease; neurological disorder;
KW gastrointestinal; developmental; vesicle trafficking disorder; infection;
KW protein-protein interaction; drug-target interaction;
KW gene expression profile; human.
XX
XX Homo sapiens.
OS
XX
FN WO2003000844-A2.
XX
PD 03-JAN-2003.
XX
PF 18-JUN-2002; 2002WO-US019360.
XX
XX 22-JUN-2001; 2001US-0300508P.
PR 06-JUL-2001; 2001US-0303445P.
PR 13-JUL-2001; 2001US-0305405P.
PR 09-AUG-2001; 2001US-0311442P.
PR 24-AUG-2001; 2001US-0314821P.
PR 29-AUG-2001; 2001US-0315992P.
PR 03-MAY-2002; 2002US-0378205P.
XX
XX (INCY-) INCYTE GENOMICS INC.
PA
XX
XX Gandhi AR, Kable AE, Swarnakar A, Hafalia AJA, Tran B, Duggan BM;
PI Warren BA, Ison CH, Honchell CD, Nguyen DB, Lu DAM, Lee EA, Yue H;
PI Forsythe TJ, Barroso I, Ramkumar J, Griffin JA, Li JX, Yang J;
PI Thangavelu K, Gietzen KJ, Ding L, Baughn MR, Borowsky ML, Yao MG;
PI Walia NK, Mason PM, Gururajan R, Lee S, Becha SD, Lee SY, Tran UK;
PI Elliott VS, Luo W, Sprague WW, Tang YT, Lu Y, Zebbarjadian Y;
XX
XX WPI; 2003-184039/18.
DR N-PSDB; AB23220.
XX
XX New isolated human PMOD polypeptide and polynucleotide, useful for
PT diagnosing, treating and preventing diseases or conditions associated
PT with the aberrant PMOD expression, e.g. cancer, AIDS, atherosclerosis and

PT infections.

PS Claim 76; Page 196; 225pp; English.

XX The invention relates to an isolated polypeptide comprising: any of 28

XX sequences of 48-1256 amino acids; a natural amino acid sequence at least

XX 90% identical to the 28 amino acid sequences, 94% identical to a sequence

CC of 703 or 267 amino acids, 96% identical to a sequence of 414 amino

CC acids, or 97% identical to a sequence of 242 amino acids, all given in

CC the specification; or a biologically active or immunogenic fragment of

CC the isolated polypeptide. The polypeptides and polynucleotides are useful

CC in diagnosing, treating and preventing diseases or conditions associated

CC with the decreased expression of protein modification and maintenance

CC molecules (PMOD), such as cell proliferative diseases (e.g. cancer,

CC atherosclerosis), autoimmune/inflammatory diseases (e.g. AIDS,

CC allergies), neurological disorders (e.g. stroke, Parkinson's disease,

CC epilepsy), gastrointestinal (e.g. ulcer, cirrhosis), reproductive (e.g.

CC endometriosis), developmental, vesicle trafficking disorders, and

CC infections (e.g. bacterial, viral, parasitic, protozoal). These are also

CC useful in assessing the effects of exogenous compounds on the expression

CC of nucleic acid and amino acid sequences of PMOD. The PMOD or its

CC fragments are useful in screening compounds for effectiveness as agonist

CC or antagonist of the polypeptides, or in altering the expression of the

CC target polynucleotide and compounds that specifically bind to or modulate

CC the activity of the polypeptide. The microarray is useful in monitoring

CC or measuring protein-protein interactions, drug-target interactions, and

CC gene expression profiles. This sequence represents a human PMOD protein

CC of the invention

XX

XX Sequence 86 AA;

Qy Query Match 53.7%; Score 404; DB 6; Length 86;

Db Best Local Similarity 98.6%; Pred. No. 4.9e-27;

Db Matches 73; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MGLSGLLPILVPFILLGDIQEPGHAEGILGKPCPKIKVECEVEIDQCTKPRDCPENMKC 60

Db 1 MGLSGLLPILVPFILLGDIQEPGHAEGILGKPCPKIKVECEVEIDQCTKPRDCPENMKC 60

Qy 61 CPFSGKCKLDPRK 74

Db 61 CPFSRGRKCKLDPRK 74

RESULT 17

ABBI2236

ID ABB12236 standard; peptide; 101 AA.

AC ABB12236;

XX

DT 11-JAN-2002 (first entry)

XX

DE Human eppin-1 homologue, SEQ ID NO:2606.

XX

KW Human; cytokine; cell proliferation; cell differentiation; growth factor;

KW haematopoiesis regulation; tissue growth; immunomodulator; activin;

KW inhibin; chemotaxis; chemokinesis; thrombolysis; oncogenesis;

KW proliferation; metastasis; cancer; tumour; haematopoietic disorder;

KW myeloid cell disorder; lymphoid cell disorder; asthma; arthritis;

KW chronic inflammatory condition; proliferative retinopathy;

KW atherosclerosis; coronary heart disease; arterial ischaemia;

KW bone disorder; osteoporosis; vascular growth disorder;

KW tissue regeneration; wound healing; infection; immune disorder;

KW cell culture; drug screening; gene therapy; antiinflammatory;

KW aniaethmatic; antiarthritic; haemostatic; antiarteriosclerotic;

KW cytosstatic; osteopathic; vasotrophic; cardiant; virucide; antibacterial;

KW antifungal; vulnuary; antiulcer.

XX

OS Homo sapiens.

XX

FN WO200157188-A2.

XX

PD 09-AUG-2001.

XX

XX 05-FEB-2001; 2001WO-US003800.

XX

XX 03-FEB-2000; 2000US-00496914.

PR 27-APR-2000; 2000US-00560875.

XX

PA (HYSE-) HYSEQ INC.

XX

XX Tang YT, Liu C, Drmanac RT;

XX

XX WPI; 2001-457740/49.

DR N-PSDB; ABA09480.

XX

XX Human proteins and DNA encoding sequences useful for preventing, treating

PT or ameliorating a medical condition in a mammalian subject e.g. arthritis

PT and cancer.

XX

XX Claim 20; Page 318; 1963pp; English.

XX

XX Sequences ABB10981-ABB12330 represent 1350 novel human polypeptides, and

CC sequences ABA08225-ABA09574 represent nucleic acids encoding them. The

CC invention also relates to vectors and recombinant host cells comprising a

CC nucleotide of the invention, methods of producing the novel polypeptides,

CC antibodies against the polypeptides, methods of detecting the nucleotides,

CC or polypeptides in a sample, and methods of identifying compounds which

CC bind to polypeptides of the invention. Although novel, many of the

CC polypeptides of the invention have homology to known proteins, thereby

CC giving an insight into their probable biological activities, and hence

CC potential therapeutic applications. The polypeptides of the invention may

CC have various activities, including cytokine, cell proliferation or cell

CC differentiation activities; stem cell growth factor activity;

CC haematopoiesis regulatory activity; tissue growth activity;

CC immunomodulatory activity; activin- or inhibin-related activities;

CC chemotactic or chemokinetic activities; haemostatic, thrombotic or

CC thrombolytic activities; receptor or ligand activities; or may be

CC involved in oncogenesis, cancer cell proliferation or metastasis.

CC Depending on their biological activities, polypeptides and nucleotides of

CC the invention are useful for preventing, treating or ameliorating medical

CC conditions, e.g., by protein or gene therapy. Such conditions include

CC cancers, haematopoietic disorders (e.g., myeloid or lymphoid cell

CC disorders), chronic inflammatory conditions (e.g., asthma or arthritis),

CC proliferative retinopathy, atherosclerosis, coronary heart disease,

CC arterial ischaemia, bone disorders (e.g., osteoporosis), and abnormal

CC vascular growth. Polypeptides involved with tissue regeneration and

CC repair (or nucleic acids encoding them) may be used to promote wound

CC healing (e.g., of burns, incisions and ulcers), while those with

CC immunomodulatory activities may be used in the treatment of viral,

CC bacterial and fungal infections in addition to immune disorders.

CC Polypeptides with growth factor activity may be used in cell cultures to

CC promote cell growth. For example, such polypeptides may be used to

CC manipulate stem cells in culture to give rise to neuroepithelial cells

CC that can be used to augment or replace cells damaged by illness,

CC autoimmune disease or accidental damage. The polypeptides and nucleotides

CC may also be used in the diagnosis of the above conditions, and in drug

CC screening techniques. The present sequence represents a novel human

CC polypeptide of the invention

XX

XX Sequence 101 AA;

Qy Query Match 53.7%; Score 404; DB 4; Length 101;

Db Best Local Similarity 98.6%; Pred. No. 5.7e-27;

Db Matches 73; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MGLSGLLPILVPFILLGDIQEPGHAEGILGKPCPKIKVECEVEIDQCTKPRDCPENMKC 60

Db 16 MGLSGLLPILVPFILLGDIQEPGHAEGILGKPCPKIKVECEVEIDQCTKPRDCPENMKC 75

Qy 61 CPFSGKCKLDPRK 74

Db 76 CPFSRGRKCKLDPRK 89

RESULT 18

disorders (e.g. Parkinson's disease and Alzheimer's disease, AIDS-related dementia, and prion disease), cardiovascular disorders (e.g. atherosclerosis, myocarditis, cardiovascular disease, and cardiopulmonary bypass complications), inflammation (e.g. hepatitis, gout, trauma, pancreatitis, sarcoidosis, dermatitis, allergic transplant rejection), blood-related disorders (thrombosis, arterial thrombosis), hyperproliferative disorders, renal disorders (e.g. acute glomerulonephritis), endocrine disorders (e.g. Addison's disease, hyperthyroidism, hyperpituitarism), liver diseases and disorders, reproductive system disorders (e.g. endometriosis), infectious diseases, and prostatic disorders. Many other diseases and disorders are listed in the specification. They also useful as a vaccine adjuvant. Further they are useful to enhance or inhibit complement mediated cell lysis, for stimulating wound and tissue repair, angiogenesis, and the repair of vascular or lymphatic diseases or disorders. They are also useful to prevent hair loss, to modulate mammalian characteristics such as body height, weight, hair colour, and to increase or decrease storage capabilities, fat content, lipid, protein, carbohydrate, vitamins, minerals, cofactors or other nutritional components. The proteins are also useful for identifying binding partners. The present sequence represents a secreted protein of the invention

XX Sequence 117 AA;

Query Match 53.3%; Score 401.5; DB 6; Length 117;
Best Local Similarity 66.0%; Pred. No. 1.1e-26;
Matches 66; Conservative 12; Mismatches 21; Indels 1; Gaps 1;

QY 29 LKQPKIKVECEVEIEIOCTKPRCPENMKCCPSGCKKCLDFKDCISMPQAGPCIA 88

DB 14 LGR-CPKIRECEFOEDVCTKDRQCDNKKCCVSCGCKLKLKQDCEMPKGTGPCIA 72

QY 89 SIPHWYNNKTKICSEFTYGGCGQNNNNFOTEAICLVCTCK 128

DB 73 YFLHWYDKKONTCSMFYGGCGQNNNNFQSKANCLNTCK 112

RESULT 21

ADG89847

ID ADG89847 standard; protein; 117 AA.

AC ADG89847;

XX 11-MAR-2004 (first entry)

DE Human secreted protein gene 24 protein #5.

Secreted protein; gene therapy; neural disorder; immune system disorders; muscular disorder; reproductive disorder; gastrointestinal disorder; pulmonary disorder; cardiovascular disorder; renal disorder; proliferative disorder; cancer; systemic lupus erythematosus; rheumatoid arthritis; multiple sclerosis; thyroiditis; anaemia; Grave's disease; diabetes; hepatitis; asthma; allergy; nephritis; Parkinson's disease; Alzheimer's disease; atherosclerosis; myocardial infarction; AIDS; infection; human.

XX Homo sapiens.

OS US2003225009-A1.

FN 04-DEC-2003.

XX 30-JAN-2002; 2002US-00058993.

XX 14-MAR-1997; 97US-0040710P.

PR 14-MAR-1997; 97US-0040762P.

PR 30-MAY-1997; 97US-0048100P.

PR 30-MAY-1997; 97US-0048189P.

PR 30-MAY-1997; 97US-0048357P.

PR 30-MAY-1997; 97US-0050934P.

PR 06-JUN-1997; 97US-0048970P.

PR 05-SEP-1997; 97US-0057765P.

PR 12-MAR-1998; 98WO-US004858.
PR 11-SEP-1998; 98US-00152060.
PR 02-FEB-2001; 2001US-0265583P.
PR 11-MAY-2001; 2001US-00852659.
PR 11-MAY-2001; 2001US-00852797.
PR 11-MAY-2001; 2001US-00853161.

XX (ROSE/) ROSEN C A.
PA (RUBE/) RUBEN S M.
PA (LIYY/) LI Y.
PA (ZENG/) ZENG Z.
PA (KYAW/) KYAW H.
PA (FISC/) FISCHER C L.
PA (LIHH/) LI H.
PA (SOPP/) SOPPET D R.
PA (GENT/) GENTZ R L.
PA (WEIY/) WEI Y.
PA (MOOR/) MOORE P A.
PA (YOUN/) YOUNG P E.
PA (GREE/) GREENE J M.
PA (FERR/) FERRIE A M.
PA (HAST/) HASTINGS G A.

XX Rosen CA, Ruben SM, Li Y, Zeng Z, Kyaw H, Fischer CL, Li H;
PI Soppet DR, Gentz RL, Wei Y, Moore PA, Young PE, Greene JM;
PI Ferrie AM, Hastings GA;

XX WPI; 2004-042167/04.

XX New polypeptides and nucleic acid molecules for diagnosing, preventing or treating diseases associated with aberrant expression or activity of the polypeptide, e.g. cancer, asthma, AIDS, Parkinson's disease or diabetes.

PS Disclosure; SEQ ID NO 120; 320pp; English.

XX The invention relates to an isolated nucleic acid molecule encoding a secreted protein that is at least 95% identical to a polynucleotide fragment of any of the nucleotide sequences listed in table 1A of the specification, which is hybridisable to the nucleotide sequences, a polynucleotide encoding a polypeptide (or a polypeptide fragment, domain or epitope of any of the amino acid sequences) listed in table 1A of the specification, a polynucleotide which is an (allelic) variant of the nucleotide sequences listed in the specification, a polynucleotide which encodes a species homologue of the above amino acid sequences, a polynucleotide capable of hybridising under stringent conditions to any of the above polynucleotides, where the polynucleotide does not hybridise under stringent conditions to a nucleic acid molecule having a nucleotide sequence of only A or T residues. Also included are a recombinant vector comprising the above nucleic acid molecule, making a recombinant host cell comprising the above nucleic acid molecule, an isolated polypeptide comprising a sequence that is at least 95% identical to the polypeptide (or its fragment, domain, epitope, secreted form, (allelic) variant or homologue) encoded by the above nucleic acid molecule, an isolated antibody that binds specifically to the above polypeptide, a recombinant host cell produced by the above method and that expresses the above polypeptide, making an isolated polypeptide, preventing, treating or ameliorating a medical condition, diagnosing a pathological condition or a susceptibility to a pathological condition in a subject, identifying a binding partner to the above polypeptide, the gene corresponding to the cDNA sequence given in the specification, and identifying an activity in a biological assay. The nucleic acid molecule and polypeptide are useful in diagnosing, preventing, prognosing or treating diseases or disorders associated with aberrant expression and/or activity of the above polypeptide, such as neural disorders, immune system disorders, muscular disorders, reproductive disorders, gastrointestinal disorders, pulmonary disorders, cardiovascular disorders, renal disorders, proliferative disorders and/or cancers. In particular, these diseases are systemic lupus erythematosus, rheumatoid arthritis, multiple sclerosis, thyroiditis, anaemia, Grave's disease, diabetes, hepatitis, asthma, allergies, nephritis, Parkinson's disease, Alzheimer's disease, atherosclerosis, myocardial infarction, AIDS and infections. The methods may be used for identifying agonists and antagonists of the polynucleotide and polypeptide. The present sequence is a protein from

XX The invention relates to an isolated polypeptide comprising an amino acid
CC sequence at least 95% identical to sequence of 28 human secreted
CC proteins, their fragment, polypeptide domain, epitope, secreted form,
CC variant, allelic variant, or species homologue, or the encoded sequence
CC included in ATCC 7921 and 97922. Also included are the encoding nucleic
CC acids, recombinant vectors, host cells, antibodies, and genes. The
CC proteins and nucleic acids are useful for diagnosing, preventing,
CC treating, prognosing or ameliorating a medical condition e.g.
CC immunodeficiencies (e.g. X-linked agammaglobulinemia, B cell
CC immunodeficiencies, severe combined immunodeficiencies), autoimmune
CC disorders (e.g. systemic erythematous, rheumatoid arthritis, multiple
CC sclerosis, autoimmune thyroiditis, autoimmune haemolytic anaemia,
CC Goodpasture's syndrome, Grave's disease, diabetes mellitus, dermatitis),
CC haematopoietic disorders, inflammatory conditions (e.g. septic shock,
CC sepsis, reperfusion injury, inflammatory bowel disease, Crohn's disease),
CC respiratory disorders (e.g. asthma and allergy), gastrointestinal
CC disorders, cancers (e.g. gastric, ovarian, lung, bladder, liver and
CC breast), central nervous system (CNS) disorders (e.g. ischaemic brain
CC injury and/or stroke, traumatic brain injury), neurodegenerative
CC disorders (e.g. Parkinson's disease and Alzheimer's disease, AIDS-related
CC dementia, and prion disease), cardiovascular disorders (e.g.
CC atherosclerosis, myocarditis, cardiovascular disease, and cardiopulmonary
CC bypass complications), inflammation (e.g. hepatitis, gout, trauma,
CC pancreatitis, sarcoidosis, dermatitis, allogeneic transplant rejection),
CC blood-related disorders (thrombosis, arterial thrombosis),
CC hyperproliferative disorders, renal disorders (e.g. acute
CC glomerulonephritis), endocrine disorders (e.g. Addison's disease,
CC hyperthyroidism, hypoparathyroidism), liver diseases and disorders,
CC reproductive system disorders (e.g. endometriosis), infectious diseases,
CC and pancreatic disorders. Many other diseases and disorders are listed in
CC the specification. They also useful as a vaccine adjuvant. Further they
CC are useful to enhance or inhibit complement mediated cell lysis, for
CC stimulating wound and tissue repair, angiogenesis, and the repair of
CC vascular or lymphatic diseases or disorders. They are also useful to
CC prevent hair loss, to modulate mammalian characteristics such as body
CC height, weight, hair colour, and to increase or decrease storage
CC capabilities fat content, lipid, protein, carbohydrate, vitamins,
CC minerals, cofactors or other nutritional components. The proteins are
CC also useful for identifying binding partners. The present sequence
CC represents a secreted protein of the invention

SQ Sequence 102 AA;

Query Match 53.1%; Score 400; DB 6; Length 102;
Best Local Similarity 66.7%; Pred. No. 1.3e-26;
Matches 64; Conservative 11; Mismatches 21; Indels 0; Gaps 0;

Oy 33 CPKIKVECEVEIDQCTKPRDCPENMKCCPFCGKKCLDFRDKICSMFQEAQPCLASIPH 92
Db 2 CPKIRECEFERDVCTKORQDNKKCCVFCGKKCLDLKQDVCEMPKETGPCLAYFLH 61
Oy 93 WYNNKTKICSEFYGGCGQNNNFQTPAICLVTK 128
Db 62 WYDKDKNTCMFVYGGCGQNNNFQSKANCLNTCK 97

RESULT 25

ADG89848

ID ADG89848 standard; protein; 102 AA.

XX AC ADG89848;

XX DT 11-MAR-2004 (first entry)

XX DE Human secreted protein gene 24 protein #6.

XX Secreted protein; gene therapy; neural disorder; immune system disorders;
KW muscular disorder; reproductive disorder; gastrointestinal disorder;
KW pulmonary disorder; cardiovascular disorder; renal disorder;
KW proliferative disorder; cancer; systemic lupus erythematosus;
KW rheumatoid arthritis; multiple sclerosis; thyroiditis; anaemia;
KW Grave's disease; diabetes; hepatitis; asthma; allergy; nephritis;

KW Parkinson's disease; Alzheimer's disease; atherosclerosis;
XX myocardial infarction; AIDS; infection; human.

OS Homo sapiens.

XX US2003225009-A1.

XX PD 04-DEC-2003.

XX 30-JAN-2002; 2002US-00059993.

PR 14-MAR-1997; 97US-0040710P.

PR 14-MAR-1997; 97US-0040762P.

PR 30-MAY-1997; 97US-0048100P.

PR 30-MAY-1997; 97US-0048189P.

PR 30-MAY-1997; 97US-0048357P.

PR 30-MAY-1997; 97US-0050934P.

PR 06-JUN-1997; 97US-0048970P.

PR 05-SEP-1997; 97US-0057765P.

PR 19-DEC-1997; 97US-0068368P.

PR 12-MAR-1998; 98WO-US0004858.

PR 11-SEP-1998; 98US-00152060.

PR 02-FEB-2001; 2001US-0265583P.

PR 11-MAY-2001; 2001US-00852659.

PR 11-MAY-2001; 2001US-00852797.

PR 11-MAY-2001; 2001US-00853161.

XX (ROSE/) ROSEN C A.

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PA (GENT/) GENTZ R L.

PA (WEIY/) WEI Y.

PA (MOOR/) MOORE P A.

PA (YOUN/) YOUNG P E.

PA (GREE/) GREENE J M.

PA (FERR/) FERRIE A M.

PA (HAST/) HASTINGS G A.

XX Rosen CA, Ruben SM, Li Y, Zeng Z, Kyaw H, Fischer CL, Li H;

PI Soppet DR, Gentz RL, Wei Y, Moore PA, Young PE, Greene JM,

PI Ferrie AM, Hastings GA;

XX WPI; 2004-042167/04.

XX New polypeptides and nucleic acid molecules for diagnosing, preventing or
PT treating diseases associated with aberrant expression or activity of the
PT polypeptide, e.g. cancer, asthma, AIDS, Parkinson's disease or diabetes.

XX Disclosure; SEQ ID NO 121; 320pp; English.

XX The invention relates to an isolated nucleic acid molecule encoding a
CC secreted protein that is at least 95% identical to a polynucleotide
CC fragment of any of the nucleotide sequences listed in table 1A of the
CC specification, which is hybridisable to the nucleotide sequences, a
CC polynucleotide encoding a polypeptide (or a polypeptide fragment, domain
CC or epitope of any of the amino acid sequences) listed in table 1A of the
CC specification, a polynucleotide which is an (allelic) variant of the
CC nucleotide sequences listed in the specification, a polynucleotide which
CC encodes a species homologue of the above amino acid sequences, a
CC polynucleotide capable of hybridising under stringent conditions to any
CC of the above polynucleotides, where the polynucleotide does not hybridise
CC under stringent conditions to a nucleic acid molecule having a nucleotide
CC sequence of only A or T residues. Also included are a recombinant vector
CC comprising the above nucleic acid molecule, making a recombinant host
CC cell comprising the above nucleic acid molecule, an isolated polypeptide
CC comprising a sequence that is at least 95% identical to the polypeptide
CC (or its fragment, domain, epitope, secreted form, (allelic) variant or
CC homologue) encoded by the above nucleic acid molecule, an isolated

antibody that binds specifically to the above polypeptide, a recombinant host cell produced by the above method and that expresses the above polypeptide, making an isolated polypeptide, preventing, treating or ameliorating a medical condition, diagnosing a pathological condition or a susceptibility to a pathological condition in a subject, identifying a binding partner to the above polypeptide, the gene corresponding to the cDNA sequence given in the specification, and identifying an activity in a biological assay. The nucleic acid molecule and polypeptide are useful in diagnosing, preventing, prognosing or treating diseases or disorders associated with aberrant expression and/or activity of the above polypeptide, such as neural disorders, immune system disorders, muscular disorders, reproductive disorders, gastrointestinal disorders, pulmonary disorders, cardiovascular disorders, renal disorders, proliferative disorders and/or cancers. In particular, these diseases are systemic lupus erythematosus, rheumatoid arthritis, multiple sclerosis, thyroiditis, anemia, Grave's disease, diabetes, hepatitis, asthma, allergies, nephritis, Parkinson's disease, Alzheimer's disease, atherosclerosis, myocardial infarction, AIDS and infections. The methods may be used for identifying agonists and antagonists of the polynucleotide and polypeptide. The present sequence is a protein from one of the 28 disclosed secreted protein genes, it is not clear whether this is an alternative expressed protein or a fragment of one of the claimed proteins.

Sequence 102 AA:

Sequence 102 AA;

	Query Match	53.1%	Score 400	DB 8	Length 102
	Best Local Similarity	66.7%	Pred. No. 1.3e-26		
	Matches 64	Conservative 11	Mismatches 21	Indels 0	Gaps 0
Qy	33	CPKIKVEVEEIIDQCTKPRDCPNMKCCPFSCGKKCLDFPKDICTSMPOEAGPCIASIPH	92		
Db	2	CPKIRECEFOERIVCVTKDRCQDNKKCCVFCSCGKKCLDLKQDYCEMPKETGPCLAYFLH	61		
Qy	93	WYNNKTKICISEFYGGCGGNNNNFQTEAICLVCTCK	128		
Db	62	WYIDKNTCTSMFYGGCGGNNNNFOSKANCLNTCK	97		

RESULT 26
ADA19813
ID ADA19813 standard: protein: 134 AA.

Mouse EPPIN protein SEQ ID NO:14.

DJ11; Kunitz-type protease inhibitor domain; antiinflammatory;
antiallergic; thrombolytic; anticoagulant; cardiant; vasotropic;
antibacterial; immunosuppressive; antineumatic; antithrptic;
neurotropic; antipruritic; vulnerary; protease inhibitor; gene therapy;
acute pancreatitis; pulmonary injury; allergy-induced protease release;
deep vein thrombosis; myocardial infarction; shock; septic shock;
hyperfibrinolytic haemorrhage; inflammatory disorder; emphysema;
idiopathic pulmonary fibrosis; rheumatoid arthritis; glomerulonephritis;
chronic inflammatory bowel disease; psoriasis; EPPIN.

XX Mus musculus.

XX PN WO2003070770-A2.

XX
PD
28-AUG-2003.

18-FEB-2003: 2003WO-EP001629.

21-FEB-2002: 2002US-0358683P.

XX
PA (GENE-) GENEPROT INC.XX
PI Bouqueleret L, Bairoch A, Niknejad A;

WPI: 2003-663849/62.

xx New engineered human Kunitz-type protease inhibitor for diagnosing,
xx preventing or treating conditions associated with excessive proteinase
PT activity, e.g. inflammation, pulmonary injuries, myocardial infarction or
PT hemorrhage.

Disclosure: Fig 1: 87pp; English.

The present invention describes an isolated, purified or recombinant DJ11 polypeptide comprising a Kunitz-type protease inhibitor domain or its biologically active portion. The polypeptide comprises at least 98 % identity to residues 77-127 of a 131 amino acid sequence (S1, see ADA19800), or to residues 52-102 of a 106 amino acid sequence (S2, see ADA19801). DJ11 has antiinflammatory, antiallergic, thrombolytic, anticoagulant, cardiac, vasotropic, antibacterial, immunosuppressive, antineumatic, antiarthritic, nephrotropic, antiparietic and vulnary activities, and can be used as a protease inhibitor and in gene therapy. Composition and methods from the present invention can be used in diagnosing, preventing or treating conditions associated with excessive proteinase activity, such as acute pancreatitis, pulmonary injury, allergy-induced protease release, deep vein thrombosis, myocardial infarction, shock (including septic shock), hyperfibrinolytic haemorrhage, and especially, inflammatory disorders (e.g. emphysema, idiopathic pulmonary fibrosis, rheumatoid arthritis, glomerulonephritis, chronic inflammatory bowel disease or psoriasis). The DJ11 proteins may be used in preserving platelet function, organ preservation or in wound healing. The polynucleotide sequence encoding DJ11 may be used as hybridisation probes, in chromosome and gene mapping, in the generation of antisense RNA and DNA, and as targets for pharmaceutical intervention. The present sequence represents a mouse EPPIN protein given in comparison with DJ11 proteins in the exemplification of the present invention.

Sequence 134 AA:

Sequence 134 AA:

Query Match	52.9%;	Score 398;	DB 7;	Length 134;
Best Local Similarity	51.9%;	Pred. No. 2.4e-26;		
Matches	67;	Conservative	25;	Mismatches 37;
			Indels	0;
			Gaps	0;

Qy	61	CPFSCGKKCLDFRKDICSNPQEA	GCPLASIPHHWYNNKTKICSEF	YTGCGCGNNNNPQTE	120
ph	61	CVFVNCGKCLNPQDLCISIPKDS	GSYCYMAVPRRWFWFNKENSTCO	VFYTGCGCGNNNNPQSO	120

RESULT 27

ADQ66734
ID ADO66734 standard: protein: 101 AA.

AA ADO66734:

DT 07-OCT-2004 (first entry)

XX
DE Novel human protein sequence #1707.[illegible]

KW gene therapy; neurological

KW cancer.

OS Homo sapiens.

PN EP1440981-A2.

28-JUL-2004.

 \mathbb{Y}

CC sequences of the invention are useful for treating diseases, e.g.
CC emphysema, idiopathic pulmonary fibrosis, adult respiratory distress
CC syndrome, cystic fibrosis, rheumatoid arthritis, organ failure,
CC glomerulonephritis or inflammatory diseases. The BTL010 protein is also
CC useful for preventing neutrophil and monocyte activation and formation of
CC active oxygen species during the oxidative burst of stimulated
CC granulocytes. It is also useful for reducing platelet activation and
CC blood coagulation. BTL010 DNA is useful in gene therapy. The present
CC sequence is human Kunitz domain (KD) peptide.

XX Sequence 58 AA;

Query Match 31.3%; Score 236; DB 8; Length 58;
Best Local Similarity 66.1%; Pred. No. 7.4e-13;
Matches 37; Conservative 8; Mismatches 11; Indels 0; Gaps 0;

Qy 73 RKDTCSPQZAGPCLASIPHHWYKTKICSEFYGGCGNNNNFQTEATCLVTCK 128
Db 1 KQDVCEMPKETGPTCLAYFLHWWYDKDNTCSMFYGGCGNNNNFQSKANCLNTCK 56

RESULT 34

ADR89980
ID ADR99980 standard; peptide; 58 AA.

XX ADR89980;

XX AC (first entry)

DT 18-NOV-2004

DE Human CAB37 protein kunitz domain peptide.

KW Kunitz domain peptide; cystic fibrosis; cystic fibrosis related disease;
KW hereditary angioedema; cancer; chronic obstructive pulmonary disease;
KW asthma; bronchitis; acute respiratory syndrome; pneumonia; bleeding;
KW cytostatic; haemostatic; CAB37 protein; human.

XX Homo sapiens.

XX US2004171794-A1.

XX 02-SEP-2004.

XX 07-FEB-2003; 2003US-00361997.

XX 07-FEB-2003; 2003US-00361997.

XX (LADN/) LADNER R C.

XX (LEYA/) LEY A C.

XX Ladner RC, Ley AC;

XX WPI; 2004-625120/60.

XX New kunitz domain peptide useful as human neutrophil elastase inhibitor
XX for the treatment of e.g. cystic fibrosis and related disease.

XX Disclosure; SEQ ID NO 5; 123pp; English.

XX The invention relates to proteins comprising kunitz domain peptide,
XX designated DPI-14 for inhibiting human neutrophil elastase, fused to
XX albumin. The invention is useful for treating cystic fibrosis and related
XX diseases, hereditary angioedema, cancer and related diseases including
XX chronic obstructive pulmonary disease, asthma, bronchitis, acute
XX respiratory syndrome, pneumonia and bleeding. The invention acts as a
XX cytostatic and haemostatic agent. The present sequence is the human CAB37
XX protein (A4) kunitz domain peptide. This sequence is used in the
XX invention.

XX Sequence 58 AA;

Query Match 31.3%; Score 236; DB 8; Length 58;
Best Local Similarity 66.1%; Pred. No. 7.4e-13;
Matches 37; Conservative 8; Mismatches 11; Indels 0; Gaps 0;

Qy 73 RKDTCSPQZAGPCLASIPHHWYKTKICSEFYGGCGNNNNFQTEATCLVTCK 128
Db 1 KQDVCEMPKETGPTCLAYFLHWWYDKDNTCSMFYGGCGNNNNFQSKANCLNTCK 56

RESULT 35

AAW75257
ID AAW75257 standard; protein; 51 AA.

XX AAW75257;

XX 29-JAN-1999 (first entry)

DE Fragment of human secreted protein encoded by gene 24.

KW Human; secreted protein; fusion protein; gene therapy; protein therapy;
KW diagnosis; tissue; cancer; tumour; neurodegenerative disorder; leukaemia;
KW developmental abnormality; foetal deficiency; blood; allergy; renal;
KW immune system; asthma; lymphocytic disease; brain; hepatic; lymphoma;
KW inflammation; ischaemic shock; Alzheimer's disease; restenosis; AIDS;
KW cognitive disorder; schizophrenia; prostate; obesity; osteoclast; thymus;
KW osteoporosis; arthritis; testis; lung; thyroiditis; thyroid; digestion;
KW endocrine; metabolism; regulation; malabsorption; gastritis; neoplasm.

XX Homo sapiens.

XX WO9840483-A2.

XX 17-SEP-1998.

XX 12-MAR-1998; 98WO-US004858.

XX 14-MAR-1997; 97US-0040710P.

XX 14-MAR-1997; 97US-0040762P.

XX 30-MAY-1997; 97US-0048100P.

XX 30-MAY-1997; 97US-0048189P.

XX 30-MAY-1997; 97US-0048357P.

XX 30-MAY-1997; 97US-0050934P.

XX 06-JUN-1997; 97US-0048970P.

XX 05-SEP-1997; 97US-0057765P.

XX 19-DEC-1997; 97US-0068368P.

XX (HUMA-) HUMAN GENOME SCI INC.

XX Ruben SM, Rosen CA, Li Y, Zeng Z, Kyaw H, Fischer CL, Li H;

XX Soppet DR, Gentz RL, Wei YF, Moore PA, Young PE, Greene JM;

XX Ferrie AM;

XX WPI; 1998-520811/44.

XX N-PSDB; AAV34309.

XX Isolated human poly-nucleotide(s) encoding secretory peptide(s) - used to
XX develop products for the diagnosis and treatment of e.g. inflammation,
XX cancers, CNS disorders or immune system disorders.

XX Disclosure; Page 24; 201pp; English.

XX This sequence represents a fragment of a secreted human protein encoded
XX by the nucleic acid molecule designated Gene 24 (AAV34309). The gene can
XX be used to generate fusion proteins by linking to the gene to a human
XX immunoglobulin Fc portion (e.g. AAV34277) for increasing the stability of
XX the fused protein as compared to the human protein only. The invention
XX relates to 28 novel genes and their fragments (nucleic acid sequences:
XX AAV34286-V34325; amino acid sequences AAV75196-W75235) which are useful
XX for preventing, treating or ameliorating medical conditions e.g. by
XX protein or gene therapy. Also, pathological conditions can be diagnosed
XX by determining the amount of the new polypeptides in a sample or by
XX determining the presence of mutations in the new polynucleotides.
XX Specific uses are described for each of the 28 polynucleotides, based on
XX which tissues they are most highly expressed in (see AAV34286 for
XX described uses)

PA (ROSE/) ROSEN C A.
PA (LIYV/) LI Y.
PA (ZENG/) ZENG Z.
PA (KYAW/) KYAW H.
PA (FISC/) FISCHER C L.
PA (LIHH/) LI H.
PA (SOPP/) SOPPET D R.
PA (GENT/) GENTZ R L.
PA (WEIY/) WEI Y.
PA (MOOR/) MOORE P A.
PA (YOUN/) YOUNG P E.
PA (GREE/) GREENE J M.
PA (FERR/) FERRIE A M.
XX
PI Ruben SM, Rosen CA, Li Y, Zeng Z, Kyaw H, Fischer CL, Li H;
PI Soppet DR, Gentz RL, Wei Y, Moore PA, Young PE, Greene JM;
PI Ferrie AM;
XX
XX WPI; 2002-574454/61.
XX
XX New nucleic acid molecules encoding 28 human secreted proteins, useful
PT for diagnosing, preventing, treating or ameliorating medical conditions
PT and as food additives or preservatives.
XX
XX Disclosure; Page 16; 209pp; English.
XX
XX AAD44854-AAD44984 represent cDNAs corresponding to 28 human secreted
CC protein genes, and AAE27097-AAE27137 represent the proteins they encode.
CC AAE27138-AAE27164 represent human secreted protein fragments. The genes
CC and their corresponding secreted proteins are useful for preventing,
CC treating or ameliorating medical conditions, e.g., by protein or gene
CC therapy. Secreted protein sequences of the invention are useful for the
CC diagnosis or treatment of disorders such as autoimmune diseases (e.g.
CC rheumatoid arthritis), hyperproliferative disorders (e.g. neoplasms of
CC the breast or liver), cerebrovascular disorders (e.g. cerebral ischaemia,
CC system disorders (e.g. Alzheimer's disease), infections caused by fungi,
CC bacteria and viruses and ocular disorders (e.g. corneal infection). The
CC polypeptides can also be used to aid wound healing and epithelial cell
CC proliferation, to prevent skin aging due to sunburn, to maintain organs
CC before transplantation, for supporting cell culture of primary tissues,
CC to regenerate tissues and in chemotaxis. They can also be used as food
CC additives or preservative to increase or decrease storage capabilities,
CC fat content, lipid, protein, carbohydrate, vitamins, minerals, cofactors
CC and other nutritional components. The present sequence represents a human
CC secreted protein fragment kunitz-type domain referred to in the
CC disclosure of the invention
XX
XX Sequence 51 AA;
SQ

Query Match 29.1%; Score 219; DB 5; Length 51;
Best Local Similarity 68.8%; Pred. No. 1.9e-11;
Matches 35; Conservative 5; Mismatches 11; Indels 0; Gaps 0;
OY 77 CSMQBPAGPCLASIPHWYNNKTKIGSEFIYGGCGNNNNFQTEAICLVTC 127
DB 1 CEMPKEGTGCLAVFLHWYDKDNTCSMFYGGCGNNNNFQSKANCLNTC 51

RESULT 38
ADG89845
ID ADG89845 standard; protein; 51 AA.
XX
XX ADG89845;
XX
XX 11-MAR-2004 (first entry)
XX
XX Human secreted protein gene 24 protein #3.
XX
XX Secreted protein; gene therapy; neural disorder; immune system disorders;
KW muscular disorder; reproductive disorder; gastrointestinal disorder;
KW pulmonary disorder; cardiovascular disorder; renal disorder;
KW proliferative disorder; cancer; systemic lupus erythematosus;

KW rheumatoid arthritis; multiple sclerosis; thyroiditis; anaemia;
KW Grave's disease; diabetes; hepatitis; asthma; allergy; nephritis;
KW Parkinson's disease; Alzheimer's disease; atherosclerosis;
KW myocardial infarction; AIDS; infection; human.
XX
OS Homo sapiens.
XX
XX US2003225009-A1.
XX
XX 04-DEC-2003.
XX
XX 30-JAN-2002; 2002US-00058993.
XX
XX 14-MAR-1997; 97US-0040710P.
XX 14-MAR-1997; 97US-0040762P.
XX 30-MAY-1997; 97US-0048100P.
XX 30-MAY-1997; 97US-0048189P.
XX 30-MAY-1997; 97US-0048357P.
XX 30-MAY-1997; 97US-0050934P.
XX 06-JUN-1997; 97US-0048970P.
XX 05-SEP-1997; 97US-0057765P.
XX 19-DEC-1997; 97US-0068368P.
XX 12-MAR-1998; 98MO-US004858.
XX 11-SEP-1998; 98US-00152060.
XX 02-FEB-2001; 2001US-0285583P.
XX 11-MAY-2001; 2001US-0085265P.
XX 11-MAY-2001; 2001US-00852797.
XX 11-MAY-2001; 2001US-00853161.
XX
XX (ROSE/) ROSEN C A.
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XX (ZENG/) ZENG Z.
XX (KYAW/) KYAW H.
XX (FISC/) FISCHER C L.
XX (LIHH/) LI H.
XX (SOPP/) SOPPET D R.
XX (GENT/) GENTZ R L.
XX (WEIY/) WEI Y.
XX (MOOR/) MOORE P A.
XX (YOUN/) YOUNG P E.
XX (GREE/) GREENE J M.
XX (FERR/) FERRIE A M.
XX (HAST/) HASTINGS G A.
XX
XX Rosen CA, Ruben SM, Li Y, Zeng Z, Kyaw H, Fischer CL, Li H;
PI Soppet DR, Gentz RL, Wei Y, Moore PA, Young PE, Greene JM;
PI Ferrie AM, Hastings GA;
XX
XX WPI; 2004-042167/04.
XX
XX New polypeptides and nucleic acid molecules for diagnosing, preventing or
PT treating diseases associated with aberrant expression or activity of the
PT polypeptide, e.g. cancer, asthma, AIDS, Parkinson's disease or diabetes.
XX
XX Disclosure; SEQ ID NO 118; 320pp; English.
XX
XX The invention relates to an isolated nucleic acid molecule encoding a
CC secreted protein that is at least 95% identical to a polynucleotide
CC fragment of any of the nucleotide sequences listed in table 1A of the
CC specification, which is hybridisable to the nucleotide sequences, a
CC polynucleotide encoding a polypeptide (or a polypeptide fragment, domain
CC or epitope of any of the amino acid sequences) listed in table 1A of the
CC specification, a polynucleotide which is an (allelic) variant of the
CC nucleotide sequences listed in the specification, a polynucleotide which
CC encodes a species homologue of the above amino acid sequences, a
CC polynucleotide capable of hybridising under stringent conditions to any
CC of the above polynucleotides, where the polynucleotide does not hybridise
CC under stringent conditions to a nucleic acid molecule having a nucleotide
CC sequence of only A or T residues. Also included are a recombinant vector
CC comprising the above nucleic acid molecule, making a recombinant host
CC cell comprising the above nucleic acid molecule, an isolated polypeptide
CC comprising a sequence that is at least 95% identical to the polypeptide

(or its fragment, domain, epitope, secreted form, (allelic) variant or homologue) encoded by the above nucleic acid molecule, an isolated antibody that binds specifically to the above polypeptide, a recombinant host cell produced by the above method and that expresses the above polypeptide, making an isolated polypeptide, preventing, treating or ameliorating a medical condition, diagnosing a pathological condition or a susceptibility to a pathological condition in a subject, identifying a binding partner to the above polypeptide, the gene corresponding to the cDNA sequence given in the specification, and identifying an activity in a biological assay. The nucleic acid molecule and polypeptide are useful in diagnosing, preventing, prognosing or treating diseases or disorders associated with aberrant expression and/or activity of the above polypeptide, such as neural disorders, immune system disorders, muscular disorders, reproductive disorders, gastrointestinal disorders, pulmonary disorders, cardiovascular disorders, renal disorders, proliferative disorders and/or cancers. In particular, these diseases are systemic lupus erythematosus, rheumatoid arthritis, multiple sclerosis, thyroiditis, anaemia, Grave's disease, diabetes, hepatitis, asthma, allergies, nephritis, Parkinson's disease, Alzheimer's disease, atherosclerosis, myocardial infarction, AIDS and infections. The methods may be used for identifying agonists and antagonists of the polynucleotide and polypeptide. The present sequence is a protein from one of the 28 disclosed secreted protein genes, it is not clear whether this is an alternative expressed protein or a fragment of one of the claimed proteins.

XX Sequence 51 AA;

Query Match 29.1%; Score 219; DB 8; Length 51;
Best Local Similarity 68.6%; Pred. No. 1.9e-11;
Matches 35; Conservative 5; Mismatches 11; Indels 0; Gaps 0;

Qy 77 CSMQEGAPCLASIPHHYNNKTKICSEFIYGGCGNNNFQTEAICLVTC 127
Db 1 CEMPKETGCLAYFLHWDYDKDNTCSMFVYGGCGNNNFQSKANCLNTC 51

RESULT 39

AAR62523
ID AAR62523 standard; peptide; 560 AA.

XX AAR62523;

XX 25-MAR-2003 (revised)
DT 06-JUN-1995 (first entry)

XX Hookworm anticoagulant.

XX Hookworm; anticoagulant; serine protease-inhibitor; blood loss; vaccine;
KW vascular disease therapy.

XX Ancylostoma caninum.

XX WO9425000-A1.

XX 10-NOV-1994.

XX 29-APR-1994; 94WO-US004707.

XX 30-APR-1993; 93US-00055988.

XX (UYVA) UNIV YALE.

XX Cappello M, Hotez PJ, Richards PE, Hawdon JM;

XX WPI; 1994-357862/44.

XX Anticoagulant protein isolated from Ancylostoma hookworm - useful to
PT prevent blood loss during infection, as vaccine and to treat vascular
PT disorders.

XX Disclosure; Page 27-29; 39pp; English.

XX

CC An anticoagulant was isolated from extracts of adult hookworm
CC (Ancylostoma caninum). Preliminary sequencing identified 2 internal
CC peptide fragments (AAR62521-22). The protein sequence of the
CC anticoagulant, predicted from a 2.3 kb clone isolated from a cDNA library
CC of adult hookworm, is given in AAR62523. The protein sequence exhibited
CC homology to the pancreatic trypsin-inhibitor (AAR62524), green mamba
CC venom (AAR62525) and tissue factor pathway inhibitors (AAR62526-8),
CC suggesting the anticoagulant to be a Kunitz-type serine protease-
CC inhibitor. (Updated on 25-MAR-2003 to correct PN field.)

XX Sequence 560 AA;

Query Match 24.8%; Score 187; DB 2; Length 560;
Best Local Similarity 44.6%; Pred. No. 9.9e-08;
Matches 33; Conservative 12; Mismatches 29; Indels 0; Gaps 0;

Qy 56 ENMKCCPFGCKCLDFRKIDICMPQAGPCLASIPHHWYNNKTKICSEFIYGGCGQNNN 115
Db 307 ESMECTYTKCAVPEPEQDTCQPTEVGPCKAMLKRYAYDNKNKNKCVRFIYGGCKGNKN 365

Qy 116 NFQTEAICLVTCCK 129

Db 367 NFESMEECTRTCKK 380

RESULT 40

ABB71150
ID ABB71150 standard; protein; 2858 AA.

XX ABB71150;

XX 26-MAR-2002 (first entry)

XX Drosophila melanogaster polypeptide SEQ ID NO 40242.

XX Drosophila; developmental biology; cell signalling; insecticide;
KW pharmaceutical.

XX Drosophila melanogaster.

XX WO200171042-A2.

XX 27-SEP-2001.

XX 23-MAR-2001; 2001WO-US009231.

XX 23-MAR-2000; 2000US-0191637P.

XX 11-JUL-2000; 2000US-00614150.

XX (PEKE) PE CORP NY.

XX Venter JC, Adams M, Li PWD, Myers EW;

XX WPI; 2001-656860/75.

XX N-PSDB; ABL15253.

XX New isolated nucleic acid detection reagent for detecting 1000 or more
PT genes from Drosophila and for elucidating cell signaling and cell-cell
PT interactions.

XX Disclosure; SEQ ID NO 40242; 21pp + Sequence Listing; English.

XX The invention relates to an isolated nucleic acid detection reagent
CC capable of detecting 1000 or more genes from Drosophila. The invention is
CC useful in developmental biology and in elucidating cell signalling and
CC cell-cell interactions in higher eukaryotes for the development of
CC insecticides, therapeutics and pharmaceutical drugs. The invention
CC discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA
CC sequences (ABL01840-ABL16175) and the encoded proteins (ABB57737-
CC ABB72072). The sequence data for this patent did not form part of the
CC printed specification, but was obtained in electronic format directly
CC from WIPO at ftp.wipo.int/pub/published_pct_sequences

XX


```
SQ Sequence 2858 AA;
Query Match 24.8%; Score 187; DB 4; Length 2858;
Best Local Similarity 33.3%; Pred. No. 4.7e-07;
Matches 38; Conservative 13; Mismatches 33; Indels 30; Gaps 5;

QY 46 DQCTKPR---DCPENM-----KCCPF---SCG-----KKCLD-----FRKD 75
1748 DRCLPKQTGDCSEKLAWHFSESEKRCVPFYSGCGGNKNNFPTLESCECHCPRQVAKD 1807

QY 76 ICSMPQAGPCLASIPHHWYKTKICSEFYGGCGNNNNFQTEAICLVTCCK 129
1808 ICEIPAEVGECAVYVTSYYDTQDQACRQFYGGCGGNENRFPPTESCLARCDR 1861

DB

QY 76 ICSMPQAGPCLASIPHHWYKTKICSEFYGGCGNNNNFQTEAICLVTCCK 129
1808 ICEIPAEVGECAVYVTSYYDTQDQACRQFYGGCGGNENRFPPTESCLARCDR 1861

DB

RESULT 41
ID ABB58064 standard; protein; 3060 AA.
XX
AC ABB58064;
XX
DT 26-MAR-2002 (first entry)
XX
DE Drosophila melanogaster polypeptide SEQ ID NO 984.
XX
KW Drosophila; developmental biology; cell signalling; insecticide;
KW pharmaceutical.
XX
OS Drosophila melanogaster.
XX
PN WO200171042-A2.
XX
PD 27-SEP-2001.
XX
PF 23-MAR-2001; 2001WO-US009231.
XX
PR 23-MAR-2000; 2000US-0191637P.
XX
PR 11-JUL-2000; 2000US-00614150.
XX
PA (PEKE ) PE CORP NY.
XX
PI Venter JC, Adams M, Li PWD, Myers EW;
XX
WPI; 2001-656860/75.
XX
N-PSDB; ABL02167.
XX
PT New isolated nucleic acid detection reagent for detecting 1000 or more
genes from Drosophila and for elucidating cell signaling and cell-cell
interactions.
XX
PS Disclosure; SEQ ID NO 984; 21pp + Sequence Listing; English.
XX
CC The invention relates to an isolated nucleic acid detection reagent
capable of detecting 1000 or more genes from Drosophila. The invention is
useful in developmental biology and in elucidating cell signalling and
cell-cell interactions in higher eukaryotes for the development of
insecticides, therapeutics and pharmaceutical drugs. The invention
discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA
sequences (ABU01840-ABL16175) and the encoded proteins (ABB57737-
ABB72072). The sequence data for this patent did not form part of the
printed specification, but was obtained in electronic format directly
from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 3060 AA;
Query Match 24.8%; Score 187; DB 4; Length 3060;
Best Local Similarity 33.3%; Pred. No. 5e-07;
Matches 38; Conservative 13; Mismatches 33; Indels 30; Gaps 5;

QY 46 DQCTKPR---DCPENM-----KCCPF---SCG-----KKCLD-----FRKD 75
1748 DRCLPKQTGDCSEKLAWHFSESEKRCVPFYSGCGGNKNNFPTLESCECHCPRQVAKD 1807

DB
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QY 76 ICSMPQAGPCLASIPHHWYKTKICSEFYGGCGNNNNFQTEAICLVTCCK 129
1808 ICEIPAEVGECAVYVTSYYDTQDQACRQFYGGCGGNENRFPPTESCLARCDR 1861

DB

RESULT 42
ID AAE39498 standard; protein; 571 AA.
XX
AC AAE39498;
XX
DT 18-DEC-2003 (first entry)
XX
DE Cloned mouse GDF-associated serum protein (GASP) 1.
XX
KW Mouse; GDF-associated serum protein; GASP; amyotrophic lateral sclerosis;
growth and differentiation factor; GDF; chronic glucocorticoid therapy;
familial periodic paralysis; paroxysmal myoglobinuria; muscular disorder;
progressive dystrophic ophthalmoplegia; adipose tissue disorder; frailty;
bone degenerative disorder; congenital myopathy; Eaton-Lambert syndrome;
muscular dystrophy; congestive obstructive pulmonary disease; cachexia;
carpal tunnel syndrome; premature gonadal failure; vitamin D deficiency;
nutritional deficiency; osteoarthritis; hyperparathyroidism; sarcopaenia;
androgen suppression; myasthenia gravis; hyperglycaemia; organ atrophy;
metabolic disorder; metabolic syndrome; anorexia nervosa; osteoporosis;
myotonia; neuroprotective; obesity; immunomodulator; diabetes.
XX
OS Mus sp.
XX
PN US2003162714-A1.
XX
PD 28-AUG-2003.
XX
PF 21-FEB-2003; 2003US-00369736.
XX
PR 21-FEB-2002; 2002US-0357845P.
XX
PR 20-DEC-2002; 2002US-0434644P.
XX
PA (AMHP ) WYETH.
XX
PI Hill JJ, Wolfman NM;
XX
WPI; 2003-756055/71.
XX
N-PSDB; AAD59931.
XX
PT Composition containing growth and differentiation factor-associated serum
protein-1, useful for treating e.g. muscular dystrophy or diabetes, also
for diagnosis.
XX
PS Example 9; Fig 13; Opp; English.
XX
CC The present invention relates to the use of a protein GDF (growth and
differentiation factor)-associated serum protein (GASP) 1 comprising
at least one follistatin domain to modulate the level or activity of
growth and differentiation factor (GDF) -8. Administration of GASP1 is
used to modulate GDF-8 for treatment of muscular disorders such as
muscular dystrophy (benign X-linked, limb-girdle, facioscapulohumeral,
myotonic, distal, oculopharyngeal, Duchenne or Fukuyama-type congenital),
progressive dystrophic ophthalmoplegia, amyotrophic lateral sclerosis,
congestive obstructive pulmonary disease, congenital myopathy (myotonia),
familial periodic paralysis, paroxysmal myoglobinuria, myasthenia gravis,
Eaton-Lambert syndrome, secondary myasthenia, organ atrophy, frailty,
carpal tunnel syndrome, paroxysmal muscle atrophy, sarcopaenia, cachexia
and other muscle wasting syndromes such as traumatic or chronic injury to
muscle, metabolic disorders such as diabetes types 1 or 2, impaired
glucose tolerance, hyperglycaemia, metabolic syndrome, insulin resistance
induced by trauma and obesity, adipose tissue disorder such as obesity,
and bone degenerative conditions such as osteoporosis, osteopaenia,
osteoarthritis, low bone mass due to chronic glucocorticoid therapy,
premature gonadal failure, vitamin D deficiency, androgen suppression,
secondary hyperparathyroidism, nutritional deficiencies and anorexia
nervosa. The present sequence is cloned mouse GDF (growth and
differentiation factor)-associated serum protein (GASP)
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XX SQ Sequence 571 AA;
Query Match 24.2%; Score 182.5; DB 7; Length 571;
Best Local Similarity 31.8%; Pred. No. 2.4e-07;
Matches 35; Conservative 12; Mismatches 34; Indels 29; Gaps 3;

Qy 47 QCTKP---RDCPENM-----KCCPF-----SCGKKCLDFRKDIC 77
Db 322 ECLKPPDSEDCGEGQTRWHFDAQANNCLTFTFGCHHNLNHFYEAACMLACMSGPLATC 381

Qy 78 SMPQEAGPCLASIPHWYNNKTKICSEFIYGGCGQNNNNFQTEAICLVTC 127
Db 382 SLPALQGFCKAYVPRWAYNSQTGLCQSPFYGCGEGNGNPFESRACEESC 431

RESULT 43
AAE39459
ID AAE39459 standard; protein; 571 AA.
XX
AC AAE39459;
XX
DT 18-DEC-2003 (first entry)
XX
DE Mouse GDF-associated serum protein (GASP)1 protein.
XX
KW Mouse; GDF-associated serum protein; GASP; amyotrophic lateral sclerosis;
KW growth and differentiation factor; GDF; chronic glucocorticoid therapy;
KW familial periodic paralysis; paroxysmal myoglobinuria; muscular disorder;
KW progressive dystrophic ophthalmoplegia; adipose tissue disorder; frailty;
KW bone degenerative disorder; congenital myopathy; Eaton-Lambert syndrome;
KW muscular dystrophy; congestive obstructive pulmonary disease; cachexia;
KW carpal tunnel syndrome; premature gonadal failure; vitamin D deficiency;
KW nutritional deficiency; osteoarthritis; hyperparathyroidism; sarcopaenia;
KW androgen suppression; myaethenia gravis; hyperglycaemia; organ atrophy;
KW metabolic disorder; metabolic syndrome; anorexia nervosa; osteoporosis;
KW myotonia; neuroprotective; obesity; immunomodulator; diabetes.
XX
OS Mus sp.
XX
FH Key Location/Qualifiers
FT Domain 105..170
FT /note= "Follistatin domain"
XX
PN US2003162714-A1.
XX
PD 28-AUG-2003.
XX
PF 21-FEB-2003; 2003US-00369736.
XX
PR 21-FEB-2002; 2002US-0357845P.
XX
PR 20-DEC-2002; 2002US-0434644P.
XX
PA (AMHP ) WYETH.
XX
PI Hill JJ, Wolfman NM;
XX
XX WPI; 2003-756055/71.
XX
DR N-PSDB; AAD59923.
XX
XX Composition containing growth and differentiation factor-associated serum
XX protein-1, useful for treating e.g. muscular dystrophy or diabetes, also
XX for diagnosis.
XX
PS Disclosure; Fig 6C; Opp; English.
XX
CC The present invention relates to the use of a protein GDF (growth and
CC differentiation factor)-associated serum protein (GASP) 1 comprising
CC at least one follistatin domain to modulate the level or activity of
CC growth and differentiation factor (GDF) -8. Administration of GASP1 is
CC used to modulate GDF-8 for treatment of muscular disorders such as
CC muscular dystrophy (benign X-linked, limb-girdle, facioscapulohumeral,
CC myotonic, distal, oculopharyngeal, Duchenne or Fukuyama-type congenital),
CC
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```
CC progressive dystrophic ophthalmoplegia, amyotrophic lateral sclerosis,
CC congestive obstructive pulmonary disease, congenital myopathy (myotonia),
CC familial periodic paralysis, paroxysmal myoglobinuria, myaethenia gravis,
CC Eaton-Lambert syndrome, secondary myasthenia, organ atrophy, frailty,
CC carpal tunnel syndrome, paroxysmal muscle atrophy, sarcopaenia, cachexia
CC and other muscle wasting syndromes such as traumatic or chronic injury to
CC muscle, metabolic disorders such as diabetes types 1 or 2, impaired
CC glucose tolerance, hyperglycaemia, metabolic syndrome, insulin resistance
CC induced by trauma and obesity, adipose tissue disorder such as obesity,
CC and bone degenerative conditions such as osteoporosis, osteopaenia,
CC osteoarthritis, low bone mass due to chronic glucocorticoid therapy,
CC premature gonadal failure, vitamin D deficiency, androgen suppression,
CC secondary hyperparathyroidism, nutritional deficiencies and anorexia
CC nervosa. The present sequence is mouse GDF (growth and differentiation
XX factor)-associated serum protein (GASP)
XX
SQ Sequence 571 AA;
Query Match 24.2%; Score 182.5; DB 7; Length 571;
Best Local Similarity 31.8%; Pred. No. 2.4e-07;
Matches 35; Conservative 12; Mismatches 34; Indels 29; Gaps 3;

Qy 47 QCTKP---RDCPENM-----KCCPF-----SCGKKCLDFRKDIC 77
Db 322 ECLKPPDSEDCGEGQTRWHFDAQANNCLTFTFGCHHNLNHFYEAACMLACMSGPLATC 381

Qy 78 SMPQEAGPCLASIPHWYNNKTKICSEFIYGGCGQNNNNFQTEAICLVTC 127
Db 382 SLPALQGFCKAYVPRWAYNSQTGLCQSPFYGCGEGNGNPFESRACEESC 431

RESULT 44
ADD93670
ID ADD93670 standard; protein; 571 AA.
XX
AC ADD93670;
XX
DT 29-JAN-2004 (first entry)
XX
DE Mouse GDF-associated serum protein 1 (GASP1).
XX
KW Mouse; GDF-associated serum protein 1; GASP1; antidiabetic; anorectic;
KW osteopathic; gene therapy.
XX
OS Mus sp.
XX
FH Key Location/Qualifiers
FT Peptide 1..29
FT /note= "Signal peptide"
FT Protein 30..571
FT /note= "Mature protein"
FT Domain 105..170
FT /note= "Follistatin domain"
FT Modified-site 313
FT /note= "potential N-glycosylation site"
FT Modified-site 514
FT /note= "potential N-glycosylation site"
XX
PN WO2003072714-A2.
XX
XX 04-SEP-2003.
XX
PD 21-FEB-2003; 2003WO-US0005150.
XX
PF 21-FEB-2002; 2002US-0357846P.
XX
PR 20-DEC-2002; 2002US-0434645P.
XX
XX (AMHP ) WYETH.
XX
PI Hill JJ, Wolfman NM;
XX
XX WPI; 2003-812402/76.
XX
DR N-PSDB; ADD93719, ADD93720.
```

XX New compositions comprising a protein containing at least one follistatin
PT domain, useful for treating muscular dystrophy (e.g. sarcopenia, and
PT cachexia), metabolic disease (e.g. diabetes or obesity), or bone
PT degenerative diseases.
XX
XX
XX Example 9; Fig 6C; 113pp; English.
PS
XX The present sequence is the protein sequence for mouse GDF-associated
CC serum protein 1 (GASPI), a protein which includes a follistatin domain
CC and which binds to growth and differentiation factor-8 (GDF-8 or
CC myostatin). The invention provides methods for modulating the effects of
CC GDF-8 on cells. These methods involve administering a protein comprising
CC at least one follistatin domain, or a nucleic acid encoding such a
CC protein. The methods are used to treat disorders relating to the level or
CC activity of GDF-8. These include a muscular disorder such as muscular
CC dystrophy (e.g. severe or benign X-linked muscular dystrophy, limb-girdle
CC dystrophy, facioscapulohumeral dystrophy, myotonic dystrophy, distal
CC muscular dystrophy, progressive dystrophic ophthalmoplegia,
CC oculopharyngeal dystrophy, Fukuyama-type congenital muscular dystrophy,
CC congenital myopathy, myotonia congenita, familial periodic paralysis,
CC paroxysmal myoglobinuria, myasthenia gravis, Eaton-Lambert syndrome,
CC secondary myasthenia, denervation atrophy, paroxysmal muscle atrophy,
CC muscle wasting syndrome, sarcopenia, and cachexia), traumatic or chronic
CC injury to muscle tissue, metabolic disease or disorder (e.g. type 2
CC diabetes, non-insulin-dependent diabetes mellitus, hyperglycaemia, or
CC obesity), adipose tissue disorder (e.g. obesity), and bone degenerative
CC disease (e.g. osteoporosis) (all claimed).

XX Sequence 571 AA;

Query Match 24.2%; Score 182.5; DB 7; Length 571;
Best Local Similarity 31.8%; Pred. No. 2.4e-07;
Matches 35; Conservative 12; Mismatches 34; Indels 29; Gaps 3;
QY 47 QCTKP---RDCPENM-----KCCPF-----SCGKCLDFRKDIC 77
DB 322 ECLKPPDSDCGEQTRHFDQAANNCLTFTFGCHNLNHPETYEACWACMSGPLATC 381
QY 78 SMOEAGCLASIPHWYNNKTKICSEFYGGCGQNNNFQTEAICLVTC 127
DB 382 SLFALQGCKAYVRWAYNSQGLCQSFVYGGCGGNFESREACEESC 431

RESULT 45
ADAL19806
ID ADAL19806 standard; peptide; 33 AA.

XX ADAL19806;
XX
XX 20-NOV-2003 (first entry)
XX Engineered human DJ11 partial amino acid sequence SEQ ID NO:7.
XX
XX DJ11; Kunitz-type protease inhibitor domain; antiinflammatory;
KW antiatheric; thrombolytic; anticoagulant; cardiant; vasotropic;
KW antibacterial; immunosuppressive; antirheumatic; antiarthritic;
KW nephrotropic; antipsoriatic; vulnary; protease inhibitor; gene therapy;
KW acute pancreatitis; pulmonary injury; allergy-induced protease release;
KW deep vein thrombosis; myocardial infarction; shock; septic shock;
KW hyperfibrinolytic haemorrhage; inflammatory disorder; emphysema;
KW idiopathic pulmonary fibrosis; rheumatoid arthritis; glomerulonephritis;
KW chronic inflammatory bowel disease; psoriasis.
XX Synthetic.
OS Homo sapiens.
XX WO2003070770-A2.
XX
XX 28-AUG-2003.
XX 18-FEB-2003; 2003WO-BP001629.
XX

21-FEB-2002; 2002US-0358683P.

(GENE-) GENEPROT INC.

Bougueleret L, Bairoch A, Niknejad A;

WPI; 2003-663849/62.

XX New engineered human Kunitz-type protease inhibitor for diagnosing,
PT preventing or treating conditions associated with excessive proteinase
PT activity, e.g. inflammation, pulmonary injuries, myocardial infarction or
PT hemorrhage.

XX Disclosure; Page 80; 87pp; English.

XX The present invention describes an isolated, purified or recombinant DJ11
CC polypeptide comprising a Kunitz-type protease inhibitor domain or its
CC biologically active portion. The polypeptide comprises at least 98 %
CC identity to residues 77-127 of a 131 amino acid sequence (S1, see
CC ADA19800), or to residues 52-102 of a 106 amino acid sequence (S2, see
CC ADA19801). DJ11 has antiinflammatory, antiatheric, thrombolytic,
CC anticoagulant, cardiant, vasotropic, antibacterial, immunosuppressive,
CC antirheumatic, antiarthritic, nephrotropic, antipsoriatic and vulnary
CC activities, and can be used as a protease inhibitor and in gene therapy.
CC Composition and methods from the present invention can be used in
CC diagnosing, preventing or treating conditions associated with excessive
CC proteinase activity, such as acute pancreatitis, pulmonary injury,
CC allergy-induced protease release, deep vein thrombosis, myocardial
CC infarction, shock (including septic shock), hyperfibrinolytic
CC haemorrhage, and especially, inflammatory disorders (e.g. emphysema,
CC idiopathic pulmonary fibrosis, rheumatoid arthritis, glomerulonephritis,
CC chronic inflammatory bowel disease or psoriasis). The DJ11 proteins may
CC be used in preserving platelet function, organ preservation or in wound
CC healing. The polynucleotide sequence encoding DJ11 may be used as
CC hybridisation probes, in chromosome and gene mapping, in the generation
CC of antisense RNA and DNA, and as targets for pharmaceutical intervention.
CC The present sequence represents a partial engineered human DJ11 protein
CC amino acid sequence from the present invention.

XX Sequence 33 AA;

Query Match 23.9%; Score 180; DB 7; Length 33;
Best Local Similarity 97.0%; Pred. No. 2.6e-08;
Matches 32; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 99 TKICSEFYGGCGQNNNFQTEAICLVTCCKYH 131

DB 1 TKICSEFYGGCGQNNNFQTEAICLVTCCKYH 33

RESULT 46

ADAL19809

ID ADAL19809 standard; peptide; 33 AA.

XX ADAL19809;

XX 20-NOV-2003 (first entry)

XX Engineered human DJ11 partial amino acid sequence SEQ ID NO:10.

XX DJ11; Kunitz-type protease inhibitor domain; antiinflammatory;
KW antiatheric; thrombolytic; anticoagulant; cardiant; vasotropic;
KW antibacterial; immunosuppressive; antirheumatic; antiarthritic;
KW nephrotropic; antipsoriatic; vulnary; protease inhibitor; gene therapy;
KW acute pancreatitis; pulmonary injury; allergy-induced protease release;
KW deep vein thrombosis; myocardial infarction; shock; septic shock;
KW hyperfibrinolytic haemorrhage; inflammatory disorder; emphysema;
KW idiopathic pulmonary fibrosis; rheumatoid arthritis; glomerulonephritis;
KW chronic inflammatory bowel disease; psoriasis.

XX Synthetic.

OS Homo sapiens.

XX

PN WO2003070770-A2.
 XX 28-AUG-2003.
 XX 18-FEB-2003; 2003WO-EP001629.
 XX 21-FEB-2002; 2002US-0358683P.
 XX (GENE-) GENEPROT INC.
 XX Bougueleret L, Bairoch A, Niknejad A;
 XX WPI; 2003-663849/62.
 XX New engineered human Kunitz-type protease inhibitor for diagnosing,
 PT preventing or treating conditions associated with excessive proteinase
 PT activity, e.g. inflammation, pulmonary injuries, myocardial infarction or
 PT hemorrhage.
 XX Disclosure; Page 82-83; 87pp; English.
 XX The present invention describes an isolated, purified or recombinant DJ11
 CC polypeptide comprising a Kunitz-type protease inhibitor domain or its
 CC biologically active portion. The polypeptide comprises at least 98 %
 CC identity to residues 77-127 of a 131 amino acid sequence (S1, see
 CC ADA19800), or to residues 52-102 of a 106 amino acid sequence (S2, see
 CC ADA19801). DJ11 has antiinflammatory, antiallergic, thrombolytic,
 CC anticoagulant, cardiac, vasotropic, antibacterial, immunosuppressive,
 CC antirheumatic, antiarthritic, nephrotropic, antipruritic and vulnerary
 CC activities, and can be used as a protease inhibitor and in gene therapy.
 CC Composition and methods from the present invention can be used in
 CC diagnosing, preventing or treating conditions associated with excessive
 CC proteinase activity, such as acute pancreatitis, pulmonary injury,
 CC allergy-induced protease release, deep vein thrombosis, myocardial
 CC infarction, shock (including septic shock), hyperfibrinolytic
 CC haemorrhage, and especially, inflammatory disorders (e.g. emphysema,
 CC idiopathic pulmonary fibrosis, rheumatoid arthritis, glomerulonephritis,
 CC chronic inflammatory bowel disease or psoriasis). The DJ11 proteins may
 CC be used in preserving platelet function, organ preservation or in wound
 CC healing. The polynucleotide sequence encoding DJ11 may be used as
 CC hybridisation probes, in chromosomes and gene mapping, in the generation
 CC of antisense RNA and DNA, and as targets for pharmaceutical intervention.
 CC The present sequence represents a partial engineered human DJ11 protein
 CC amino acid sequence from the present invention.
 XX Sequence 33 AA;
 SQ Query Match 23.9%; Score 180; DB 7; Length 33;
 Best Local Similarity 97.0%; Pred. No. 2.6e-08;
 Matches 32; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Qy 99 TKICSEFIYGGCGQNNNNFQTEAICLVTKCKYH 131
 Db 1 TKICSEFIYGGCGQNNNNFQTEAICLVTKCKYH 33
 RESULT 47
 AAR99146
 ID AAR99146 standard; protein; 58 AA.
 XX AAR99146;
 AC AAR99146;
 XX 12-FEB-1997 (first entry)
 DT Aprotinin-like Kunitz domain.
 DE Aprotinin; Kunitz domain; human neutrophil elastase; hNE;
 XX connective tissue; alpha 1 protease inhibitor; API; neutrophil;
 KW alpha1 antitrypsin; respiratory disorder; cystic fibrosis;
 KW smokers emphysema.
 XX Synthetic.
 OS
 XX

PN WO9620278-A2.
 XX 04-JUL-1996.
 XX 15-DEC-1995; 95WO-US016349.
 XX 16-DEC-1994; 94US-00358160.
 XX (PROT-) PROTEIN ENG CORP.
 XX Ley AC, Ladner RC, Guterman SK, Roberts BL, Markland W, Kent RB;
 XX WPI; 1996-321851/32.
 DR New engineered inhibitors of human neutrophil elastase - contg. aprotinin
 PT -like Kunitz domain for treating, e.g. cystic fibrosis or other
 PT respiratory disorders.
 XX Example 23; Page 47; 105pp; English.
 PS Genetically engineered human derived Kunitz domains can be used to
 CC inhibit human neutrophil elastase, an enzyme involved in the elimination
 CC of pathogens and the restructuring of connective tissue. In cases of
 CC reduction of the circulating alpha-1-protease inhibitor (API or alpha
 CC antitrypsin), or the inactivation of API by oxidation (smokers
 CC emphysema), extensive destruction of the lung tissue may result from
 CC uncontrolled elastolytic activity of human neutrophil elastase. Other
 CC respiratory disorders such as cystic fibrosis are thought to be caused by
 CC human neutrophil elastase release by neutrophils. The genetically
 CC engineered human derived Kunitz domains can be used to treat such
 CC respiratory disorders. See AAR99146-R99211
 XX Sequence 58 AA;
 SQ Query Match 23.5%; Score 177; DB 2; Length 58;
 Best Local Similarity 56.4%; Pred. No. 8.1e-08;
 Matches 31; Conservative 5; Mismatches 19; Indels 0; Gaps 0;
 Qy 73 RKDICSMPQAGRCIASIPHWYNNKTKICSEFIYGGCGQNNNNFQTEAICLVTC 127
 Db 1 RPDFCLLPAETGCRAMIPRFYNNAKSGKCEPFYGGCGGNANNFKTEECRRTC 55
 RESULT 48
 AAE13096
 ID AAE13096 standard; peptide; 43 AA.
 XX AAE13096;
 AC AAE13096;
 XX 28-JAN-2002 (first entry)
 DT Human serine proteinase inhibitor BTL.009 peptide fragment #2.
 XX Human; BTL.009 protein; serine proteinase inhibitor; cytosstatic;
 KW nephrotropic; idiopathic pulmonary fibrosis; cystic fibrosis; emphysema;
 KW rheumatoid arthritis; adult respiratory distress syndrome; angioplasty;
 KW blood coagulation; glomerulonephritis; prophylactic; platelet activation;
 KW neutrophil; monocyte; granulocyte; organ failure; inflammatory disease;
 KW elastase inhibitor; chymotrypsin inhibitor; lung injury; vascular injury;
 KW therapeutic.
 XX Homo sapiens.
 OS
 XX US6294648-B1.
 PN 25-SEP-2001.
 XX 20-JUL-1999; 99US-00358569.
 PF 20-JUL-1999; 99US-00358569.
 XX (FARB) BAYER CORP.
 XX

SQ Sequence 503 AA;

Query Match 23.0%; Score 173.5; DB 5; Length 503;
Best Local Similarity 31.8%; Pred. No. 1.3e-06;
Matches 35; Conservative 10; Mismatches 36; Indels 29; Gaps 3;
Qy 47 QCTKP---RDCPENM-----KCCPF-----SCGKKCLDFRKDIC 77
Db 258 ECLKPPDSEDCGEQTRWHFDAQANNCLTFTFGHCHRNLNHFETYEACMLACMSGPLAAC 317
Qy 78 SMPQAGFCLASIPHWYNKTKICSEFIYGCQGNNNNFQTEAICLVTC 127
Db 318 SLPALQGCKAYAPWAYNSQTQCQSFYGGCEGNGNPFESREACEESC 367

Search completed: September 21, 2005, 16:36:48
Job time : 87.9233 secs

Qy 61 CPFSGKKCLDFRDKCSMPQAGPCLASIPHHWYNNKTKICSEFYGGCGGNNNFOTE 120
Db 61 CVFSGKKCLDLKQDCEMPKETGCLAYFLHWWYDKDNTCSMFVYGGCGGNNNFQSK 120
Qy 121 AICLVTK 128
Db 121 ANCLNTCK 128

RESULT 2

US-09-358-569D-10
; Sequence 10, Application US/09358569D
; Patent No. 6294648
; GENERAL INFORMATION:
; APPLICANT: Delaria, Kathy
; APPLICANT: Roczniaak, Steve
; APPLICANT: Davies, Christopher
; TITLE OF INVENTION: Protein Having Proteinase Inhibitor Activity
; FILE REFERENCE: MSB-7259
; CURRENT APPLICATION NUMBER: US/09/358,569D
; CURRENT FILING DATE: 1999-07-20
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 10
; LENGTH: 64
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Extension of
; OTHER INFORMATION: Seq id 1
US-09-358-569D-10

Query Match 32.1%; Score 242; DB 3; Length 64;
Best Local Similarity 65.5%; Pred. No. 5.5e-17;
Matches 38; Conservative 8; Mismatches 12; Indels 0; Gaps 0;

Qy 71 DFRDKCSMPQAGPCLASIPHHWYNNKTKICSEFYGGCGGNNNFOTEICLVTK 128
Db 1 DLKQDCEMPKETGCLAYFLHWWYDKDNTCSMFVYGGCGGNNNFQSKANCLNTCK 58

RESULT 3

US-09-369-494-8
; Sequence 8, Application US/09369494
; Patent No. 6180607
; GENERAL INFORMATION:
; APPLICANT: Davies, Christopher
; APPLICANT: Chen, Dadong
; APPLICANT: Roczniaak, Steve
; TITLE OF INVENTION: Protein Having Proteinase Inhibitor Activity
; FILE REFERENCE: MSB-7260
; CURRENT APPLICATION NUMBER: US/09/369,494
; CURRENT FILING DATE: 1999-08-05
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 8
; LENGTH: 58
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:fragment from
; OTHER INFORMATION: computer database
US-09-369-494-8

Query Match 31.3%; Score 236; DB 3; Length 58;
Best Local Similarity 66.1%; Pred. No. 1.9e-16;
Matches 37; Conservative 8; Mismatches 11; Indels 0; Gaps 0;

Qy 73 RKDICSMPQAGPCLASIPHHWYNNKTKICSEFYGGCGGNNNFOTEICLVTK 128
Db 1 KQDCEMPKETGCLAYFLHWWYDKDNTCSMFVYGGCGGNNNFQSKANCLNTCK 56

RESULT 4

US-09-569-670-8
; Sequence 8, Application US/09569670
; Patent No. 6689582
; GENERAL INFORMATION:
; APPLICANT: Davies, Christopher
; APPLICANT: Chen, Dadong
; APPLICANT: Roczniaak, Steve
; TITLE OF INVENTION: Protein Having Proteinase Inhibitor Activity
; FILE REFERENCE: MSB-7260
; CURRENT APPLICATION NUMBER: US/09/569,670
; CURRENT FILING DATE: 2000-05-12
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 8
; LENGTH: 58
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:fragment from
; OTHER INFORMATION: computer database
US-09-569-670-8

Query Match 31.3%; Score 236; DB 4; Length 58;
Best Local Similarity 66.1%; Pred. No. 1.9e-16;
Matches 37; Conservative 8; Mismatches 11; Indels 0; Gaps 0;

Qy 73 RKDICSMPQAGPCLASIPHHWYNNKTKICSEFYGGCGGNNNFOTEICLVTK 128
Db 1 KQDCEMPKETGCLAYFLHWWYDKDNTCSMFVYGGCGGNNNFQSKANCLNTCK 56

RESULT 5

US-09-358-569D-8
; Sequence 8, Application US/09358569D
; Patent No. 6294648
; GENERAL INFORMATION:
; APPLICANT: Delaria, Kathy
; APPLICANT: Roczniaak, Steve
; APPLICANT: Davies, Christopher
; TITLE OF INVENTION: Protein Having Proteinase Inhibitor Activity
; FILE REFERENCE: MSB-7259
; CURRENT APPLICATION NUMBER: US/09/358,569D
; CURRENT FILING DATE: 1999-07-20
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 8
; LENGTH: 54
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:derived from
; OTHER INFORMATION: EST sequence database
US-09-358-569D-8

Query Match 30.9%; Score 233; DB 3; Length 54;
Best Local Similarity 68.5%; Pred. No. 3.6e-16;
Matches 37; Conservative 6; Mismatches 11; Indels 0; Gaps 0;

Qy 75 DICSMPQAGPCLASIPHHWYNNKTKICSEFYGGCGGNNNFOTEICLVTK 128
Db 1 DVCEMPKETGCLAYFLHWWYDKDNTCSMFVYGGCGGNNNFQSKANCLNTCK 54

RESULT 6

US-09-358-569D-1
; Sequence 1, Application US/09358569D
; Patent No. 6294648
; GENERAL INFORMATION:
; APPLICANT: Delaria, Kathy
; APPLICANT: Roczniaak, Steve
; APPLICANT: Davies, Christopher

;; TITLE OF INVENTION: Protein Having Proteinase Inhibitor Activity
;; FILE REFERENCE: MSB-7259
;; CURRENT APPLICATION NUMBER: US/09/358,569D
;; CURRENT FILING DATE: 1999-07-20
;; NUMBER OF SEQ ID NOS: 15
;; SOFTWARE: PatentIn Ver. 2.0
;; SEQ ID NO 1
;; LENGTH: 55
;; TYPE: PRT
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; OTHER INFORMATION: Description of Artificial Sequence: derived from
;; OTHER INFORMATION: EST sequence database
US-09-358-569D-1

Query Match 30.7%; Score 231; DB 3; Length 55;
Best Local Similarity 65.5%; Pred. No. 5.7e-16;
Matches 36; Conservative 8; Mismatches 11; Indels 0; Gaps 0;
Qy 73 RKDICSMPQEAGPCLASIPHWYNNKTKICSEFYGGCGGNNNNFQTEAICLVTC 127
:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||
Db 1 KQDVCMPKGTGCPCLAYELHWYDKDNTCSMFVYGGCGGNNNNFQSKANCLNTC 55

RESULT 7
US-08-358-160-113
; Sequence 113, Application US/08358160
; Patent No. 5663143
; GENERAL INFORMATION:
; APPLICANT: LEY, Arthur C.
; APPLICANT: LADNER, Robert C.
; APPLICANT: GUTERMAN, Sonia K.
; APPLICANT: ROBERTS, Bruce L.
; APPLICANT: MARKLAND, William
; APPLICANT: KENT, Rachel B.
; TITLE OF INVENTION: ENGINEERED HUMAN-DERIVED KUNITZ
; TITLE OF INVENTION: DOMAINS THAT INHIBIT HUMAN NEUTROPHIL ELASTASE
; NUMBER OF SEQUENCES: 234
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W. Suite 300
; CITY: Washington
; STATE: District of Columbia
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/358,160
; FILING DATE: 16-DEC-1994
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/133,031
; FILING DATE: 13-OCT-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/009,319
; FILING DATE: 26-JAN-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/664,989
; FILING DATE: 01-MAR-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/487,063
; FILING DATE: 02-MAR-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/240,160
; FILING DATE: 02-SEP-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Cooper, Iver P.
; REGISTRATION NUMBER: 28,005
; REFERENCE/DOCKET NUMBER: LEY=1

;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 202-628-5197
;; TELEFAX: 202-737-3528
;; TELEX: 248633
;; INFORMATION FOR SEQ ID NO: 113:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 66 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
US-08-358-160-113

Query Match 24.7%; Score 186; DB 1; Length 66;
Best Local Similarity 50.0%; Pred. No. 2e-11;
Matches 28; Conservative 13; Mismatches 15; Indels 0; Gaps 0;
Qy 73 RKDICSMPQEAGPCLASIPHWYNNKTKICSEFYGGCGGNNNNFQTEAICLVTC 128
:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||
Db 4 KRDICLPPEQGPCKGRIPRYFYNPASRMCSFYGGCKGNKNNFKTKAECVCRACR 59

RESULT 8
5466783-7
; Patent No. 5466783
; APPLICANT: Wun, Tze-Chain; Kretzmer, Kuniko K.; Broze, George J. Jr.
; TITLE OF INVENTION: HUMAN TISSUE FACTOR INHIBITOR
; NUMBER OF SEQUENCES: 26
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/93,285
; FILING DATE: 15-JUL-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 566,280
; FILING DATE: 13-AUG-1990
; APPLICATION NUMBER: 123,753
; FILING DATE: 23-NOV-1987
; APPLICATION NUMBER: 77,366
; FILING DATE: 23-JUL-1987
; SEQ ID NO: 7
; LENGTH: 79
5466783-7

Query Match 24.7%; Score 186; DB 6; Length 79;
Best Local Similarity 50.0%; Pred. No. 2.4e-11;
Matches 28; Conservative 13; Mismatches 15; Indels 0; Gaps 0;
Qy 73 RKDICSMPQEAGPCLASIPHWYNNKTKICSEFYGGCGGNNNNFQTEAICLVTC 128
:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||
Db 4 KRDICLPPEQGPCKGRIPRYFYNPASRMCSFYGGCKGNKNNFKTKAECVCRACR 59

RESULT 9
5466783-7
; Patent No. 5466783
; APPLICANT: Wun, Tze-Chain; Kretzmer, Kuniko K.; Broze, George J. Jr.
; TITLE OF INVENTION: HUMAN TISSUE FACTOR INHIBITOR
; NUMBER OF SEQUENCES: 26
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/93,285
; FILING DATE: 15-JUL-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 566,280
; FILING DATE: 13-AUG-1990
; APPLICATION NUMBER: 123,753
; FILING DATE: 23-NOV-1987
; APPLICATION NUMBER: 77,366
; FILING DATE: 23-JUL-1987
; SEQ ID NO: 7
; LENGTH: 79
5466783-7

Query Match 24.7%; Score 186; DB 6; Length 79;
Best Local Similarity 50.0%; Pred. No. 2.4e-11;
Matches 28; Conservative 13; Mismatches 15; Indels 0; Gaps 0;

Qy 73 RKDICTMPQEAGPCLASIPHWYNNKTKICSEFYGGCGGNNNFOTEIACLVTCK 128
:::|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:
Db 4 KRDIQLPPEOGCPKGIRPYFYNPASRNCESEFYGGCGKNNFFTKAEVCACR 59

RESULT 10
US-08-358-160-71
; Sequence 71, Application US/08358160
; Patent No. 5663143
; GENERAL INFORMATION:
; APPLICANT: LEY, Arthur C.
; APPLICANT: LADNER, Robert C.
; APPLICANT: GUTERMAN, Sonia K.
; APPLICANT: ROBERTS, Bruce L.
; APPLICANT: MARKLAND, William
; APPLICANT: KENT, Rachel B.
; TITLE OF INVENTION: ENGINEERED HUMAN-DERIVED KUNITZ
; TITLE OF INVENTION: DOMAINS THAT INHIBIT HUMAN NEUTROPHIL ELASTASE
; NUMBER OF SEQUENCES: 234
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W. Suite 300
; CITY: Washington
; STATE: District of Columbia
; COUNTRY: USA
; ZIP: 20004

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, COMPUTER READABLE FORM:
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, MEDIUM TYPE: Floppy disk
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, COMPUTER: IBM PC compatible
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, OPERATING SYSTEM: PC-DOS/MS-DOS
,
, SOFTWARE: Patent In Release #1.0, Version #1.25
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, CURRENT APPLICATION DATA:
,
, APPLICATION NUMBER: US/08/358,160
,
, FILING DATE: 16-DEC-1994
,
, CLASSIFICATION: 514
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,
, PRIOR APPLICATION DATA: US 08/133,031
, APPLICATION NUMBER: US 08/133,031
, FILING DATE: 13-OCT-1993
, PRIOR APPLICATION DATA:
, APPLICATION NUMBER: US 08/009,319
, FILING DATE: 26-JAN-1993
, PRIOR APPLICATION DATA:
, APPLICATION NUMBER: US 07/664,989
, FILING DATE: 01-MAR-1991
, PRIOR APPLICATION DATA:
, APPLICATION NUMBER: US 07/487,063
, FILING DATE: 02-MAR-1990
, PRIOR APPLICATION DATA:
, APPLICATION NUMBER: US 07/240,160
, FILING DATE: 02-SEP-1988
```

FILING DATE: 02-SEP-1988
 ATTORNEY/AGENT INFORMATION:
 NAME: Cooper, Iver P.
 REGISTRATION NUMBER: 28,005
 REFERENCE/DOCKET NUMBER: LEY=1
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 202-628-5197
 TELEFAX: 202-737-3528
 TELEX: 248633
 INFORMATION FOR SEQ ID NO: 71:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 58 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-358-160-71

Query Match 23.5%; Score 177; DB 1; Length 58;
Best Local Similarity 56.4%; Pred. No. 1.4e-10;

	Matches	31: Conservative	5: Mismatches	19: Indels	0: Gaps	0:
Qy	73	RKDICSMPOAGPCLASIPHHWYKTKICSEFIYGCQCGNNNNFOTEACLVT	C	127		
Db	1	RPDFCLLPAAETGPGCRAMIPRFYVNAKSGKCEPIYGCQCGNNNNFTEECR	C	55		

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RESULT 11
US-09-358-569D-13
; Sequence 13, Application US/09358569D
; Patent No. 6294648
; GENERAL INFORMATION:
; APPLICANT: Delaria, Kathy
; APPLICANT: Rocznia, Steve
; APPLICANT: Davies, Christopher
; TITLE OF INVENTION: Protein Having Proteinase Inhibitor Activity
; FILE REFERENCE: MSB-7259
; CURRENT APPLICATION NUMBER: US/09/358,569D
; CURRENT FILING DATE: 1999-07-20
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 13
; LENGTH: 43
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Artificial
; OTHER INFORMATION: sequence derived from EST database
US-09-358-569D-13

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Query Match 23.2%; Score 175; DB 3; Length 43;
Best Local Similarity 69.0%; Pred. NO. 1.6e-10;
Matches 29; Conservative 4; Mismatches 9; Indels

QY 87 LASIPHWNNKTKIKCSBFYGGCGGNNNNFQTAICLVCTK 128
|||||
1 LAFTLHWYDKDNTCSMEVYGGCGGNNNNFQSKANCLNTCK 42
|||||

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RESULT 12
US-09-358-569D-9
; Sequence 9, Application US/09358569D
; Patent No. 6294648
; GENERAL INFORMATION:
; APPLICANT: Delaria, Kathy
; APPLICANT: Roczniak, Steve
; APPLICANT: Davies, Christopher
; TITLE OF INVENTION: Protein Having Proteinase Inhibitor Activity
; FILE REFERENCE: MSB-7259
; CURRENT APPLICATION NUMBER: US/09/358,569D
; CURRENT FILING DATE: 1999-07-20
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 9
; LENGTH: 54
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:derived from
; OTHER INFORMATION: EST sequence database
US-09-358-569D-9

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Query Match      23.2%; Score 175; DB 3; Length 54;
Best Local Similarity 50.0%; Pred. No. 2e-10;
Matches 27; Conservative 10; Mismatches 17; Indels 0; Gaps 0;

Qy 75 DICSMPOEAGPCLASIPHWYNNKTKICSFYICGGCGNNNNFQTEAICLVTC 128
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1 DICOLPOARCEKAAALLRYFNSTSNACBPETVGGCGNNNNFETTEMCLURIC 54
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

```

RESULT 13
US-08-358-160-123


```
; APPLICANT: LADNER, Robert C.
; APPLICANT: GUTERMAN, Sonia K.
; APPLICANT: ROBERTS, Bruce L.
; APPLICANT: MARKLAND, William
; APPLICANT: KENT, Rachel B.
; TITLE OF INVENTION: ENGINEERED HUMAN-DERIVED KUNITZ
; TITLE OF INVENTION: DOMAINS THAT INHIBIT HUMAN NEUTROPHIL ELASTASE
; NUMBER OF SEQUENCES: 234
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W. Suite 300
; CITY: Washington
; STATE: District of Columbia
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/358,160
; FILING DATE: 16-DEC-1994
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/133,031
; FILING DATE: 13-OCT-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/009,319
; FILING DATE: 26-JAN-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/664,989
; FILING DATE: 01-MAR-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/487,063
; FILING DATE: 02-MAR-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/240,160
; FILING DATE: 02-SEP-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Cooper, Iver P.
; REGISTRATION NUMBER: 28,005
; REFERENCE/DOCKET NUMBER: LEY=1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; TELEX: 248633
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 58 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-358-160-18

Query Match      23.0%; Score 173; DB 1; Length 58;
Best Local Similarity 50.0%; Pred. No. 3.4e-10;
Matches 28; Conservative 7; Mismatches 21; Indels 0; Gaps 0;

Qy 73 RKDSCMPQEGAGPCLASIPHWYNNKTKICSEFYGGCGGNNNFQTEAICLVTK 128
Db 1 RPDFQLGYSAGPCVAMPFRIFYNGASMACQTFVYGGCGMGNFVTEKDCIQCR 56

RESULT 16
5466783-4
;Patent No. 5466783
; APPLICANT: Wun, Tze-Chein.;Kretzmer, Kuniko K.;Broze,
;George J. Jr.
; TITLE OF INVENTION: HUMAN TISSUE FACTOR INHIBITOR
; NUMBER OF SEQUENCES: 26
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US 08/009,319
; FILING DATE: 26-JAN-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/664,989
; FILING DATE: 01-MAR-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/487,063
; FILING DATE: 02-MAR-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/240,160
; FILING DATE: 02-SEP-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Cooper, Iver P.
; REGISTRATION NUMBER: 28,005
; REFERENCE/DOCKET NUMBER: LEY=1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; TELEX: 248633
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 58 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-358-160-18
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; APPLICATION NUMBER: US/08/93,285
; FILING DATE: 15-JUL-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 566,280
; FILING DATE: 13-AUG-1990
; APPLICATION NUMBER: 123,753
; FILING DATE: 23-NOV-1987
; APPLICATION NUMBER: 77,366
; FILING DATE: 23-JUL-1987
; SEQ ID NO:4:
; LENGTH: 77
5466783-4

Query Match      22.4%; Score 169; DB 6; Length 77;
Best Local Similarity 46.3%; Pred. No. 1.1e-09;
Matches 25; Conservative 12; Mismatches 17; Indels 0; Gaps 0;

Qy 75 DCSMPQEGAGPCLASIPHWYNNKTKICSEFYGGCGGNNNFQTEAICLVTK 128
Db 6 DLQQLPQARGFCKAALLRYFYBSTSNACEPFTYGGCGGNNNFETTEMCLRICE 59

RESULT 17
5466783-4
;Patent No. 5466783
; APPLICANT: Wun, Tze-Chein.;Kretzmer, Kuniko K.;Broze,
;George J. Jr.
; TITLE OF INVENTION: HUMAN TISSUE FACTOR INHIBITOR
; NUMBER OF SEQUENCES: 26
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/93,285
; FILING DATE: 15-JUL-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 566,280
; FILING DATE: 13-AUG-1990
; APPLICATION NUMBER: 123,753
; FILING DATE: 23-NOV-1987
; APPLICATION NUMBER: 77,366
; FILING DATE: 23-JUL-1987
; SEQ ID NO:4:
; LENGTH: 77
5466783-4

Query Match      22.4%; Score 169; DB 6; Length 77;
Best Local Similarity 46.3%; Pred. No. 1.1e-09;
Matches 25; Conservative 12; Mismatches 17; Indels 0; Gaps 0;

Qy 75 DCSMPQEGAGPCLASIPHWYNNKTKICSEFYGGCGGNNNFQTEAICLVTK 128
Db 6 DLQQLPQARGFCKAALLRYFYBSTSNACEPFTYGGCGGNNNFETTEMCLRICE 59

RESULT 18
US-09-910-430-8
; Sequence 8, Application US/09910430
; Patent No. 6794166
; GENERAL INFORMATION:
; APPLICANT: Godfroi, Edmond
; APPLICANT: Bollen, Alex
; APPLICANT: Leboulle, Gerard
; TITLE OF INVENTION: IDENTIFICATION AND MOLECULAR CHARACTERIZATION OF
; TITLE OF INVENTION: PROTEINS, EXPRESSED IN THE IXODES RICINUS SALIVARY
; TITLE OF INVENTION: GLANDS
; FILE REFERENCE: VANM229.001CPI
; CURRENT APPLICATION NUMBER: US/09/910,430
; CURRENT FILING DATE: 2001-07-19
; PRIOR APPLICATION NUMBER: PCT/BE00/00061
; PRIOR FILING DATE: 2000-06-06
; PRIOR APPLICATION NUMBER: GB 9913425.6
; PRIOR FILING DATE: 1999-06-09
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 8
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; LENGTH: 86
; TYPE: PRT
; ORGANISM: Ixodes ricinus
US-09-910-430-8

Query Match      22.3%; Score 168; DB 4; Length 86;
Best Local Similarity 48.1%; Pred. No. 1.6e-09;
Matches 25; Conservative 11; Mismatches 16; Indels 0; Gaps 0;

QY 77 CSMQPEAGPCLASIPHHWYKTKICSEFIYGGCGNNNNFOTEICLVTK 128
DB 31 CKLPDDGCRARISYFDRKTKCKEYFGCGEGNENNFENITTCQECR 82

; MOLECULE TYPE: protein
US-08-358-160-10

Query Match      22.2%; Score 167; DB 1; Length 58;
Best Local Similarity 50.0%; Pred. No. 1.3e-09;
Matches 28; Conservative 6; Mismatches 22; Indels 0; Gaps 0;

QY 73 RKDTCMPQEGAGPCLASIPHHWYKTKICSEFIYGGCGNNNNFOTEICLVTK 128
DB 1 RPDFCQLGYSAGPCVAMPFRYFYNGTSMACETFYGGCMGNGNMFVTEKCLQTCR 56

RESULT 20
US-08-358-160-11
; Sequence 11, Application US/08358160
; Patent No. 5663143
; GENERAL INFORMATION:
; APPLICANT: LEY, Arthur C.
; APPLICANT: LADNER, Robert C.
; APPLICANT: GUTERMAN, Sonia K.
; APPLICANT: ROBERTS, Bruce L.
; APPLICANT: MARKLAND, William
; APPLICANT: KENT, Rachel B.
; TITLE OF INVENTION: ENGINEERED HUMAN-DERIVED KUNITZ
; NUMBER OF SEQUENCES: 234
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W. Suite 300
; CITY: Washington
; STATE: District of Columbia
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/358,160
; FILING DATE: 16-DEC-1994
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/133,031
; FILING DATE: 13-OCT-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/009,319
; FILING DATE: 26-JAN-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/664,989
; FILING DATE: 01-MAR-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/487,063
; FILING DATE: 02-MAR-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/240,160
; FILING DATE: 02-SEP-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Cooper, Iver P.
; REGISTRATION NUMBER: 28,005
; REFERENCE/DOCKET NUMBER: LEY=1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; TELEX: 248633
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 58 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-358-160-11
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; APPLICANT: ROBERTS, Bruce L.
; APPLICANT: MARKLAND, William
; APPLICANT: KENT, Rachel B.
; TITLE OF INVENTION: ENGINEERED HUMAN-DERIVED KUNITZ
; TITLE OF INVENTION: DOMAINS THAT INHIBIT HUMAN NEUTROPHIL ELASTASE
; NUMBER OF SEQUENCES: 234
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W. Suite 300
; CITY: Washington
; STATE: District of Columbia
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/358,160
; FILING DATE: 16-DEC-1994
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/133,031
; FILING DATE: 13-OCT-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/009,319
; FILING DATE: 26-JAN-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/664,989
; FILING DATE: 01-MAR-1991
; APPLICATION NUMBER: US 07/487,063
; FILING DATE: 02-MAR-1990
; APPLICATION NUMBER: US 07/240,160
; FILING DATE: 02-SEP-1988
; NAME: Cooper, Iver P.
; REGISTRATION NUMBER: 28,005
; REFERENCE/DOCKET NUMBER: LEY=1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; TELEX: 248633
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 58 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-358-160-1
;
; Query Match 22.0%; Score 166; DB 1; Length 58;
; Best Local Similarity 47.3%; Pred. No. 1.7e-09;
; Matches 26; Conservative 8; Mismatches 21; Indels 0; Gaps 0;
;
; QY 73 RKDICSMPQEGPCLASIPHWYNNKTKICSEFYGGCGGNNNFQTEAICLVTC 127
; DB 1 RPDFCLEPYTGPCVAMPFRFYNAKAGLCQTFVYGGCGGNGNFKSABDCMRTC 55
;
; RESULT 24
; US-08-358-160-15
; Sequence 15, Application US/08358160
; Patent No. 5663143
; GENERAL INFORMATION:
; APPLICANT: LEY, Arthur C.
; APPLICANT: LADNER, Robert C.
; APPLICANT: GUTERMAN, Sonia K.
; APPLICANT: ROBERTS, Bruce L.
; APPLICANT: MARKLAND, William
```

```
; APPLICANT: KENT, Rachel B.
; TITLE OF INVENTION: ENGINEERED HUMAN-DERIVED KUNITZ
; TITLE OF INVENTION: DOMAINS THAT INHIBIT HUMAN NEUTROPHIL ELASTASE
; NUMBER OF SEQUENCES: 234
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W. Suite 300
; CITY: Washington
; STATE: District of Columbia
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/358,160
; FILING DATE: 16-DEC-1994
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/133,031
; FILING DATE: 13-OCT-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/009,319
; FILING DATE: 26-JAN-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/664,989
; FILING DATE: 01-MAR-1991
; APPLICATION NUMBER: US 07/487,063
; FILING DATE: 02-MAR-1990
; APPLICATION NUMBER: US 07/240,160
; FILING DATE: 02-SEP-1988
; NAME: Cooper, Iver P.
; REGISTRATION NUMBER: 28,005
; REFERENCE/DOCKET NUMBER: LEY=1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; TELEX: 248633
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 58 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-358-160-15
;
; Query Match 22.0%; Score 166; DB 1; Length 58;
; Best Local Similarity 48.2%; Pred. No. 1.7e-09;
; Matches 27; Conservative 8; Mismatches 21; Indels 0; Gaps 0;
;
; QY 73 RKDICSMPQEGPCLASIPHWYNNKTKICSEFYGGCGGNNNFQTEAICLVTC 128
; DB 1 KEDFCQLGYSAGPCVAMPFRFYNGTSMACETFFYGGCGGNGNFTVEKDCQTCR 56
;
; RESULT 25
; US-08-358-160-26
; Sequence 26, Application US/08358160
; Patent No. 5663143
; GENERAL INFORMATION:
; APPLICANT: LEY, Arthur C.
; APPLICANT: LADNER, Robert C.
; APPLICANT: GUTERMAN, Sonia K.
; APPLICANT: ROBERTS, Bruce L.
; APPLICANT: MARKLAND, William
; APPLICANT: KENT, Rachel B.
; TITLE OF INVENTION: ENGINEERED HUMAN-DERIVED KUNITZ
```

```
; TITLE OF INVENTION: DOMAINS THAT INHIBIT HUMAN NEUTROPHIL ELASTASE
; NUMBER OF SEQUENCES: 234
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W. Suite 300
; CITY: Washington
; STATE: District of Columbia
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/358,160
; FILING DATE: 16-DEC-1994
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/133,031
; FILING DATE: 13-OCT-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/009,319
; FILING DATE: 26-JAN-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/664,989
; FILING DATE: 01-MAR-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/487,063
; FILING DATE: 02-MAR-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/240,160
; FILING DATE: 02-SEP-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Cooper, Iver P.
; REGISTRATION NUMBER: 28,005
; REFERENCE/DOCKET NUMBER: LEY=1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; TELEX: 248633
; INFORMATION FOR SEQ ID NO: 26:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 58 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-358-160-26

Query Match 22.0%; Score 166; DB 1; Length 58;
Best Local Similarity 47.3%; Pred. No. 1.7e-09;
Matches 26; Conservative 8; Mismatches 21; Indels 0; Gaps 0;

Qy 73 RKDTCSPQEQAGPCLASIPHWYNNKTKICSEFYGGCGQNNNFQTEAICLVTC 127
Db 1 RPDFCLEPPYTGPCIAFPFRFYNAKAGLCQTFVYGGCMGNGNFKSAEDCMRTC 55

RESULT 26
US-08-358-160-27
; Sequence 27, Application US/08358160
; Patent No. 5663143
; GENERAL INFORMATION:
; APPLICANT: LEY, Arthur C.
; APPLICANT: LADNER, Robert C.
; APPLICANT: GUTERMAN, Sonia K.
; APPLICANT: ROBERTS, Bruce L.
; APPLICANT: MARKLAND, William
; APPLICANT: KENT, Rachel B.
; TITLE OF INVENTION: ENGINEERED HUMAN-DERIVED KUNITZ
; TITLE OF INVENTION: DOMAINS THAT INHIBIT HUMAN NEUTROPHIL ELASTASE
; NUMBER OF SEQUENCES: 234
```

```
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W. Suite 300
; CITY: Washington
; STATE: District of Columbia
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/358,160
; FILING DATE: 16-DEC-1994
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/133,031
; FILING DATE: 13-OCT-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/009,319
; FILING DATE: 26-JAN-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/664,989
; FILING DATE: 01-MAR-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/487,063
; FILING DATE: 02-MAR-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/240,160
; FILING DATE: 02-SEP-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Cooper, Iver P.
; REGISTRATION NUMBER: 28,005
; REFERENCE/DOCKET NUMBER: LEY=1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; TELEX: 248633
; INFORMATION FOR SEQ ID NO: 27:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 62 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-358-160-27

Query Match 22.0%; Score 166; DB 1; Length 62;
Best Local Similarity 47.3%; Pred. No. 1.8e-09;
Matches 26; Conservative 8; Mismatches 21; Indels 0; Gaps 0;

Qy 73 RKDTCSPQEQAGPCLASIPHWYNNKTKICSEFYGGCGQNNNFQTEAICLVTC 127
Db 5 RPDFCLEPPYTGPCIAFPFRFYNAKAGLCQTFVYGGCMGNGNFKSAEDCMRTC 59

RESULT 27
US-09-270-767-46540
; Sequence 46540, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 46540
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
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STREET:	3000 K Street, N.W., Suite 500	STREET:	3000 K Street, N.W., Suite 500
CITY:	Washington	CITY:	Washington
STATE:	D.C.	STATE:	D.C.
COUNTRY:	USA	COUNTRY:	USA
ZIP:	20007-5109	ZIP:	20007-5109
COMPUTER READABLE FORM:		COMPUTER READABLE FORM:	
MEDIUM TYPE:	Floppy disk	MEDIUM TYPE:	Floppy disk
COMPUTER:	IBM PC compatible	COMPUTER:	IBM PC compatible
OPERATING SYSTEM:	PC-DOS/MS-DOS	OPERATING SYSTEM:	PC-DOS/MS-DOS
SOFTWARE:	PatentIn Release #1.0, Version #1.30	SOFTWARE:	PatentIn Release #1.0, Version #1.30
APPLICATION DATA:		APPLICATION DATA:	
APPLICATION NUMBER:	US/08/829,876	APPLICATION NUMBER:	US/08/829,876
FILING DATE:		FILING DATE:	
CLASSIFICATION:		CLASSIFICATION:	
PRIOR APPLICATION DATA:		PRIOR APPLICATION DATA:	
APPLICATION NUMBER:	US 08/436,555	APPLICATION NUMBER:	US 08/436,555
FILING DATE:	08-MAY-1995	FILING DATE:	08-MAY-1995
ATTORNEY/AGENT INFORMATION:		ATTORNEY/AGENT INFORMATION:	
NAME:	Pelto, Don J.	NAME:	Bent, Stephen
REGISTRATION NUMBER:	33,754	REGISTRATION NUMBER:	29,768
REFERENCE/DOCKET NUMBER:	56324/106/SCNO	REFERENCE/DOCKET NUMBER:	056324/0106
TELECOMMUNICATION INFORMATION:		TELECOMMUNICATION INFORMATION:	
TELEPHONE:	(202)672-5300	TELEPHONE:	(202)672-5300
TELEFAX:	(202)672-5399	TELEFAX:	(202)672-5399
TELEX:	904136	TELEX:	904136
INFORMATION FOR SEQ ID NO: 214:		INFORMATION FOR SEQ ID NO: 214:	
SEQUENCE CHARACTERISTICS:		SEQUENCE CHARACTERISTICS:	
LENGTH:	61 amino acids	LENGTH:	61 amino acids
TYPE:	amino acid	TYPE:	amino acid
STRANDEDNESS:	single	STRANDEDNESS:	single
TOPOLOGY:	linear	TOPOLOGY:	linear
MOLECULE TYPE:	protein	MOLECULE TYPE:	protein
US-08-829-876-214		US-08-829-876-214	
Query Match	21.8%; Score 164; DB 2; Length 61;	Query Match	21.8%; Score 164; DB 3; Length 61;
Best Local Similarity	46.3%; Pred. No. 2.8e-09;	Best Local Similarity	46.3%; Pred. No. 2.8e-09;
Matches	25; Conservative 9; Mismatches 20; Indels 0; Gaps 0;	Matches	25; Conservative 9; Mismatches 20; Indels 0; Gaps 0;
QY	74 KDICSMPOEAGPCLASIPHWYKTKICSEFIYGGCGNNNFQTEAICLVTC 127	QY	74 KDICSMPOEAGPCLASIPHWYKTKICSEFIYGGCGNNNFQTEAICLVTC 127
Db	4 REVCSQAETGFCRALIPRWYFDVTEGKCAPFFYGGCGNNRNFDTTEYCMVNC 57	Db	4 REVCSQAETGFCRAATQHWFVDTGKCAPFFYGGCGNNRNFDTTEYCMVNC 57
RESULT 33		RESULT 34	
US-09-234-874A-211		US-09-234-874A-214	
Sequence 211, Application US/09234874A		Sequence 214, Application US/09234874A	
Patent No. 6376648		Patent No. 6376648	
GENERAL INFORMATION:		GENERAL INFORMATION:	
APPLICANT:	White, Tyler R.	APPLICANT:	White, Tyler R.
Damm, Deborah		Damm, Deborah	
Lesikar, David D.		Lesikar, David D.	
McFadden, Kathleen		McFadden, Kathleen	
Garrick, Brett L.		Garrick, Brett L.	
TITLE OF INVENTION:	PROTEASE INHIBITOR PEPTIDES	TITLE OF INVENTION:	PROTEASE INHIBITOR PEPTIDES
NUMBER OF SEQUENCES:	228	NUMBER OF SEQUENCES:	228
CORRESPONDENCE ADDRESS:		CORRESPONDENCE ADDRESS:	
ADDRESS:	Foley & Lardner	ADDRESS:	Foley & Lardner
STREET:	3000 K Street, N.W., Suite 500	STREET:	3000 K Street, N.W., Suite 500
CITY:	Washington	CITY:	Washington
STATE:	D.C.	STATE:	D.C.
COUNTRY:	USA	COUNTRY:	USA
ZIP:	20007-5109	ZIP:	20007-5109
COMPUTER READABLE FORM:		COMPUTER READABLE FORM:	
MEDIUM TYPE:	Floppy disk	MEDIUM TYPE:	Floppy disk
COMPUTER:	IBM PC compatible	COMPUTER:	IBM PC compatible
OPERATING SYSTEM:	PC-DOS/MS-DOS	OPERATING SYSTEM:	PC-DOS/MS-DOS
SOFTWARE:	PatentIn Release #1.0, Version #1.30	SOFTWARE:	PatentIn Release #1.0, Version #1.30
APPLICATION DATA:		APPLICATION DATA:	
APPLICATION NUMBER:	US/09/234,874A	APPLICATION NUMBER:	US/09/234,874A
FILING DATE:	11-Jun-2001	FILING DATE:	11-Jun-2001
PRIOR APPLICATION DATA:		PRIOR APPLICATION DATA:	
APPLICATION NUMBER:	08/436,555	APPLICATION NUMBER:	08/436,555
FILING DATE:	08-MAY-1995	FILING DATE:	08-MAY-1995
ATTORNEY/AGENT INFORMATION:		ATTORNEY/AGENT INFORMATION:	
NAME:	Bent, Stephen	NAME:	Bent, Stephen
REGISTRATION NUMBER:	29,768	REGISTRATION NUMBER:	29,768
REFERENCE/DOCKET NUMBER:	056324/0106	REFERENCE/DOCKET NUMBER:	056324/0106
TELECOMMUNICATION INFORMATION:		TELECOMMUNICATION INFORMATION:	
TELEPHONE:	(202)672-5300	TELEPHONE:	(202)672-5300
TELEFAX:	(202)672-5399	TELEFAX:	(202)672-5399
TELEX:	904136	TELEX:	904136
INFORMATION FOR SEQ ID NO: 214:		INFORMATION FOR SEQ ID NO: 214:	
SEQUENCE CHARACTERISTICS:		SEQUENCE CHARACTERISTICS:	
LENGTH:	61 amino acids	LENGTH:	61 amino acids
TYPE:	amino acid	TYPE:	amino acid
STRANDEDNESS:	single	STRANDEDNESS:	single
TOPOLOGY:	linear	TOPOLOGY:	linear
MOLECULE TYPE:	protein	MOLECULE TYPE:	protein
SEQUENCE DESCRIPTION:	SEQ ID NO: 214:	SEQUENCE DESCRIPTION:	SEQ ID NO: 214:

STREET: Suite 300
CITY: Washington,
STATE: DC
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORDPERFECT 4.2
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/664,989B
FILING DATE: 19910301
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US89/03731
FILING DATE: 01-SEP-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/487,063
FILING DATE: 02-MAR-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/240,160
FILING DATE: 02-SEP-1988
ATTORNEY/AGENT INFORMATION:
NAME: Cooper, Iver P.
REGISTRATION NUMBER: 28005
REFERENCE/DOCKET NUMBER: LADNER 7
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
INFORMATION FOR SEQ ID NO: 84:
SEQUENCE CHARACTERISTICS:
LENGTH: 58 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear
MOLECULE TYPE: protein
US-07-664-989B-84

Query Match 21.6%; Score 163; DB 1; Length 58;
Best Local Similarity 47.3%; Pred. No. 3.3e-09;
Matches 26; Conservative 8; Mismatches 21; Indels 0; Gaps 0;

QY 73 RKDICSMPQAGPCLASIPHWYKTKICSEFIYGGCGGNNNFQTEAICLVTC 127
Db 1 RPDFCLEPPYTGPCVAMPFRFYNAKAGLCQTFMYGGCGKGNFKSAEDCMRTC 55

RESULT 38
US-08-358-160-12
Sequence 12, Application US/08358160
Patent No. 5663143
GENERAL INFORMATION:
APPLICANT: LEY, Arthur C.
APPLICANT: LADNER, Robert C.
APPLICANT: GUTERMAN, Sonia K.
APPLICANT: ROBERTS, Bruce L.
APPLICANT: MARKLAND, William
APPLICANT: KENT, Rachel B.
TITLE OF INVENTION: ENGINEERED HUMAN-DERIVED KUNITZ
NUMBER OF SEQUENCES: 234
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NETMARK
STREET: 419 Seventh Street, N.W. Suite 300
CITY: Washington
STATE: District of Columbia
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/358,160
FILING DATE: 16-DEC-1994
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/133,031
FILING DATE: 13-OCT-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/009,319
FILING DATE: 26-JAN-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/664,989
FILING DATE: 01-MAR-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/487,063
FILING DATE: 02-MAR-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/240,160
FILING DATE: 02-SEP-1988
ATTORNEY/AGENT INFORMATION:
NAME: Cooper, Iver P.
REGISTRATION NUMBER: 28,005
REFERENCE/DOCKET NUMBER: LEY=1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
TELEX: 248633
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 58 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-358-160-12

Query Match 21.6%; Score 163; DB 1; Length 58;
Best Local Similarity 48.2%; Pred. No. 3.3e-09;
Matches 27; Conservative 6; Mismatches 23; Indels 0; Gaps 0;

QY 73 RKDICSMPQAGPCLASIPHWYKTKICSEFIYGGCGGNNNFQTEAICLVTC 128
Db 1 RPDFCQLGYSTGPCVAMPFRFYNGTSMACETFOYGGCMGNGNFVTEKDCLOICR 56

RESULT 39
US-08-358-160-61
Sequence 61, Application US/08358160
Patent No. 5663143
GENERAL INFORMATION:
APPLICANT: LEY, Arthur C.
APPLICANT: LADNER, Robert C.
APPLICANT: GUTERMAN, Sonia K.
APPLICANT: ROBERTS, Bruce L.
APPLICANT: MARKLAND, William
APPLICANT: KENT, Rachel B.
TITLE OF INVENTION: ENGINEERED HUMAN-DERIVED KUNITZ
NUMBER OF SEQUENCES: 234
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NETMARK
STREET: 419 Seventh Street, N.W. Suite 300
CITY: Washington
STATE: District of Columbia
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/358,160

; FILING DATE: 16-DEC-1994
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/133,031
; FILING DATE: 13-OCT-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/009,319
; FILING DATE: 26-JAN-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/664,989
; FILING DATE: 01-MAR-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/487,063
; FILING DATE: 02-MAR-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/240,160
; FILING DATE: 02-SEP-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Cooper, Iver P.
; REGISTRATION NUMBER: 28,005
; REFERENCE/DOCKET NUMBER: LEV=1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; TELEX: 248633
; INFORMATION FOR SEQ ID NO: 61:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 58 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-358-160-61

Query Match 21.6%; Score 163; DB 1; Length 58;
Best Local Similarity 47.3%; Pred. No. 3.3e-09;
Matches 26; Conservative 8; Mismatches 21; Indels 0; Gaps 0;

Qy 73 RKDTCSPQEAAGPCLASIPHWYNNKTKICSEFYGGCGGNNNNFOTEAIICLVTC 127
Db 1 RPDFCLEPPYTGPCVAMPFRIFYNAKAGLCQTFWYGGCGGNNNFKAEDCMRTC 55

RESULT 40
US-08-463-155A-56
; Sequence 56, Application US/08463155A
; Patent No. 5780265
; GENERAL INFORMATION:
; APPLICANT: Dennis, Mark S.
; APPLICANT: Lazarus, Robert A.
; TITLE OF INVENTION: KUNITZ TYPE PLASMA KALLIKREIN INHIBITORS
; NUMBER OF SEQUENCES: 72
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/463,155A
; FILING DATE: 05-Jun-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Kubinec, Jeffrey S.
; REGISTRATION NUMBER: 36,575
; REFERENCE/DOCKET NUMBER: P0944
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/952-8228
; TELEFAX: 415/952-8228
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 56:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 58 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
; US-08-463-432B-56

Query Match 21.6%; Score 163; DB 1; Length 58;
Best Local Similarity 48.1%; Pred. No. 3.3e-09;
Matches 26; Conservative 8; Mismatches 20; Indels 0; Gaps 0;

Qy 74 KDICSMPEQAGPCLASIPHWYNNKTKICSEFYGGCGGNNNNFOTEAIICLVTC 127
Db 2 REVCSQAEDGPCRAAIPRWYFDVTGKCAFFIYGGCGGNRNNFDTEEYCAAVC 55

RESULT 42
US-08-676-124-69
; Sequence 69, Application US/08676124
; Patent No. 6010880
; GENERAL INFORMATION:

; TELEPHONE: 415/225-8228
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 56:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 58 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
; US-08-463-155A-56

Query Match 21.6%; Score 163; DB 1; Length 58;
Best Local Similarity 48.1%; Pred. No. 3.3e-09;
Matches 26; Conservative 8; Mismatches 20; Indels 0; Gaps 0;

Qy 74 KDICSMPEQAGPCLASIPHWYNNKTKICSEFYGGCGGNNNNFOTEAIICLVTC 127
Db 2 REVCSQAEDGPCRAAIPRWYFDVTGKCAFFIYGGCGGNRNNFDTEEYCAAVC 55

RESULT 41
US-08-463-432B-56
; Sequence 56, Application US/08463432B
; Patent No. 5786328
; GENERAL INFORMATION:
; APPLICANT: Dennis, Mark S.
; APPLICANT: Lazarus, Robert A.
; TITLE OF INVENTION: KUNITZ TYPE PLASMA KALLIKREIN INHIBITORS
; NUMBER OF SEQUENCES: 72
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/463,432B
; FILING DATE: 05-Jun-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Kubinec, Jeffrey S.
; REGISTRATION NUMBER: 36,575
; REFERENCE/DOCKET NUMBER: P0944-2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/225-8228
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 56:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 58 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
; US-08-463-432B-56

Query Match 21.6%; Score 163; DB 1; Length 58;
Best Local Similarity 48.1%; Pred. No. 3.3e-09;
Matches 26; Conservative 8; Mismatches 20; Indels 0; Gaps 0;

Qy 74 KDICSMPEQAGPCLASIPHWYNNKTKICSEFYGGCGGNNNNFOTEAIICLVTC 127
Db 2 REVCSQAEDGPCRAAIPRWYFDVTGKCAFFIYGGCGGNRNNFDTEEYCAAVC 55

RESULT 42
US-08-676-124-69
; Sequence 69, Application US/08676124
; Patent No. 6010880
; GENERAL INFORMATION:

APPLICANT: MARKLAND, William
APPLICANT: LADNER, Robert Charles
TITLE OF INVENTION: INHIBITORS OF HUMAN PLASMIN DERIVED
TITLE OF INVENTION: FROM FROM THE KUNITZ DOMAINS
NUMBER OF SEQUENCES: 137
CORRESPONDENCE ADDRESS:
ADDRESSEE: Browdy and Neimark
STREET: 419 Seventh Street N.W., Ste. 300
CITY: Washington
STATE: D.C.
COUNTRY: United States of America
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/676,124
FILING DATE:
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/00298
FILING DATE: 11-JAN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/179,658
FILING DATE: 11-JAN-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/208,265
FILING DATE: 10-MAR-1994
ATTORNEY/AGENT INFORMATION:
NAME: COOPER, IVER P.
REGISTRATION NUMBER: 28,005
REFERENCE/DOCKET NUMBER: MARKLAND=3B
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
INFORMATION FOR SEQ ID NO: 69:
SEQUENCE CHARACTERISTICS:
LENGTH: 58 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-676-124-69

Query Match 21.6%; Score 163; DB 3; Length 58;
Best Local Similarity 47.2%; Pred. No. 3.3e-09;
Matches 25; Conservative 8; Mismatches 20; Indels 0; Gaps 0;

QY 75 DICSMPQAGPCLASIPHWYNNKTKICSEFYGGCGGNNNNFQTEAICLVTC 127
Db 3 DICKLPKDTGPRARFDKWDYDPTKSCFEFVYGGCGGNNKFGSQKECKVC 55

RESULT 43
US-09-414-878-69
Sequence 69, Application US/09414878
Patent No. 6071723
GENERAL INFORMATION:
APPLICANT: DYAX CORP
APPLICANT: MARKLAND, William
APPLICANT: LADNER, Robert C
TITLE OF INVENTION: Inhibitors of Human Plasmin Derived
TITLE OF INVENTION: From The Kunitz Domains
NUMBER OF SEQUENCES: 139
CORRESPONDENCE ADDRESS:
ADDRESSEE: Yankwich & Associates
STREET: 130 Bishop Allen Drive
CITY: Cambridge
STATE: Massachusetts
COUNTRY: USA
ZIP: 02139

COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5-inch diskette
COMPUTER: IBM PC compatible
OPERATING SYSTEM: Microsoft Windows 98
SOFTWARE: Microsoft Word 97 SR-1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/414,878
FILING DATE: (concurrently herewith)
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/240,136
FILING DATE: 29-JAN-1999
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/676,124
FILING DATE: 07-JAN-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/00298
FILING DATE: 11-JAN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/208,265
FILING DATE: 10-MAR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/179,685
FILING DATE: 11-JAN-1994
ATTORNEY/AGENT INFORMATION:
NAME: YANKWICH, Leon R
REGISTRATION NUMBER: 30,237
NAME: ZWICKER, Kenneth P
REGISTRATION NUMBER: 43,310
REFERENCE/DOCKET NUMBER: DYX-007.2P US-2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-491-4343
TELEFAX: 617-491-8801
INFORMATION FOR SEQ ID NO: 69:
SEQUENCE CHARACTERISTICS:
LENGTH: 58 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-414-878-69

Query Match 21.6%; Score 163; DB 3; Length 58;
Best Local Similarity 47.2%; Pred. No. 3.3e-09;
Matches 25; Conservative 8; Mismatches 20; Indels 0; Gaps 0;

QY 75 DICSMPQAGPCLASIPHWYNNKTKICSEFYGGCGGNNNNFQTEAICLVTC 127
Db 3 DICKLPKDTGPRARFDKWDYDPTKSCFEFVYGGCGGNNKFGSQKECKVC 55

RESULT 44
US-09-240-136-69
Sequence 69, Application US/09240136
Patent No. 6103499
GENERAL INFORMATION:
APPLICANT: DYAX CORP
APPLICANT: MARKLAND, William
APPLICANT: LADNER, Robert C
TITLE OF INVENTION: Inhibitors of Human Plasmin Derived
TITLE OF INVENTION: From The Kunitz Domains
NUMBER OF SEQUENCES: 139
CORRESPONDENCE ADDRESS:
ADDRESSEE: Yankwich & Associates
STREET: 130 Bishop Allen Drive
CITY: Cambridge
STATE: Massachusetts
COUNTRY: USA
ZIP: 02139
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5-inch diskette
COMPUTER: IBM PC compatible
OPERATING SYSTEM: Microsoft Windows 98

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; SOFTWARE: Microsoft Word 97 SR-1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/240.136
; FILING DATE: (concurrently herewith)
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/676,124
; FILING DATE: 07-JAN-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/00298
; FILING DATE: 11-JAN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/208,265
; FILING DATE: 10-MAR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/179,685
; FILING DATE: 11-JAN-1994
; NAME: YANKWICH, Leon R
; ATTORNEY/AGENT INFORMATION:
; REGISTRATION NUMBER: 30,237
; NAME: ZWICKER, Kenneth P
; REGISTRATION NUMBER: 43,310
; REFERENCE/DOCKET NUMBER: DYX-007.2P US-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-491-4343
; TELEFAX: 617-491-8801
; INFORMATION FOR SEQ ID NO: 69:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 58 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-240-136-69

Query Match 21.6%; Score 163; DB 3; Length 58;
Best Local Similarity 47.2%; Pred. No. 3.3e-09;
Matches 25; Conservative 8; Mismatches 20; Indels 0; Gaps 0;

Qy 75 DCSMPQAGCLASIPHWYNNKTKICSEFYGGCGQNNNFQTEAICLVTC 127
|||:::|||:::|||:::|||:::|||:::|||:::|||:::|||:::|||
Db 3 DICKLPKDTGPCRARFDKWKYDPNTKSCFEFVYGGCGGNENKFGSQKECKVC 55

RESULT 45
US-09-638-770A-69
; Sequence 69, Application US/09638770A
; Patent No. 6423498
; GENERAL INFORMATION:
; APPLICANT: DYAX CORP
; MARKLAND, William
; LADNER, Robert C
; TITLE OF INVENTION: Inhibitors of Human Plasmin Derived
; From The Kunitz Domains
; NUMBER OF SEQUENCES: 140
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Yankwich & Associates
; STREET: 130 Bishop Allen Drive
; CITY: Cambridge
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02139
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5-inch diskette
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: Microsoft Windows 98
; SOFTWARE: Microsoft Word 97 SR-1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/638,770A
; FILING DATE: 15-Aug-2000
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/676,124
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; FILING DATE: 07-JAN-1997
; APPLICATION NUMBER: PCT/US95/00298
; FILING DATE: 11-JAN-1995
; APPLICATION NUMBER: 08/208,265
; FILING DATE: 10-MAR-1994
; APPLICATION NUMBER: 08/179,685
; FILING DATE: 11-JAN-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: ZWICKER, Kenneth P
; REGISTRATION NUMBER: 43,310
; REFERENCE/DOCKET NUMBER: DYX-007.2P US-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-491-4343
; TELEFAX: 617-491-8801
; INFORMATION FOR SEQ ID NO: 69:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 58 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 69:
; US-09-638-770A-69

Query Match 21.6%; Score 163; DB 4; Length 58;
Best Local Similarity 47.2%; Pred. No. 3.3e-09;
Matches 25; Conservative 8; Mismatches 20; Indels 0; Gaps 0;

Qy 75 DCSMPQAGCLASIPHWYNNKTKICSEFYGGCGQNNNFQTEAICLVTC 127
|||:::|||:::|||:::|||:::|||:::|||:::|||:::|||:::|||
Db 3 DICKLPKDTGPCRARFDKWKYDPNTKSCFEFVYGGCGGNENKFGSQKECKVC 55

RESULT 46
US-08-829-876-180
; Sequence 180, Application US/08829876
; Patent No. 5962266
; GENERAL INFORMATION:
; APPLICANT: White, Tyler R.
; APPLICANT: Damm, Deborah
; APPLICANT: Lesikar, David D.
; APPLICANT: McFadden, Kathleen
; APPLICANT: Garrick, Brett L.
; TITLE OF INVENTION: PROTEASE INHIBITOR PEPTIDES
; NUMBER OF SEQUENCES: 228
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/829,876
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/436,555
; FILING DATE: 08-MAY-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Peltó, Don J.
; REGISTRATION NUMBER: 33,754
; REFERENCE/DOCKET NUMBER: 56324/106/SCNO
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 180:
```



```
;
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/234,874A
; FILING DATE: 11-Jun-2001
; APPLICATION DATA:
; APPLICATION NUMBER: 08/436,555
; FILING DATE: 08-MAY-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Bent, Stephen
; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 056324/0106
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 218:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 61 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 218:
US-09-234-874A-218

Query Match      21.6%; Score 163; DB 3; Length 61;
Best Local Similarity 46.3%; Pred. No. 3.5e-09;
Matches 25; Conservative 10; Mismatches 19; Indels 0; Gaps 0;

Qy 74 KDICSMPEAGPCLASIPHWYNNKTKICSEFIYGGCGGNNNNFQTEAICLVTC 127
Db 4 REVCSEQAESGFCRAAIYHWYFDVTEGKCAPFFYGGCGGNRRNFDTEYCMAVC 57

RESULT 50
US-09-234-873A-180
; Sequence 180, Application US/09234873A
; Patent No. 6613890
; GENERAL INFORMATION:
; APPLICANT: White, Tyler R.
; Damm, Deborah
; Lesikar, David D.
; McFadden, Kathleen
; Garrick, Brett L.
; TITLE OF INVENTION: PROTEASE INHIBITOR PEPTIDES
; NUMBER OF SEQUENCES: 228
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/234,873A
; FILING DATE: 21-Jan-1999
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/829,876
; FILING DATE: 02-APR-1997
; APPLICATION NUMBER: 08/436,555
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;
; FILING DATE: 08-MAY-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Bent, Stephen
; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 056324/0116
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 180:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 61 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 180:
US-09-234-873A-180

Query Match      21.6%; Score 163; DB 4; Length 61;
Best Local Similarity 46.3%; Pred. No. 3.5e-09;
Matches 25; Conservative 8; Mismatches 21; Indels 0; Gaps 0;

Qy 74 KDICSMPEAGPCLASIPHWYNNKTKICSEFIYGGCGGNNNNFQTEAICLVTC 127
Db 4 REVCSEQAETGPCRAGIPRWYFDVTEGKCAPFFYGGCGGNRRNFDTEYCMAVC 57

Search completed: September 21, 2005, 16:42:16
Job time : 29.9587 secs
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OM protein - protein search, using sw model

Run on: September 21, 2005, 16:33:14 ; Search time 81.9233 Seconds
(without alignments)
650.835 Million cell updates/sec

Title: US-10-807-204-1
Perfect score: 753
Sequence: 1 MGLSGLFILVFFILLGDIQ.....GNNNFQTEAICLVTCCKYH 131

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1826521 seqs, 407012169 residues

Total number of hits satisfying chosen parameters: 1826521

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Listing first 50 summaries

Database : Published Applications AA:*
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2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep.*
3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep.*
4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep.*
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13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep.*
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15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep.*
16: /cgn2_6/ptodata/2/pubpaa/US10D_PUBCOMB.pep.*
17: /cgn2_6/ptodata/2/pubpaa/US10E_PUBCOMB.pep.*
18: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep.*
19: /cgn2_6/ptodata/2/pubpaa/US11A_PUBCOMB.pep.*
20: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep.*
21: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*
22: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	753	100.0	131	16 US-10-807-204-1	Sequence 1, Appli
2	753	100.0	131	16 US-10-807-204-12	Sequence 12, Appl
3	731	97.1	131	16 US-10-807-204-15	Sequence 15, Appl
4	625	83.0	106	16 US-10-807-204-2	Sequence 2, Appli
5	551	73.2	98	16 US-10-807-204-9	Sequence 9, Appli
6	432	65.3	136	16 US-10-807-204-16	Sequence 16, Appl
7	467	62.0	133	9 US-09-853-161-75	Sequence 75, Appl
8	467	62.0	133	9 US-09-852-659A-75	Sequence 75, Appl
9	467	62.0	133	9 US-09-852-797-75	Sequence 75, Appl
10	467	62.0	133	15 US-10-058-993-75	Sequence 75, Appl
11	467	62.0	133	16 US-10-807-204-13	Sequence 13, Appl

12	404	53.7	86	17	US-10-480-988-21	Sequence 21, Appl
13	404	53.7	101	15	US-10-276-774-2606	Sequence 2606, Ap
14	401.5	53.3	117	9	US-09-852-659A-119	Sequence 119, App
15	401.5	53.3	117	15	US-10-058-993-120	Sequence 120, App
16	400	53.1	102	9	US-09-852-659A-120	Sequence 120, App
17	400	53.1	102	15	US-10-058-993-121	Sequence 121, App
18	398	52.9	134	16	US-10-807-204-14	Sequence 14, Appl
19	258	34.3	43	16	US-10-807-204-5	Sequence 5, Appli
20	236	31.3	58	16	US-10-361-997-5	Sequence 5, Appli
21	236	31.3	58	17	US-10-931-153-21	Sequence 21, Appl
22	219	29.1	51	15	US-10-058-993-118	Sequence 118, App
23	197	26.2	759	17	US-10-825-692-48	Sequence 48, Appl
24	184	24.4	64	10	US-09-896-095-160	Sequence 160, App
25	184	24.4	64	14	US-10-038-722-103	Sequence 103, App
26	184	24.4	64	15	US-10-115-134-17	Sequence 17, App
27	182.5	24.2	571	14	US-10-369-736-3	Sequence 3, Appli
28	182.5	24.2	571	14	US-10-369-736-49	Sequence 49, Appl
29	182.5	24.2	571	14	US-10-369-738-3	Sequence 3, Appli
30	182.5	24.2	571	14	US-10-369-738-49	Sequence 49, Appl
31	182.5	24.2	571	19	US-11-028-058-3	Sequence 3, Appli
32	182.5	24.2	571	19	US-11-028-058-49	Sequence 49, Appl
33	180	23.9	33	16	US-10-807-204-7	Sequence 7, Appli
34	180	23.9	33	16	US-10-807-204-10	Sequence 10, Appl
35	177	23.5	58	14	US-10-038-722-5	Sequence 5, Appli
36	175	23.2	67	10	US-09-896-095-147	Sequence 147, App
37	175	23.2	67	14	US-10-038-722-90	Sequence 90, Appl
38	175	23.2	67	15	US-10-115-134-4	Sequence 4, Appli
39	173.5	23.0	503	14	US-10-007-280A-233	Sequence 233, App
40	173.5	23.0	576	9	US-09-794-589-2	Sequence 2, Appli
41	173.5	23.0	576	14	US-10-315-380-2	Sequence 2, Appli
42	173.5	23.0	576	14	US-10-369-736-7	Sequence 7, Appli
43	173.5	23.0	576	14	US-10-369-738-7	Sequence 7, Appli
44	173.5	23.0	576	19	US-11-028-058-7	Sequence 7, Appli
45	173.5	23.0	640	14	US-10-369-736-5	Sequence 5, Appli
46	173.5	23.0	640	14	US-10-369-738-5	Sequence 5, Appli
47	173.5	23.0	640	19	US-11-028-058-5	Sequence 5, Appli
48	173	23.0	58	14	US-10-038-722-17	Sequence 17, Appl
49	173	23.0	58	14	US-10-038-722-18	Sequence 18, Appl
50	173	23.0	58	14	US-10-038-722-19	Sequence 19, Appl

ALIGNMENTS

US-10-807-204-1
RESULT 1
; Sequence 1, Application US/10807204
; Publication No. US20040229312A1
; GENERAL INFORMATION:
; APPLICANT: Bougueleret, Lydie
; APPLICANT: Bairoch, Amos
; APPLICANT: Niknejad, Anne
; TITLE OF INVENTION: Engineered Human Kunitz-Type Protease
; TITLE OF INVENTION: Inhibitor
; FILE REFERENCE: 54720-8015.US00
; CURRENT APPLICATION NUMBER: US/10/807,204
; CURRENT FILING DATE: 2004-03-22
; PRIOR APPLICATION NUMBER: PCT/EP03/01629
; PRIOR FILING DATE: 2003-02-18
; PRIOR APPLICATION NUMBER: US 60/358,683
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; TYPE: PRT
; LENGTH: 131
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (1)...(131)
; OTHER INFORMATION: eppin-like precursor
; FEATURE:
; NAME/KEY: SIGNAL

```

; LOCATION: (1)...(25)
; OTHER INFORMATION: predicted by signalp 2.0
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (26)...(131)
; OTHER INFORMATION: mature peptide
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (77)...(127)
; OTHER INFORMATION: Kunitz domain predicted by pfscan
; FEATURE:
; NAME/KEY: DISULFID
; LOCATION: (33)...(61)
; OTHER INFORMATION: predicted disulfide bond
; FEATURE:
; NAME/KEY: DISULFID
; LOCATION: (40)...(65)
; OTHER INFORMATION: predicted disulfide bond
; FEATURE:
; NAME/KEY: DISULFID
; LOCATION: (48)...(60)
; OTHER INFORMATION: predicted disulfide bond
; FEATURE:
; NAME/KEY: DISULFID
; LOCATION: (54)...(69)
; OTHER INFORMATION: predicted disulfide bond
; FEATURE:
; NAME/KEY: DISULFID
; LOCATION: (77)...(127)
; OTHER INFORMATION: predicted disulfide bond
; FEATURE:
; NAME/KEY: DISULFID
; LOCATION: (86)...(110)
; OTHER INFORMATION: predicted disulfide bond
; FEATURE:
; NAME/KEY: DISULFID
; LOCATION: (102)...(123)
; OTHER INFORMATION: predicted disulfide bond
US-10-807-204-1

Query Match      100.0%; Score 753; DB 16; Length 131;
Best Local Similarity 100.0%; Pred. No. 4.8e-65;
Matches 131; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MGLSGLLPILVPFILLGDIQEPGHAEGILGKPCPKIKVECEVEEIDQCTKPRDCPENMKC 60
Db 1 MGLSGLLPILVPFILLGDIQEPGHAEGILGKPCPKIKVECEVEEIDQCTKPRDCPENMKC 60

Qy 61 CPFSCKKCLDFRKDICSMPQAGPCLASIPHHWYNNKTKICSEFIYGGCGGNNNNFQTE 120
Db 61 CPFSCKKCLDFRKDICSMPQAGPCLASIPHHWYNNKTKICSEFIYGGCGGNNNNFQTE 120

Qy 121 AICLVTCCKYH 131
Db 121 AICLVTCCKYH 131

RESULT 3
US-10-807-204-15
; Sequence 15, Application US/10807204
; Publication No. US20040229312A1
; GENERAL INFORMATION:
; APPLICANT: Bougueleret, Lydie
; APPLICANT: Bairoch, Amos
; APPLICANT: Niknejad, Anne
; TITLE OF INVENTION: Engineered Human Kunitz-Type Protease
; TITLE OF INVENTION: Inhibitor
; FILE REFERENCE: 54720-8015.US00
; CURRENT APPLICATION NUMBER: US/10/807,204
; CURRENT FILING DATE: 2004-03-22
; PRIOR APPLICATION NUMBER: PCT/EP03/01629
; PRIOR FILING DATE: 2003-02-18
; PRIOR APPLICATION NUMBER: US 60/358,683
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15
; LENGTH: 131
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-807-204-15

Query Match      97.1%; Score 731; DB 16; Length 131;
Best Local Similarity 98.5%; Pred. No. 6.5e-63;
Matches 129; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 MGLSGLLPILVPFILLGDIQEPGHAEGILGKPCPKIKVECEVEEIDQCTKPRDCPENMKC 60
Db 1 MGLSGLLPILVPFILLGDIQEPGHAEGILGKPCPKIKVECEVEEIDQCTKPRDCPENMKC 60

Qy 61 CPFSCKKCLDFRKDICSMPQAGPCLASIPHHWYNNKTKICSEFIYGGCGGNNNNFQTE 120
Db 61 CPFSCKKCLDFRKDICSMPQAGPCLASIPHHWYNNKTKICSEFIYGGCGGNNNNFQTE 120

Qy 121 AICLVTCCKYH 131
Db 121 AICLVTCCKYH 131

RESULT 4
US-10-807-204-2
; Sequence 2, Application US/10807204
; Publication No. US20040229312A1
; GENERAL INFORMATION:
; APPLICANT: Bougueleret, Lydie
; APPLICANT: Bairoch, Amos
; APPLICANT: Niknejad, Anne
; TITLE OF INVENTION: Engineered Human Kunitz-Type Protease
; TITLE OF INVENTION: Inhibitor
; FILE REFERENCE: 54720-8015.US00
; CURRENT APPLICATION NUMBER: US/10/807,204
; CURRENT FILING DATE: 2004-03-22
; PRIOR APPLICATION NUMBER: PCT/EP03/01629
; PRIOR FILING DATE: 2003-02-18
; PRIOR APPLICATION NUMBER: US 60/358,683

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; APPLICANT: Bougueleret, Lydie
; APPLICANT: Bairoch, Amos
; APPLICANT: Niknejad, Anne
; TITLE OF INVENTION: Engineered Human Kunitz-Type Protease
; TITLE OF INVENTION: Inhibitor
; FILE REFERENCE: 54720-8015.US00
; CURRENT APPLICATION NUMBER: US/10/807,204
; CURRENT FILING DATE: 2004-03-22
; PRIOR APPLICATION NUMBER: PCT/EP03/01629
; PRIOR FILING DATE: 2003-02-18
; PRIOR APPLICATION NUMBER: US 60/358,683
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 106
; TYPE: PRT
; ORGANISM: Homo sapiens
; NAME/KEY: VARIANT
; LOCATION: (1)...(106)
; OTHER INFORMATION: mature form
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (52)...(102)
; OTHER INFORMATION: Kunitz domain predicted by pfscan
; FEATURE:
; NAME/KEY: DISULFID
; LOCATION: (8)...(36)
; OTHER INFORMATION: predicted disulfide bond
; FEATURE:
; NAME/KEY: DISULFID
; LOCATION: (15)...(40)
; OTHER INFORMATION: predicted disulfide bond
; FEATURE:
; NAME/KEY: DISULFID
; LOCATION: (29)...(44)
; OTHER INFORMATION: predicted disulfide bond
; NAME/KEY: DISULFID
; LOCATION: (52)...(102)
; OTHER INFORMATION: predicted disulfide bond
; NAME/KEY: DISULFID
; LOCATION: (61)...(85)
; OTHER INFORMATION: predicted disulfide bond
; NAME/KEY: DISULFID
; LOCATION: (77)...(98)
; OTHER INFORMATION: predicted disulfide bond
US-10-807-204-2
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Query Match 83.0%; Score 625; DB 16; Length 106;
Best Local Similarity 100.0%; Pred. No. 9.6e-53;
Matches 106; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 26 EGLGKPCPKIKVECEVEEIDQTKPRDCPENMKCCPFSCGKKCLDFRDKDICSMPQEAGP 85
Db 1 EGLGKPCPKIKVECEVEEIDQTKPRDCPENMKCCPFSCGKKCLDFRDKDICSMPQEAGP 60

QY 86 CLASIPHHWYNNKTKICSEFIYGGCGQNNNNFQTEAICLVTCCKYH 131
Db 61 CLASIPHHWYNNKTKICSEFIYGGCGQNNNNFQTEAICLVTCCKYH 106
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RESULT 5

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US-10-807-204-9
; Sequence 9, Application US/10807204
; Publication No. US20040229312A1
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; GENERAL INFORMATION:
; APPLICANT: Bougueleret, Lydie
; APPLICANT: Bairoch, Amos
; APPLICANT: Niknejad, Anne
; TITLE OF INVENTION: Engineered Human Kunitz-Type Protease
; TITLE OF INVENTION: Inhibitor
; FILE REFERENCE: 54720-8015.US00
; CURRENT APPLICATION NUMBER: US/10/807,204
; CURRENT FILING DATE: 2004-03-22
; PRIOR APPLICATION NUMBER: PCT/EP03/01629
; PRIOR FILING DATE: 2003-02-18
; PRIOR APPLICATION NUMBER: US 60/358,683
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 98
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-807-204-9

Query Match 73.2%; Score 551; DB 16; Length 98;
Best Local Similarity 99.0%; Pred. No. 1.3e-45;
Matches 97; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MGLSGLLPILVPFILLGDIQEPGHAEGILGKPCPKIKVECEVEEIDQTKPRDCPENMKC 60
Db 1 MGLSGLLPILVPFILLGDIQEPGHAEGILGKPCPKIKVECEVEEIDQTKPRDCPENMKC 60

QY 61 CPFGCGKKCLDFRDKDICSMPQEAGPCLASIPHHWYNNK 98
Db 61 CPFGSGKKCLDFRDKDICSMPQEAGPCLASIPHHWYNNK 98
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RESULT 6

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US-10-807-204-16
; Sequence 16, Application US/10807204
; Publication No. US20040229312A1
; GENERAL INFORMATION:
; APPLICANT: Bougueleret, Lydie
; APPLICANT: Bairoch, Amos
; APPLICANT: Niknejad, Anne
; TITLE OF INVENTION: Engineered Human Kunitz-Type Protease
; TITLE OF INVENTION: Inhibitor
; FILE REFERENCE: 54720-8015.US00
; CURRENT APPLICATION NUMBER: US/10/807,204
; CURRENT FILING DATE: 2004-03-22
; PRIOR APPLICATION NUMBER: PCT/EP03/01629
; PRIOR FILING DATE: 2003-02-18
; PRIOR APPLICATION NUMBER: US 60/358,683
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 16
; LENGTH: 136
; TYPE: PRT
; ORGANISM: Mus musculus
; US-10-807-204-16
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Query Match 65.3%; Score 492; DB 16; Length 136;
Best Local Similarity 62.8%; Pred. No. 9.4e-40;
Matches 81; Conservative 20; Mismatches 28; Indels 0; Gaps 0;

QY 1 MGLSGLLPILVPFILLGDIQEPGHAEGILGKPCPKIKVECEVEEIDQTKPRDCPENMKC 60
Db 1 MGLWGLLPILVPFILLGDIQEPGHAEGILGKPCPKIKVECEVEEIDQTKPRDCPENMKC 60

QY 61 CPFGCGKKCLDFRDKDICSMPQEAGPCLASIPHHWYNNKTKICSEFIYGGCGQNNNNFQTE 120
Db 61 CLFGCGKKCLDFRDKDICSMPQEAGPCLASIPHHWYNNKTKICSEFIYGGCGQNNNNFQTE 120

QY 121 AICLVTCCK 129
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Db      121 GICTVCK 129

RESULT 7
US-09-853-161-75
; Sequence 75, Application US/09853161
; Patent No. US20020076756A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 28 Human Secreted Proteins
; FILE REFERENCE: P2003P3
; CURRENT APPLICATION NUMBER: US/09/853,161
; CURRENT FILING DATE: 2001-05-11
; PRIOR APPLICATION NUMBER: 60/265,583
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: 09/152,060
; PRIOR FILING DATE: 1998-09-11
; PRIOR APPLICATION NUMBER: PCT/US98/04858
; PRIOR FILING DATE: 1998-03-12
; PRIOR APPLICATION NUMBER: 60/040,762
; PRIOR FILING DATE: 1997-03-14
; PRIOR APPLICATION NUMBER: 60/040,710
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/048,189
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/057,765
; PRIOR FILING DATE: 1997-09-05
; PRIOR APPLICATION NUMBER: 60/048,970
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/068,368
; PRIOR FILING DATE: 1997-12-19
; NUMBER OF SEQ ID NOS: 118
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 75
; LENGTH: 133
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-853-161-75

Query Match      62.0%; Score 467; DB 9; Length 133;
Best Local Similarity 60.9%; Pred. No. 2.4e-37;
Matches 78; Conservative 18; Mismatches 32; Indels 0; Gaps 0;

Qy      1 MGLSGLLPILVFPFLLGDIQEPGHAEGILGKPCPKIKVECEVEEIDQCTKPRDCPENMKC 60
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      1 MGSSGLLSLLVLFVLLANVGPGLTDLWLPFRRCPKIRECECFQBRDVCTKDRQCQDNKKC 60

Qy      61 CPFSCGKKCLDFRKIDICSMPOEAGPCLASIPHHWYNNKTKICSEFFIYGGCGGNNNFQTE 120
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      61 CVFSCGKKCLDLKQDVCCEMPKETGCLAYFLHWWYDKDKNTCSMFYVYGGCGGNNNFQSK 120

Qy      121 AICLVTK 128
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Db      121 ANCLNTCK 128

RESULT 9
US-09-852-797-75
; Sequence 75, Application US/09852797
; Patent No. US20020172994A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 28 Human Secreted Proteins
; FILE REFERENCE: P2003P2
; CURRENT APPLICATION NUMBER: US/09/852,797
; CURRENT FILING DATE: 2001-05-11
; PRIOR APPLICATION NUMBER: 60/265,583
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: 09/152,060
; PRIOR FILING DATE: 1998-09-11
; PRIOR APPLICATION NUMBER: PCT/US98/04858
; PRIOR FILING DATE: 1998-03-12
; PRIOR APPLICATION NUMBER: 60/040,762
; PRIOR FILING DATE: 1997-03-14
; PRIOR APPLICATION NUMBER: 60/040,710
; PRIOR FILING DATE: 1997-03-14
; PRIOR APPLICATION NUMBER: 60/050,934
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/048,100
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/048,357

Query Match      62.0%; Score 467; DB 9; Length 133;
Best Local Similarity 60.9%; Pred. No. 2.4e-37;
Matches 78; Conservative 18; Mismatches 32; Indels 0; Gaps 0;

Qy      1 MGLSGLLPILVFPFLLGDIQEPGHAEGILGKPCPKIKVECEVEEIDQCTKPRDCPENMKC 60
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      1 MGSSGLLSLLVLFVLLANVGPGLTDLWLPFRRCPKIRECECFQBRDVCTKDRQCQDNKKC 60

Qy      61 CPFSCGKKCLDFRKIDICSMPOEAGPCLASIPHHWYNNKTKICSEFFIYGGCGGNNNFQTE 120
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      61 CVFSCGKKCLDLKQDVCCEMPKETGCLAYFLHWWYDKDKNTCSMFYVYGGCGGNNNFQSK 120

Qy      121 AICLVTK 128
      |||||
Db      121 ANCLNTCK 128

RESULT 8
US-09-852-659A-75
; Sequence 75, Application US/09852659A
; Patent No. US20020077287A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 28 Human Secreted Proteins
; FILE REFERENCE: P2003P4
; CURRENT APPLICATION NUMBER: US/09/852,659A
; CURRENT FILING DATE: 2001-05-11
; PRIOR APPLICATION NUMBER: 60/265,583
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; PRIOR FILING DATE: 1997-05-30
 ; PRIOR APPLICATION NUMBER: 60/048,189
 ; PRIOR FILING DATE: 1997-05-30
 ; PRIOR APPLICATION NUMBER: 60/057,765
 ; PRIOR FILING DATE: 1997-09-05
 ; PRIOR APPLICATION NUMBER: 60/048,970
 ; PRIOR FILING DATE: 1997-06-06
 ; PRIOR APPLICATION NUMBER: 60/068,368
 ; PRIOR FILING DATE: 1997-12-19
 ; NUMBER OF SEQ ID NOS: 118
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 75
 ; LENGTH: 133
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-09-852-797-75

Query Match 62.0%; Score 467; DB 9; Length 133;
 Best Local Similarity 60.9%; Pred. No. 2.4e-37;
 Matches 78; Conservative 18; Mismatches 32; Indels 0; Gaps 0;
 Qy 1 MGLSGLLPILVPFILLGDIQEPGHAEGILGKPCPKIKVECEVEIDQCTKPRDCPENMKC 60
 Db 1 MGSSGLLSLLVLFVLLANVQGPGLTDLWLPFRPCPKIRECECFQERDVCTKDRQCQDNKKC 60
 Qy 61 CPFGCGKKCLDFRKDICSMPQEAAGPCLASIPHHWYNNKTKICSEFIYGGCCGNNNNFQTE 120
 Db 61 CVFGCGKKCLDLKQDVCMPKGTGCLAYFLHWWYDKKDNKTCSEMFVYGGCCGNNNNFQSK 120
 Qy 121 AICLVTK 128
 Db 121 ANCLNTCK 128

RESULT 10
 US-10-058-993-75
 ; Sequence 75, Application US/10058993
 ; Publication No. US20030225009A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Rosen et al.
 ; TITLE OF INVENTION: 28 Human Secreted Proteins
 ; FILE REFERENCE: P2003PS
 ; CURRENT APPLICATION NUMBER: US/10/058,993
 ; CURRENT FILING DATE: 2002-01-30
 ; PRIOR APPLICATION NUMBER: 09/852,659
 ; PRIOR FILING DATE: 2001-05-11
 ; PRIOR APPLICATION NUMBER: 09/852,797
 ; PRIOR FILING DATE: 2001-05-11
 ; PRIOR APPLICATION NUMBER: 09/853,161
 ; PRIOR FILING DATE: 2001-05-11
 ; PRIOR APPLICATION NUMBER: 60/265,583
 ; PRIOR FILING DATE: 2001-02-02
 ; PRIOR APPLICATION NUMBER: 09/152,060
 ; PRIOR FILING DATE: 1998-09-11
 ; PRIOR APPLICATION NUMBER: PCT/US98/04858
 ; PRIOR FILING DATE: 1998-03-12
 ; PRIOR APPLICATION NUMBER: 60/068,368
 ; PRIOR FILING DATE: 1997-12-19
 ; PRIOR APPLICATION NUMBER: 60/057,765
 ; PRIOR FILING DATE: 1997-09-05
 ; PRIOR APPLICATION NUMBER: 60/048,970
 ; PRIOR FILING DATE: 1997-06-05
 ; PRIOR APPLICATION NUMBER: 60/050,934
 ; PRIOR FILING DATE: 1997-05-30
 ; PRIOR APPLICATION NUMBER: 60/048,100
 ; PRIOR FILING DATE: 1997-05-30
 ; PRIOR APPLICATION NUMBER: 60/048,189
 ; PRIOR FILING DATE: 1997-05-30
 ; PRIOR APPLICATION NUMBER: 60/048,357
 ; PRIOR FILING DATE: 1997-05-30
 ; PRIOR APPLICATION NUMBER: 60/040,710
 ; PRIOR FILING DATE: 1997-03-14
 ; PRIOR APPLICATION NUMBER: 60/040,762

; PRIOR FILING DATE: 1997-03-14
 ; NUMBER OF SEQ ID NOS: 122
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 75
 ; LENGTH: 133
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-10-058-993-75
 Query Match 62.0%; Score 467; DB 15; Length 133;
 Best Local Similarity 60.9%; Pred. No. 2.4e-37;
 Matches 78; Conservative 18; Mismatches 32; Indels 0; Gaps 0;
 Qy 1 MGLSGLLPILVPFILLGDIQEPGHAEGILGKPCPKIKVECEVEIDQCTKPRDCPENMKC 60
 Db 1 MGSSGLLSLLVLFVLLANVQGPGLTDLWLPFRPCPKIRECECFQERDVCTKDRQCQDNKKC 60
 Qy 61 CPFGCGKKCLDFRKDICSMPQEAAGPCLASIPHHWYNNKTKICSEFIYGGCCGNNNNFQTE 120
 Db 61 CVFGCGKKCLDLKQDVCMPKGTGCLAYFLHWWYDKKDNKTCSEMFVYGGCCGNNNNFQSK 120
 Qy 121 AICLVTK 128
 Db 121 ANCLNTCK 128

RESULT 11
 US-10-807-204-13
 ; Sequence 13, Application US/10807204
 ; Publication No. US20040229312A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Bougueleret, Lydie
 ; APPLICANT: Bairoch, Amos
 ; APPLICANT: Niknejad, Anne
 ; TITLE OF INVENTION: Engineered Human Kunitz-Type Protease
 ; TITLE OF INVENTION: Inhibitor
 ; FILE REFERENCE: 54720-8015.US00
 ; CURRENT APPLICATION NUMBER: US/10/807,204
 ; CURRENT FILING DATE: 2004-03-22
 ; PRIOR APPLICATION NUMBER: PCT/EP03/01629
 ; PRIOR FILING DATE: 2003-02-18
 ; PRIOR APPLICATION NUMBER: US 60/358,683
 ; PRIOR FILING DATE: 2002-02-21
 ; NUMBER OF SEQ ID NOS: 16
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 13
 ; LENGTH: 133
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-10-807-204-13

Query Match 62.0%; Score 467; DB 16; Length 133;
 Best Local Similarity 60.9%; Pred. No. 2.4e-37;
 Matches 78; Conservative 18; Mismatches 32; Indels 0; Gaps 0;
 Qy 1 MGLSGLLPILVPFILLGDIQEPGHAEGILGKPCPKIKVECEVEIDQCTKPRDCPENMKC 60
 Db 1 MGSSGLLSLLVLFVLLANVQGPGLTDLWLPFRPCPKIRECECFQERDVCTKDRQCQDNKKC 60
 Qy 61 CPFGCGKKCLDFRKDICSMPQEAAGPCLASIPHHWYNNKTKICSEFIYGGCCGNNNNFQTE 120
 Db 61 CVFGCGKKCLDLKQDVCMPKGTGCLAYFLHWWYDKKDNKTCSEMFVYGGCCGNNNNFQSK 120
 Qy 121 AICLVTK 128
 Db 121 ANCLNTCK 128
 RESULT 12
 US-10-480-988-21
 ; Sequence 21, Application US/10480988
 ; Publication No. US20050069877A1
 ; GENERAL INFORMATION:

APPLICANT: GANDHI, Ameena R.; KABLE, Amy E.;
APPLICANT: SWARNAKAR, Anita; HAFALIA, April J.A.;
APPLICANT: TRAN, Bao, DUGGAN, Brendan M.;
APPLICANT: WARREN, Bridget A.; ISON, Craig H.;
APPLICANT: HONCHELL, Cynthia D.; NGUYEN, Dannel B.;
APPLICANT: LU, Dyung Aina M.; LEE, Ernestine A.;
APPLICANT: YUE, Henry; FORSYTHE, Ian J.;
APPLICANT: BARROSO, Ines; RAMKUMAR, Jayalaxmi;
APPLICANT: GRIFFIN, Jennifer A.; LI, Joana X.;
APPLICANT: YANG, Junning; THANGAVELU, Kavitha;
APPLICANT: GIETZEN, Kimberly J.; DING, Li;
APPLICANT: BAUGHN, Mariah R.; BOROWSKY, Mark L.;
APPLICANT: YAO, Monique G.; CHAWLA, Narinder K.;
APPLICANT: MASON, Patricia M.; GURURAJAN, Rajagopal;
APPLICANT: LEE, Sally; BECHA, Shanya D.;
APPLICANT: LEE, Soo Yeun; TRAN, Uyen K.;
APPLICANT: ELLIOTT, Vicki S.; LUO, Wen;
APPLICANT: SPRAGUE, William W.; TANG, Y. Tom;
APPLICANT: LU, Yan; ZEBARJADIAN, Yeganeh
TITLE OF INVENTION: PROTEIN MODIFICATION AND MAINTENANCE MOLECULES
FILE REFERENCE: PP-1040 USN
CURRENT APPLICATION NUMBER: US/10/480,988
CURRENT FILING DATE: 2003-12-16
PRIOR APPLICATION NUMBER: PCT/US02/19360
PRIOR FILING DATE: 2002-06-18
PRIOR APPLICATION NUMBER: US 60/300,508
PRIOR FILING DATE: 2001-06-22
PRIOR APPLICATION NUMBER: US 60/303,445
PRIOR FILING DATE: 2001-07-06
PRIOR APPLICATION NUMBER: US 60/305,405
PRIOR FILING DATE: 2001-07-13
PRIOR APPLICATION NUMBER: US 60/311,442
PRIOR FILING DATE: 2001-08-09
PRIOR APPLICATION NUMBER: US 60/314,821
PRIOR FILING DATE: 2001-08-24
PRIOR APPLICATION NUMBER: US 60/315,992
PRIOR FILING DATE: 2001-08-29
PRIOR APPLICATION NUMBER: US 60/378,205
PRIOR FILING DATE: 2002-05-03
NUMBER OF SEQ ID NOS: 56
SOFTWARE: PERL Program
SEQ ID NO 21
LENGTH: 86
TYPE: PRT
ORGANISM: Homo sapiens
NAME/KEY: misc feature
OTHER INFORMATION: Incyte ID No: 7675588CD1
US-10-480-988-21
Query Match 53.7%; Score 404; DB 17; Length 86;
Best Local Similarity 98.6%; Pred. No. 2e-31; Indels 0; Gaps 0;
Matches 73; Conservative 0; Mismatches 1;
Qy 1 MGLSGLLPILVPFILLGDIQBPQHAEGILGKPCPKIKVECEVEEIDQCTKPRDCPENMKC 60
Db 1 MGLSGLLPILVPFILLGDIQBPQHAEGILGKPCPKIKVECEVEEIDQCTKPRDCPENMKC 60
Qy 61 CPFSCKGKCLDFRK 74
Db 61 CPFSRGKKCLDFRK 74
RESULT 13
US-10-276-774-2606
Sequence 2606, Application US/10276774
Publication No. US20040053245A1
GENERAL INFORMATION:
APPLICANT: Hyseq, Inc.
APPLICANT: Tang, Y, Tom et al
TITLE OF INVENTION: NO. US20040053245A1el Nucleic Acids and Polypeptides
FILE REFERENCE: 21272-030
CURRENT APPLICATION NUMBER: US/10/276,774

CURRENT FILING DATE: 2002-11-18
PRIOR APPLICATION NUMBER: 09/560,875
PRIOR FILING DATE: 2000-04-27
PRIOR APPLICATION NUMBER: 09/496,914
PRIOR FILING DATE: 2000-02-03
NUMBER OF SEQ ID NOS: 2700
SOFTWARE: Custom
SEQ ID NO 2606
LENGTH: 101
TYPE: PRT
ORGANISM: Homo sapiens
US-10-276-774-2606
Query Match 53.7%; Score 404; DB 15; Length 101;
Best Local Similarity 98.6%; Pred. No. 2.3e-31; Indels 0; Gaps 0;
Matches 73; Conservative 0; Mismatches 1;
Qy 1 MGLSGLLPILVPFILLGDIQBPQHAEGILGKPCPKIKVECEVEEIDQCTKPRDCPENMKC 60
Db 16 MGLSGLLPILVPFILLGDIQBPQHAEGILGKPCPKIKVECEVEEIDQCTKPRDCPENMKC 75
Qy 61 CPFSCKGKCLDFRK 74
Db 76 CPFSRGKKCLDFRK 89
RESULT 14
US-09-852-659A-119
Sequence 119, Application US/09852659A
Patent No. US20020077287A1
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: 28 Human Secreted Proteins
FILE REFERENCE: P2003P4
CURRENT APPLICATION NUMBER: US/09/852,659A
CURRENT FILING DATE: 2001-05-11
PRIOR APPLICATION NUMBER: 60/265,583
PRIOR FILING DATE: 2001-02-02
PRIOR APPLICATION NUMBER: 09/152,060
PRIOR FILING DATE: 1998-09-11
PRIOR APPLICATION NUMBER: PCT/US98/04858
PRIOR FILING DATE: 1998-03-12
PRIOR APPLICATION NUMBER: 60/040,762
PRIOR FILING DATE: 1997-03-14
PRIOR APPLICATION NUMBER: 60/040,710
PRIOR FILING DATE: 1997-03-14
PRIOR APPLICATION NUMBER: 60/050,934
PRIOR FILING DATE: 1997-05-30
PRIOR APPLICATION NUMBER: 60/048,100
PRIOR FILING DATE: 1997-05-30
PRIOR APPLICATION NUMBER: 60/048,357
PRIOR FILING DATE: 1997-05-30
PRIOR APPLICATION NUMBER: 60/048,189
PRIOR FILING DATE: 1997-05-30
PRIOR APPLICATION NUMBER: 60/057,765
PRIOR FILING DATE: 1997-09-05
PRIOR APPLICATION NUMBER: 60/048,970
PRIOR FILING DATE: 1997-06-06
PRIOR APPLICATION NUMBER: 60/068,368
PRIOR FILING DATE: 1997-12-19
NUMBER OF SEQ ID NOS: 121
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 119
LENGTH: 117
TYPE: PRT
ORGANISM: Homo sapiens
US-09-852-659A-119
Query Match 53.3%; Score 401.5; DB 9; Length 117;
Best Local Similarity 66.0%; Pred. No. 4.7e-31; Indels 1; Gaps 1;
Matches 66; Conservative 12; Mismatches 21;
Qy 29 LGKPCPKIKVECEVEEIDQCTKPRDCPENMKCCPFCGKCKLDFRKIDCSMPQAGPCLA 88


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; PRIOR APPLICATION NUMBER: 60/068,368
; PRIOR FILING DATE: 1997-12-19
; PRIOR APPLICATION NUMBER: 60/057,765
; PRIOR FILING DATE: 1997-09-05
; PRIOR APPLICATION NUMBER: 60/048,970
; PRIOR FILING DATE: 1997-06-05
; PRIOR APPLICATION NUMBER: 60/050,934
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/048,100
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/048,189
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/048,357
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/040,710
; PRIOR FILING DATE: 1997-03-14
; PRIOR APPLICATION NUMBER: 60/040,762
; PRIOR FILING DATE: 1997-03-14
; NUMBER OF SEQ ID NOS: 122
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 121
; LENGTH: 102
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-058-993-121

Query Match      53.1%; Score 400; DB 15; Length 102;
Best Local Similarity 66.7%; Pred. No. 5.7e-31;
Matches 64; Conservative 11; Mismatches 21; Indels 0; Gaps 0;

Qy 33 CPKIKVECEVEEIDQCTKPRDCPENMKCCPFSCGKKCLDPRKDCISMPEQAGPCLASIPH 92
Db 2 CPKIRECECFQERDVCTKRDQCQDNKKCCVFCGKKCLDLKQDVCEMPKETGTGCLAYFLH 61

Qy 93 WYWNKTKICSEFYGGCGQNNNFQTEAICLVTK 128
Db 62 WYDCKONTCSMFYVGGCGQNNNFQSKANCLNTCK 97

RESULT 18
US-10-807-204-14
; Sequence 14, Application US/10807204
; Publication No. US20040229312A1
; GENERAL INFORMATION:
; APPLICANT: Bougueleret, Lydie
; APPLICANT: Bairoch, Amos
; APPLICANT: Niknejad, Anne
; TITLE OF INVENTION: Engineered Human Kunitz-Type Protease
; FILE REFERENCE: 54720-8015.US00
; CURRENT APPLICATION NUMBER: US/10/807,204
; CURRENT FILING DATE: 2004-03-22
; PRIOR APPLICATION NUMBER: PCT/EP03/01629
; PRIOR FILING DATE: 2003-02-18
; PRIOR APPLICATION NUMBER: US 60/358,683
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14
; LENGTH: 134
; TYPE: PRT
; ORGANISM: Mus musculus
; US-10-807-204-14

Query Match      52.9%; Score 398; DB 16; Length 134;
Best Local Similarity 51.9%; Pred. No. 1.2e-30;
Matches 67; Conservative 25; Mismatches 37; Indels 0; Gaps 0;

Qy 1 MGLSGLLPILVPIILGDIQSPGHAEGILGKPCPKIKVECEVEEIDQCTKPRDCPENMKC 60
Db 1 MKLSGFSVILVFLGLARVQGPSLADLFFPRRCFRFEECEHQERDLCTDRDCPKKEKC 60

Qy 61 CPFSGKKCLDFRKDCISMPEQAGPCLASIPHWYNNKTKICSEFYGGCGQNNNFQTE 120
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Db 61 CVFNCGKKCLNPQDICSPLKSGCYCMAYPRRWFNKENSTCQVFIYGGCGQNNNFQSQ 120
Qy 121 AICLVTKCK 129
Db 121 SICQACEK 129

RESULT 19
US-10-807-204-5
; Sequence 5, Application US/10807204
; Publication No. US20040229312A1
; GENERAL INFORMATION:
; APPLICANT: Bougueleret, Lydie
; APPLICANT: Bairoch, Amos
; APPLICANT: Niknejad, Anne
; TITLE OF INVENTION: Engineered Human Kunitz-Type Protease
; FILE REFERENCE: 54720-8015.US00
; CURRENT APPLICATION NUMBER: US/10/807,204
; CURRENT FILING DATE: 2004-03-22
; PRIOR APPLICATION NUMBER: PCT/EP03/01629
; PRIOR FILING DATE: 2003-02-18
; PRIOR APPLICATION NUMBER: US 60/358,683
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 43
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-807-204-5

Query Match      34.3%; Score 258; DB 16; Length 43;
Best Local Similarity 100.0%; Pred. No. 1.3e-17;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 32 PCPKIKVECEVEEIDQCTKPRDCPENMKCCPFSCGKKCLDFRK 74
Db 1 PCPKIKVECEVEEIDQCTKPRDCPENMKCCPFSCGKKCLDFRK 43

RESULT 20
US-10-361-997-5
; Sequence 5, Application US/10361997
; Publication No. US20040171794A1
; GENERAL INFORMATION:
; APPLICANT: Ladner, Robert Charles
; APPLICANT: Ley, Arthur C.
; TITLE OF INVENTION: KUNITZ DOMAIN PEPTIDES
; FILE REFERENCE: 3421.1015-000
; CURRENT APPLICATION NUMBER: US/10/361,997
; CURRENT FILING DATE: 2003-02-07
; PRIOR APPLICATION NUMBER: US 60/355,547
; PRIOR FILING DATE: 2002-02-07
; NUMBER OF SEQ ID NOS: 84
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 58
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-361-997-5

Query Match      31.3%; Score 236; DB 16; Length 58;
Best Local Similarity 66.1%; Pred. No. 2.4e-15;
Matches 37; Conservative 8; Mismatches 11; Indels 0; Gaps 0;

Qy 73 RKDTCSPQBPAGPCLASIPHWYNNKTKICSEFYGGCGQNNNFQTEAICLVTK 128
Db 1 KQDVCEMPKETGTGCLAYFLHWDKDKDNTCSMFYVGGCGQNNNFQSKANCLNTCK 56

RESULT 21
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```
US-10-931-153-21
; Sequence 21, Application US/10931153
; Publication No. US20050089515A1
; GENERAL INFORMATION:
; APPLICANT: Ley, Arthur C.
; APPLICANT: Sato, Aaron K.
; APPLICANT: Ladner, Robert C.
; APPLICANT: Stochl, Mark
; TITLE OF INVENTION: POLY-PEGYLATED PROTEASE INHIBITORS
; FILE REFERENCE: 10280-119001
; CURRENT APPLICATION NUMBER: US/10/931,153
; CURRENT FILING DATE: 2004-08-30
; PRIOR APPLICATION NUMBER: US 60/498,845
; PRIOR FILING DATE: 2003-08-29
; PRIOR APPLICATION NUMBER: US 60/598,967
; PRIOR FILING DATE: 2004-08-04
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 21
; LENGTH: 58
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-931-153-21

Query Match 31.3%; Score 236; DB 17; Length 58;
Best Local Similarity 66.1%; Pred. No. 2.4e-15;
Matches 37; Conservative 8; Mismatches 11; Indels 0; Gaps 0;

QY 73 RKDICSMPQAGPCLASIPHHWYNNKTKICSEFIYGGCGGNNNNFQTEAICLVTC 128
Db 1 KQDVCEMPKETGCLAYFLHMYDKDNTCSMFVYGGCGGNNNNFQSKANCLNTCK 56

RESULT 22
US-10-058-993-118
; Sequence 118, Application US/10058993
; Publication No. US20030225009A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 28 Human Secreted Proteins
; FILE REFERENCE: PZ003PS
; CURRENT APPLICATION NUMBER: US/10/058,993
; CURRENT FILING DATE: 2002-01-30
; PRIOR APPLICATION NUMBER: 09/852,659
; PRIOR FILING DATE: 2001-05-11
; PRIOR APPLICATION NUMBER: 09/852,797
; PRIOR FILING DATE: 2001-05-11
; PRIOR APPLICATION NUMBER: 09/853,161
; PRIOR FILING DATE: 2001-05-11
; PRIOR APPLICATION NUMBER: 60/265,583
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: 09/152,060
; PRIOR FILING DATE: 1998-09-11
; PRIOR APPLICATION NUMBER: PCT/US98/04858
; PRIOR FILING DATE: 1998-03-12
; PRIOR APPLICATION NUMBER: 60/068,368
; PRIOR FILING DATE: 1997-12-19
; PRIOR APPLICATION NUMBER: 60/057,765
; PRIOR FILING DATE: 1997-09-05
; PRIOR APPLICATION NUMBER: 60/048,970
; PRIOR FILING DATE: 1997-06-05
; PRIOR APPLICATION NUMBER: 60/050,934
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/048,100
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/048,189
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/048,357
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/040,710
; PRIOR FILING DATE: 1997-03-14
; PRIOR APPLICATION NUMBER: 60/040,762
; PRIOR FILING DATE: 1997-03-14
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; NUMBER OF SEQ ID NOS: 122
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 118
; LENGTH: 51
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-058-993-118

Query Match 29.1%; Score 219; DB 15; Length 51;
Best Local Similarity 68.6%; Pred. No. 9.4e-14;
Matches 35; Conservative 5; Mismatches 11; Indels 0; Gaps 0;

QY 77 CSMPQAGPCLASIPHHWYNNKTKICSEFIYGGCGGNNNNFQTEAICLVTC 127
Db 1 CEMPKETGCLAYFLHMYDKDNTCSMFVYGGCGGNNNNFQSKANCLNTC 51

RESULT 23
US-10-825-692-48
; Sequence 48, Application US/10825692
; Publication No. US20050042322A1
; GENERAL INFORMATION:
; APPLICANT: Hotez, Peter
; APPLICANT: Ashcom, James
; APPLICANT: Bdamchian, Mahnaz
; APPLICANT: Zhan, Bin
; APPLICANT: Wang, Yan
; APPLICANT: Hawdon, John
; APPLICANT: Loukas, Alexander
; APPLICANT: Williamson, Angela
; APPLICANT: Jones, Brian
; APPLICANT: Bethony, Jeffrey
; APPLICANT: Goud, Gaddam
; APPLICANT: Botazzi, Maria E.
; APPLICANT: Mendez, Susana
; TITLE OF INVENTION: Hookworm Vaccine
; FILE REFERENCE: 03740007aa
; CURRENT APPLICATION NUMBER: US/10/825,692
; CURRENT FILING DATE: 2004-04-16
; PRIOR APPLICATION NUMBER: US 60/329,533
; PRIOR FILING DATE: 2001-10-17
; PRIOR APPLICATION NUMBER: US 60/332,007
; PRIOR FILING DATE: 2001-11-23
; PRIOR APPLICATION NUMBER: US 60/375,404
; PRIOR FILING DATE: 2002-04-26
; PRIOR APPLICATION NUMBER: PCT US02/33106
; PRIOR FILING DATE: 2002-10-17
; NUMBER OF SEQ ID NOS: 114
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 48
; LENGTH: 759
; TYPE: PRT
; ORGANISM: Ancylostoma caninum
US-10-825-692-48

Query Match 26.2%; Score 197; DB 17; Length 759;
Best Local Similarity 46.1%; Pred. No. 2e-10;
Matches 35; Conservative 13; Mismatches 26; Indels 2; Gaps 1;

QY 56 ENMKCCPFCGKKCL--DFRKDICSMPQAGPCLASIPHHWYNNKTKICSEFIYGGCG 113
Db 560 ETMEDCTTCTCEQRLAKPELEKDVCSQPTAGPCRASIPRYGYDSKKRCKVKFTYGGCKGN 619

QY 114 NNNFQTEAICLVTCCK 129
Db 620 GNRFTKNECEKTKCR 635

RESULT 24
US-09-896-095-160
; Sequence 160, Application US/09896095
; Publication No. US20030219886A1
; GENERAL INFORMATION:
```


Thu Sep 22 07:16:43 2005

; Publication No. US20030162714A1
; GENERAL INFORMATION:
; APPLICANT: HILL, JENNIFER J.
; APPLICANT: WOLFMAN, NEIL M.
; TITLE OF INVENTION: FOLLISTATIN DOMAIN CONTAINING PROTEINS
; FILE REFERENCE: 08702.0014-00
; CURRENT APPLICATION NUMBER: US/10/369,736
; CURRENT FILING DATE: 2003-02-21
; PRIOR APPLICATION NUMBER: 60/357,846
; PRIOR FILING DATE: 2002-02-21
; PRIOR APPLICATION NUMBER: 60/434,645
; PRIOR FILING DATE: 2002-12-20
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 49
; LENGTH: 571
; TYPE: PRT
; ORGANISM: Mus sp.
US-10-369-736-49

Query Match 24.2%; Score 182.5; DB 14; Length 571;
Best Local Similarity 31.8%; Pred. No. 3.8e-09;
Matches 35; Conservative 12; Mismatches 34; Indels 29; Gaps 3;
QY 47 QCTKP---RDCPENM-----KCCPF-----SCGKKCLDFRKDIC 77
DB 322 ECLKPPDSDCGEQTRWHFDAQANNCLTFTFGCHHNLNHPETYEACMLACMSGPLATC 381
QY 78 SMPQAGPCLASIPHWYNNKTKICSEFYGGCGQNNNFQTEAICLVTC 127
DB 382 SLPALQGPCKAYVPRWAYNSQTGLCSFYVGGCEGNGNPFESREACEESC 431

RESULT 29
US-10-369-738-3
; Sequence 3, Application US/10369738
; Publication No. US20030180306A1
; GENERAL INFORMATION:
; APPLICANT: HILL, JENNIFER J.
; APPLICANT: WOLFMAN, NEIL M.
; TITLE OF INVENTION: FOLLISTATIN DOMAIN CONTAINING PROTEINS
; FILE REFERENCE: 08702.0014-00
; CURRENT APPLICATION NUMBER: US/10/369,738
; CURRENT FILING DATE: 2003-02-21
; PRIOR APPLICATION NUMBER: 60/357,846
; PRIOR FILING DATE: 2002-02-21
; PRIOR APPLICATION NUMBER: 60/434,645
; PRIOR FILING DATE: 2002-12-20
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 571
; TYPE: PRT
; ORGANISM: Mus sp.
US-10-369-738-3

Query Match 24.2%; Score 182.5; DB 14; Length 571;
Best Local Similarity 31.8%; Pred. No. 3.8e-09;
Matches 35; Conservative 12; Mismatches 34; Indels 29; Gaps 3;
QY 47 QCTKP---RDCPENM-----KCCPF-----SCGKKCLDFRKDIC 77
DB 322 ECLKPPDSDCGEQTRWHFDAQANNCLTFTFGCHHNLNHPETYEACMLACMSGPLATC 381
QY 78 SMPQAGPCLASIPHWYNNKTKICSEFYGGCGQNNNFQTEAICLVTC 127
DB 382 SLPALQGPCKAYVPRWAYNSQTGLCSFYVGGCEGNGNPFESREACEESC 431

RESULT 30
US-10-369-738-49
; Sequence 49, Application US/10369738
; Publication No. US20030180306A1

; GENERAL INFORMATION:
; APPLICANT: HILL, JENNIFER J.
; APPLICANT: WOLFMAN, NEIL M.
; TITLE OF INVENTION: FOLLISTATIN DOMAIN CONTAINING PROTEINS
; FILE REFERENCE: 08702.0014-00
; CURRENT APPLICATION NUMBER: US/10/369,738
; CURRENT FILING DATE: 2003-02-21
; PRIOR APPLICATION NUMBER: 60/357,846
; PRIOR FILING DATE: 2002-02-21
; PRIOR APPLICATION NUMBER: 60/434,645
; PRIOR FILING DATE: 2002-12-20
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 49
; LENGTH: 571
; TYPE: PRT
; ORGANISM: Mus sp.
US-10-369-738-49

Query Match 24.2%; Score 182.5; DB 14; Length 571;
Best Local Similarity 31.8%; Pred. No. 3.8e-09;
Matches 35; Conservative 12; Mismatches 34; Indels 29; Gaps 3;
QY 47 QCTKP---RDCPENM-----KCCPF-----SCGKKCLDFRKDIC 77
DB 322 ECLKPPDSDCGEQTRWHFDAQANNCLTFTFGCHHNLNHPETYEACMLACMSGPLATC 381
QY 78 SMPQAGPCLASIPHWYNNKTKICSEFYGGCGQNNNFQTEAICLVTC 127
DB 382 SLPALQGPCKAYVPRWAYNSQTGLCSFYVGGCEGNGNPFESREACEESC 431

RESULT 31
US-11-028-058-3
; Sequence 3, Application US/11028058
; Publication No. US20050106154A1
; GENERAL INFORMATION:
; APPLICANT: HILL, JENNIFER J.
; APPLICANT: WOLFMAN, NEIL M.
; TITLE OF INVENTION: FOLLISTATIN DOMAIN CONTAINING PROTEINS
; FILE REFERENCE: 08702.0015-00
; CURRENT APPLICATION NUMBER: US/11/028,058
; CURRENT FILING DATE: 2005-01-04
; PRIOR APPLICATION NUMBER: US/10/369,736
; PRIOR FILING DATE: 2003-02-21
; PRIOR APPLICATION NUMBER: 60/357,846
; PRIOR FILING DATE: 2002-02-21
; PRIOR APPLICATION NUMBER: 60/434,645
; PRIOR FILING DATE: 2002-12-20
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 571
; TYPE: PRT
; ORGANISM: Mus sp.
US-11-028-058-3

Query Match 24.2%; Score 182.5; DB 19; Length 571;
Best Local Similarity 31.8%; Pred. No. 3.8e-09;
Matches 35; Conservative 12; Mismatches 34; Indels 29; Gaps 3;
QY 47 QCTKP---RDCPENM-----KCCPF-----SCGKKCLDFRKDIC 77
DB 322 ECLKPPDSDCGEQTRWHFDAQANNCLTFTFGCHHNLNHPETYEACMLACMSGPLATC 381
QY 78 SMPQAGPCLASIPHWYNNKTKICSEFYGGCGQNNNFQTEAICLVTC 127
DB 382 SLPALQGPCKAYVPRWAYNSQTGLCSFYVGGCEGNGNPFESREACEESC 431

RESULT 32
US-11-028-058-49
; Sequence 49, Application US/11028058

```

; Publication No. US20050106154A1
; GENERAL INFORMATION:
; APPLICANT: HILL, JENNIFER J.
; APPLICANT: WOLFMAN, NEIL M.
; TITLE OF INVENTION: FOLLICULIN DOMAIN CONTAINING PROTEINS
; FILE REFERENCE: 08702.0015-00
; CURRENT APPLICATION NUMBER: US/11/028,058
; CURRENT FILING DATE: 2005-01-04
; PRIOR APPLICATION NUMBER: US/10/369,736
; PRIOR FILING DATE: 2003-02-21
; PRIOR APPLICATION NUMBER: 60/357,846
; PRIOR FILING DATE: 2002-02-21
; PRIOR APPLICATION NUMBER: 60/434,645
; PRIOR FILING DATE: 2002-12-20
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: Patentin ver. 2.1
; SEQ ID NO 49
; LENGTH: 571
; TYPE: PRT
; ORGANISM: Mus sp.
US-11-028-058-49

Query Match      24.2%; Score 182.5; DB 19; Length 571;
Best Local Similarity 31.8%; Pred. No. 3.8e-09;
Matches 35; Conservative 12; Mismatches 34; Indels 29; Gaps 3;

Qy 47 OCTXP---RDCPENM-----KCCPF-----SCGKKCLDFRKDIK 77
Db 322 ECLKPPDSEDCEGEQTRWHFDAQANCLITFTFGHCHHNLNHFETYEACMLACNSGLATC 381

Qy 78 SMPQAGPCLASIPHWYNNKTKICSEFIYGGCGQNNNNFQTEAICLVTC 127
Db 382 SLPALQGPCKAYVPRWAYNSQTGLCQSFYGGCGEGNNGNFSREACRESC 431

RESULT 33
US-10-807-204-7
; Sequence 7, Application US/10807204
; Publication No. US20040229312A1
; GENERAL INFORMATION:
; APPLICANT: Bougueleret, Lydie
; APPLICANT: Baïroch, Amos
; APPLICANT: Niknejad, Anne
; TITLE OF INVENTION: Engineered Human Kunitz-Type Protease
; FILE REFERENCE: 54720-8015.US00
; CURRENT APPLICATION NUMBER: US/10/807,204
; CURRENT FILING DATE: 2004-03-22
; PRIOR APPLICATION NUMBER: PCT/EP03/01629
; PRIOR FILING DATE: 2003-02-18
; PRIOR APPLICATION NUMBER: US 60/358,683
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 33
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-807-204-7

Query Match      23.9%; Score 180; DB 16; Length 33;
Best Local Similarity 97.0%; Pred. No. 3.6e-10;
Matches 32; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 99 TKICSEFIYGGCGQNNNNFQTEAICLVTCCKKYH 131
Db 1 TKICSEFIYGGCGQNNNNFQTEAICLVTCCKKYH 33

RESULT 34
US-10-807-204-10
; Sequence 10, Application US/10807204
; Publication No. US20040229312A1

```

```

; GENERAL INFORMATION:
; APPLICANT: Bougueleret, Lydie
; APPLICANT: Baïroch, Amos
; APPLICANT: Niknejad, Anne
; TITLE OF INVENTION: Engineered Human Kunitz-Type Protease
; FILE REFERENCE: 54720-8015.US00
; CURRENT APPLICATION NUMBER: US/10/807,204
; CURRENT FILING DATE: 2004-03-22
; PRIOR APPLICATION NUMBER: PCT/EP03/01629
; PRIOR FILING DATE: 2003-02-18
; PRIOR APPLICATION NUMBER: US 60/358,683
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 33
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-807-204-10

Query Match      23.9%; Score 180; DB 16; Length 33;
Best Local Similarity 97.0%; Pred. No. 3.6e-10;
Matches 32; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 99 TKICSEFIYGGCGQNNNNFQTEAICLVTCCKKYH 131
Db 1 TKICSEFIYGGCGQNNNNFQTEAICLVTCCKKYH 33

RESULT 35
US-10-038-722-5
; Sequence 5, Application US/10038722
; Publication No. US20030175919A1
; GENERAL INFORMATION:
; APPLICANT: LEY, Arthur C.
; APPLICANT: GUTERMAN, Sonia K.
; APPLICANT: MARKLAND, William
; APPLICANT: KENT, Rachel B.
; APPLICANT: ROBERTS, Bruce L.
; APPLICANT: LADNER, Robert C.
; TITLE OF INVENTION: ITI-D1 KUNITZ DOMAIN MUTANTS AS nHE INHIBITORS
; FILE REFERENCE: LEY=1B
; CURRENT APPLICATION NUMBER: US/10/038,722
; CURRENT FILING DATE: 2002-01-08
; PRIOR APPLICATION NUMBER: US 08/849,406
; PRIOR FILING DATE: 1999-07-21
; PRIOR APPLICATION NUMBER: PCT/US95/16349
; PRIOR FILING DATE: 1995-12-15
; PRIOR APPLICATION NUMBER: US 08/358,160
; PRIOR FILING DATE: 1994-12-16
; NUMBER OF SEQ ID NOS: 129
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 5
; LENGTH: 58
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Consensus Kunitz domain
US-10-038-722-5

Query Match      23.5%; Score 177; DB 14; Length 58;
Best Local Similarity 56.4%; Pred. No. 1.2e-09;
Matches 31; Conservative 5; Mismatches 19; Indels 0; Gaps 0;

Qy 73 RKDICSMPQAGPCLASIPHWYNNKTKICSEFIYGGCGQNNNNFQTEAICLVTC 127
Db 1 RPDCLLPATETGPCRAMIPRFYNNKSGKCEPFYGGCGGNANNFKTEECRRTC 55

RESULT 36
US-09-896-095-147
; Sequence 147, Application US/09896095

```



```
US-09-794-589-2
; Sequence 2, Application US/09794589
; Patent No. US20020004224A1
; GENERAL INFORMATION:
; TITLE OF INVENTION: KUNITZ DOMAIN POLYPEPTIDE ZKUN8
; FILE REFERENCE: 00-01
; CURRENT APPLICATION NUMBER: US/09/794,589
; CURRENT FILING DATE: 2001-02-27
; PRIOR APPLICATION NUMBER: US 60/186,069
; PRIOR FILING DATE: 2000-02-29
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 576
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-794-589-2

Query Match      23.0%; Score 173.5; DB 9; Length 576;
Best Local Similarity 31.8%; Pred. No. 2.8e-08;
Matches 35; Conservative 10; Mismatches 36; Indels 29; Gaps 3;

Qy 47 QCTKP---RDCPENM-----KCCPF-----SCGKKCLDPRKDIC 77
Db 327 ECLKPPDSEDCGEQTRWHFDAQANNCLTFTFGHCHRNLNHFYEAACMLACMSGPLAAC 386
Qy 78 SMPQEAGPCLASIPHWYNNKTKICSEFIYGGCGQNNNNFQTEAICLVTC 127
Db 387 SLPALQGPCKAYAPRWAYNSQTQCQSFYVYGGCEGNGNPFESREACEBSC 436

RESULT 41
US-10-315-380-2
; Sequence 2, Application US/10315380
; Publication No. US20030129577A1
; GENERAL INFORMATION:
; APPLICANT: Sheppard, Paul O.
; TITLE OF INVENTION: KUNITZ DOMAIN POLYPEPTIDE ZKUN8
; FILE REFERENCE: 00-01
; CURRENT APPLICATION NUMBER: US/10/315,380
; CURRENT FILING DATE: 2002-12-09
; PRIOR APPLICATION NUMBER: US/09/794,589
; PRIOR FILING DATE: 2001-02-27
; PRIOR APPLICATION NUMBER: US 60/186,069
; PRIOR FILING DATE: 2000-02-29
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 576
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-315-380-2

Query Match      23.0%; Score 173.5; DB 14; Length 576;
Best Local Similarity 31.8%; Pred. No. 2.8e-08;
Matches 35; Conservative 10; Mismatches 36; Indels 29; Gaps 3;

Qy 47 QCTKP---RDCPENM-----KCCPF-----SCGKKCLDPRKDIC 77
Db 327 ECLKPPDSEDCGEQTRWHFDAQANNCLTFTFGHCHRNLNHFYEAACMLACMSGPLAAC 386
Qy 78 SMPQEAGPCLASIPHWYNNKTKICSEFIYGGCGQNNNNFQTEAICLVTC 127
Db 387 SLPALQGPCKAYAPRWAYNSQTQCQSFYVYGGCEGNGNPFESREACEBSC 436

RESULT 42
US-10-369-736-7
; Sequence 7, Application US/10369736
; Publication No. US20030162714A1
; GENERAL INFORMATION:
; APPLICANT: HILL, JENNIFER J.
```

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; APPLICANT: WOLFMAN, NEIL M.
; TITLE OF INVENTION: FOLLISTATIN DOMAIN CONTAINING PROTEINS
; FILE REFERENCE: 08702.0015-00
; CURRENT APPLICATION NUMBER: US/10/369,736
; CURRENT FILING DATE: 2003-02-21
; PRIOR APPLICATION NUMBER: 60/357,846
; PRIOR FILING DATE: 2002-02-21
; PRIOR APPLICATION NUMBER: 60/434,645
; PRIOR FILING DATE: 2002-12-20
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
; LENGTH: 576
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-369-736-7

Query Match      23.0%; Score 173.5; DB 14; Length 576;
Best Local Similarity 31.8%; Pred. No. 2.8e-08;
Matches 35; Conservative 10; Mismatches 36; Indels 29; Gaps 3;

Qy 47 QCTKP---RDCPENM-----KCCPF-----SCGKKCLDPRKDIC 77
Db 327 ECLKPPDSEDCGEQTRWHFDAQANNCLTFTFGHCHRNLNHFYEAACMLACMSGPLAAC 386
Qy 78 SMPQEAGPCLASIPHWYNNKTKICSEFIYGGCGQNNNNFQTEAICLVTC 127
Db 387 SLPALQGPCKAYAPRWAYNSQTQCQSFYVYGGCEGNGNPFESREACEBSC 436

RESULT 43
US-10-369-738-7
; Sequence 7, Application US/10369738
; Publication No. US20030180306A1
; GENERAL INFORMATION:
; APPLICANT: HILL, JENNIFER J.
; APPLICANT: WOLFMAN, NEIL M.
; TITLE OF INVENTION: FOLLISTATIN DOMAIN CONTAINING PROTEINS
; FILE REFERENCE: 08702.0014-00
; CURRENT APPLICATION NUMBER: US/10/369,738
; CURRENT FILING DATE: 2003-02-21
; PRIOR APPLICATION NUMBER: 60/357,846
; PRIOR FILING DATE: 2002-02-21
; PRIOR APPLICATION NUMBER: 60/434,645
; PRIOR FILING DATE: 2002-12-20
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
; LENGTH: 576
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-369-738-7

Query Match      23.0%; Score 173.5; DB 14; Length 576;
Best Local Similarity 31.8%; Pred. No. 2.8e-08;
Matches 35; Conservative 10; Mismatches 36; Indels 29; Gaps 3;

Qy 47 QCTKP---RDCPENM-----KCCPF-----SCGKKCLDPRKDIC 77
Db 327 ECLKPPDSEDCGEQTRWHFDAQANNCLTFTFGHCHRNLNHFYEAACMLACMSGPLAAC 386
Qy 78 SMPQEAGPCLASIPHWYNNKTKICSEFIYGGCGQNNNNFQTEAICLVTC 127
Db 387 SLPALQGPCKAYAPRWAYNSQTQCQSFYVYGGCEGNGNPFESREACEBSC 436

RESULT 44
US-11-028-058-7
; Sequence 7, Application US/11028058
; Publication No. US20050106154A1
; GENERAL INFORMATION:
; APPLICANT: HILL, JENNIFER J.
; APPLICANT: WOLFMAN, NEIL M.
```



```

; APPLICANT: LEY, Arthur C.
; APPLICANT: GUTERMAN, Sonia K.
; APPLICANT: MARKLAND, William
; APPLICANT: KENT, Rachel B.
; APPLICANT: ROBERTS, Bruce L.
; APPLICANT: LADNER, Robert C.
; TITLE OF INVENTION: ITI-D1 KUNITZ DOMAIN MUTANTS AS nHE INHIBITORS
; FILE REFERENCE: LEY=1B
; CURRENT APPLICATION NUMBER: US/10/038,722
; CURRENT FILING DATE: 2002-01-08
; PRIOR APPLICATION NUMBER: US 08/849,406
; PRIOR FILING DATE: 1999-07-21
; PRIOR APPLICATION NUMBER: PCT/US95/16349
; PRIOR FILING DATE: 1995-12-15
; PRIOR APPLICATION NUMBER: US 08/358,160
; PRIOR FILING DATE: 1994-12-16
; NUMBER OF SEQ ID NOS: 129
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 17
; LENGTH: 58
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: BITI-E7-141
US-10-038-722-17

Query Match      23.0%; Score 173; DB 14; Length 58;
Best Local Similarity 50.0%; Pred. No. 3e-09;
Matches 28; Conservative 7; Mismatches 21; Indels 0; Gaps 0;

Qy 73 RKDICSMPQEAGPCLASIPHWYNNKTKICSEFYGGCGQNNNNFQTEAICLVTK 128
Db 1 RPDFCQLGYSAGPCVAMFFRYFYNGTSMACQTFVYGGCMGNGNNFVTEKDCLOT 56

RESULT 49
US-10-038-722-18
; Sequence 18, Application US/10038722
; Publication No. US20030175919A1
; GENERAL INFORMATION:
; APPLICANT: LEY, Arthur C.
; APPLICANT: GUTERMAN, Sonia K.
; APPLICANT: MARKLAND, William
; APPLICANT: KENT, Rachel B.
; APPLICANT: ROBERTS, Bruce L.
; APPLICANT: LADNER, Robert C.
; TITLE OF INVENTION: ITI-D1 KUNITZ DOMAIN MUTANTS AS nHE INHIBITORS
; FILE REFERENCE: LEY=1B
; CURRENT APPLICATION NUMBER: US/10/038,722
; CURRENT FILING DATE: 2002-01-08
; PRIOR APPLICATION NUMBER: US 08/849,406
; PRIOR FILING DATE: 1999-07-21
; PRIOR APPLICATION NUMBER: PCT/US95/16349
; PRIOR FILING DATE: 1995-12-15
; PRIOR APPLICATION NUMBER: US 08/358,160
; PRIOR FILING DATE: 1994-12-16
; NUMBER OF SEQ ID NOS: 129
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 18
; LENGTH: 58
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: MUTT26A
US-10-038-722-18

Query Match      23.0%; Score 173; DB 14; Length 58;
Best Local Similarity 50.0%; Pred. No. 3e-09;
Matches 28; Conservative 7; Mismatches 21; Indels 0; Gaps 0;

Qy 73 RKDICSMPQEAGPCLASIPHWYNNKTKICSEFYGGCGQNNNNFQTEAICLVTK 128
Db 1 RPDFCQLGYSAGPCVAMFFRYFYNGTSMACQTFVYGGCMGNGNNFVTEKDCLOT 56
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RESULT 50
US-10-038-722-19
; Sequence 19, Application US/10038722
; Publication No. US20030175919A1
; GENERAL INFORMATION:
; APPLICANT: LEY, Arthur C.
; APPLICANT: GUTERMAN, Sonia K.
; APPLICANT: MARKLAND, William
; APPLICANT: KENT, Rachel B.
; APPLICANT: ROBERTS, Bruce L.
; APPLICANT: LADNER, Robert C.
; TITLE OF INVENTION: ITI-D1 KUNITZ DOMAIN MUTANTS AS nHE INHIBITORS
; FILE REFERENCE: LEY=1B
; CURRENT APPLICATION NUMBER: US/10/038,722
; CURRENT FILING DATE: 2002-01-08
; PRIOR APPLICATION NUMBER: US 08/849,406
; PRIOR FILING DATE: 1999-07-21
; PRIOR APPLICATION NUMBER: PCT/US95/16349
; PRIOR FILING DATE: 1995-12-15
; PRIOR APPLICATION NUMBER: US 08/358,160
; PRIOR FILING DATE: 1994-12-16
; NUMBER OF SEQ ID NOS: 129
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 19
; LENGTH: 58
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: MUTQB
US-10-038-722-19

Query Match      23.0%; Score 173; DB 14; Length 58;
Best Local Similarity 50.0%; Pred. No. 3e-09;
Matches 28; Conservative 7; Mismatches 21; Indels 0; Gaps 0;

Qy 73 RKDICSMPQEAGPCLASIPHWYNNKTKICSEFYGGCGQNNNNFQTEAICLVTK 128
Db 1 RPDFCQLGYSAGPCVAMFFRYFYNGTSMACQTFVYGGCMGNGNNFVTEKDCLOT 56

Search completed: September 21, 2005, 16:45:51
Job time : 83.9233 secs
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493/1; 2555/1; 2720/1; 2739/3; 2819/1
F:220-274/Domain: animal Kunitz-type proteinase inhibitor homology <BPII>
F:343-395/Domain: animal Kunitz-type proteinase inhibitor homology <BPI2>
F:442-495/Domain: animal Kunitz-type proteinase inhibitor homology <BPI3>
F:546-598/Domain: animal Kunitz-type proteinase inhibitor homology <BPI4>
F:654-706/Domain: animal Kunitz-type proteinase inhibitor homology <BPI5>
F:1662-1716/Domain: animal Kunitz-type proteinase inhibitor homology <BPI6>
F:1787-1839/Domain: animal Kunitz-type proteinase inhibitor homology <BPI7>
F:1845-1895/Domain: animal Kunitz-type proteinase inhibitor homology <BPI8>
F:1952-2004/Domain: animal Kunitz-type proteinase inhibitor homology <BPI9>
F:2097-2152/Domain: animal Kunitz-type proteinase inhibitor homology <BPI0>

Query Match 22.7%; Score 171; DB 2; Length 2844;
Best Local Similarity 30.4%; Pred. No. 5.8e-07;
Matches 35; Conservative 14; Mismatches 34; Indels 32; Gaps 3;

QY 37 KVECEV-----EETDQTKPRDCPENMK-----CCPFCGKKCLDFR 73
DB 388 RHECEMYCARLQCEGSPURIGEEAQRCONNAQCPSSECKADQGVCCP-----RK 438

QY 74 KDICSMPOBAGPCLASIPHWYNNKTKICSEFIYGGCGGNNNNFQTEAICLVTK 128
DB 439 QTICAPLRIGDCTENVKRYWYNARTQCOMFEYTGCGGNDNNFDSIMDCQNFCK 493

RESULT 7
T23573
hypothetical protein K10D3.4 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C:Accession: T23573
R:McMurray, A.
submitted to the EMBL Data Library, June 1996
A:Reference number: Z15762
A:Accession: T23573
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-922 <WIL>
A:Cross-references: UNIPROT:Q21418; EMBL:Z75545; PIDN:CAA99886.1; GSPDB:GN00019; CESP:K10D3
A:Experimental source: clone K10D3
C:Genetic:
A:Gene: CESP:K10D3.4
A:Map position: 1
A:Introns: 60/1; 228/1; 278/1; 355/1; 743/1; 802/1; 885/2

Query Match 22.5%; Score 169.5; DB 2; Length 922;
Best Local Similarity 31.9%; Pred. No. 3.1e-07;
Matches 45; Conservative 14; Mismatches 53; Indels 29; Gaps 7;

QY 11 VPFILGDIQEPGHAEGILGKPCPKIKVECEV-----BEIDQCTKPRDCPENMKC----- 60
DB 328 IQFSYLG---QGGNFNNFLSQDHCEKFCRILCSAGE---PLKSSGGERNMECSPTGSCA 381

QY 61 --CP--FSC-----GKKCLDFKDTCSMPQEGAGPCLASIPHWYNNKTKICSEFIY 107
DB 382 NSCPSTHSCSTSGSTTFGVCPCPRQYVCKLPREQNGCTYSNRWFWNAKTGNCBEFIY 441

QY 108 GCGGNNNNFQTEAICLVTK 128
DB 442 SGGCGNANNFETYKQCYCR 462

RESULT 8
D88550
protein ZC84.6 [imported] - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
C:Accession: D88550
R:anonymous, The C. elegans Sequencing Consortium.
Science 282, 2012-2018, 1998
A:Title: Genome sequence of the nematode C. elegans: a platform for investigating biological processes
A:Reference number: A75000; MUID:99069613; PMID:9851916
A:Note: see websites genome.wustl.edu/gac/c_elegans/ and www_sanger.ac.uk/Projects/c_elegans/

A:Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; and
A:Accession: D88550
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-1474 <STO>
A:Cross-references: UNIPROT:O62504; GB:chr_III; PIDN:CAA79570.1; PID:G3881447; GSPDB:GN00019
C:Genetic:
A:Gene: ZC84.6
A:Map position: 3

Query Match 22.2%; Score 167.5; DB 2; Length 1474;
Best Local Similarity 27.1%; Pred. No. 6.8e-07;
Matches 38; Conservative 17; Mismatches 44; Indels 41; Gaps 5;

QY 12 PFILGDIQEPGHAEGILGKPCPKIKVECEV-----BEIDQCTKPRDCP 55
DB 369 PFTYLG---AGGNNNNFLS-----RIDCELYCARLQCDRGNPLRIGDVTQSCASNNDP 419

QY 56 ENMK-----CCPFCGKKCLDFKDTCSMPQEGAGPCLASIPHWYNNKTKICSEFIY 108
DB 420 SSHECKMDQAVCCP-----RMQTICTOPLRVGNCDSRVRYWYSAATRECOSFEYT 470

QY 109 GCGGNNNNFQTEAICLVTK 128
DB 471 GCGGNNNNFETLVDCQTECR 490

RESULT 9
A44180
taicatoxin serine proteinase inhibitor component - Australian taipan
C:Species: Oxyuranus scutellatus scutellatus (Australian taipan)
C:Date: 27-Apr-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
C:Accession: A44180
R:Possani, L.D.; Martin, B.M.; Yatani, A.; Mochca-Morales, J.; Zamudio, F.Z.; Gurrola, G.
Toxicon 30, 1343-1364, 1992
A:Title: Isolation and physiological characterization of taicatoxin, a complex toxin with
A:Reference number: A44180; MUID:93134601; PMID:1485334
A:Accession: A44180
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-62 <POS>
A:Cross-references: UNIPROT:Q7LZE4
A:Experimental source: subsp. scutellatus, venom
A:Note: sequence extracted from NCBI backbone (NCBIP:122482)
C:Superfamily: basic proteinase inhibitor; animal Kunitz-type proteinase inhibitor homol
C:Keywords: serine proteinase inhibitor
F:7-57/Domain: animal Kunitz-type proteinase inhibitor homology <BPI>

Query Match 21.4%; Score 161; DB 2; Length 62;
Best Local Similarity 49.1%; Pred. No. 1.9e-07;
Matches 27; Conservative 8; Mismatches 20; Indels 0; Gaps 0;

QY 73 RKDICSMPOBAGPCLASIPHWYNNKTKICSEFIYGGCGGNNNNFQTEAICLVTC 127
DB 3 RPKFCHLPKPGPCRAALPRFYNNPHSKQCEKFIYGGCHGNANKFTPDCENYTC 57

RESULT 10
JH0773
Alzheimer's disease amyloid beta protein precursor - African clawed frog
C:Species: Xenopus laevis (African clawed frog)
C:Date: 10-Jun-1993 #sequence_revision 10-Jun-1993 #text_change 13-Aug-1999
C:Accession: JH0773
R:Okado, H.; Okamoto, H.
Biochem. Biophys. Res. Commun. 189, 1561-1568, 1992
A:Title: A Xenopus homologue of the human beta-amyloid precursor protein: developmental
A:Reference number: JH0773; MUID:93129227; PMID:1282805
A:Accession: JH0773
A:Molecule type: mRNA
A:Residues: 1-747 <OKA>
A:Cross-references: GB:S52417; NID:G263150; PIDN:AAB24853.1; PID:G263151
A:Experimental source: larva
C:Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase i

A;Residues: 1-75 <LAF>
A;Cross-references: GB:M24546; GB:M24547; NID:G341202; PIDN:AAAC13654.1; PID:G516074
R;Johnstone, E.M.; Chaney, M.O.; Moore, R.E.; Ward, K.E.; Norris, F.H.; Little, S.P.
Biochem. Biophys. Res. Commun. 163, 1248-1255, 1989
A;Title: Alzheimer's disease amyloid peptide is encoded by two exons and shows similarity
A;Reference number: A33260; MUID:8932030; PMID:2675837
A;Accession: A33260
A;Molecule type: DNA
A;Residues: 656-737 <JOH>
A;Cross-references: GB:M29270; NID:G178863; PIDN:AAAS1768.1; PID:G178865
R;Pirelli, F.; Levy, E.; van Duinen, S.G.; Bots, G.T.A.M.; Luyendijk, W.; Frangione, B.
Biochem. Biophys. Res. Commun. 170, 301-307, 1990
A;Title: Expression of a normal and variant Alzheimer's beta-protein gene in amyloid of
A;Reference number: A35486; MUID:90321244; PMID:2196878
A;Accession: A35486
A;Molecule type: DNA
A;Residues: 672-710 <PREL>
A;Note: 693-Gln was found in DNA isolated from HCHWA-D patients
R;Yoshikai, S.I.; Sasaki, H.; Doh-ura, K.; Furuya, H.; Sakaki, Y.
Gene 87, 257-263, 1990
A;Title: Genomic organization of the human amyloid beta-protein precursor gene.
A;Reference number: I39451; MUID:90236318; PMID:2110105
A;Accession: I39451
A;Status: nucleic acid sequence not shown; translation not shown; translated from GB/EMBL
A;Molecule type: DNA
A;Residues: 1-770 <YOSI>
A;Cross-references: GB:M33112; NID:G178613; PIDN:AAB59502.1; PID:G178616
A;Accession: I39451
A;Status: nucleic acid sequence not shown; translation not shown; translated from GB/EMBL
A;Molecule type: DNA
A;Residues: 1-530, 'QWLMVPVAPFAWEAKVGR' <YOS2>
A;Cross-references: GB:M34875; NID:G178608; PIDN:AAB59501.1; PID:G178615
R;Yoshikai, S.I.; Sasaki, H.; Doh-ura, K.; Furuya, H.; Sakaki, Y.
Gene 102, 291-292, 1991
A;Reference number: A59020; MUID:91340168; PMID:1908403
A;Contents: annotation; erratum
A;Note: revised physical map for reference I39451
R;Levy, E.; Carman, M.D.; Fernandez-Madrid, I.J.; Power, M.D.; Lieberburg, I.; van Duinen
Science 248, 1124-1126, 1990
A;Title: Mutation of the Alzheimer's disease amyloid gene in hereditary cerebral hemorrh
A;Reference number: I39453; MUID:90260663; PMID:2111584
A;Accession: I39453
A;Status: translated from GB/EMBL/DBBJ
A;Molecule type: DNA
A;Residues: 656-737 <LEV>
A;Cross-references: GB:M37896; NID:G178618; PIDN:AAAS1727.1; PID:G178620
A;Note: a mutation with 693-Gln is presented
R;Murrell, J.; Farlow, M.; Ghetti, B.; Benson, M.D.
Science 254, 97-99, 1991
A;Title: A mutation in the amyloid precursor protein associated with hereditary Alzheimer
A;Reference number: I59562; MUID:92022553; PMID:1925564
A;Accession: I59562
A;Status: translated from GB/EMBL/DBBJ
A;Molecule type: DNA
A;Residues: 689-716, 'F', 718-737 <MUR>
A;Cross-references: GB:S57665; NID:G236720; PIDN:AAB19991.1; PID:G236721
R;Kamino, K.; Orr, H.T.; Payami, H.; Wijesman, E.M.; Alonso, M.E.; Pulst, S.M.; Anderson,
araki, S.E.; Korenberg, J.R.; Sharma, V.; Kukull, W.; Larson, E.; Heston, L.L.; Martin,
Am. J. Hum. Genet. 51, 998-1014, 1992
A;Title: Linkage and mutational analysis of familial Alzheimer disease kindreds for the
A;Reference number: A44017; MUID:93035397; PMID:1415269
A;Accession: A44017
A;Molecule type: DNA
A;Residues: 687-692, 'G', 694-718 <KAMI>
A;Cross-references: GB:S45135; NID:G257377; PIDN:AAB23645.1; PID:G257378
A;Experimental source: Familial Alzheimer disease family SB
A;Note: sequence extracted from NCBI backbone (NCBIP:115374)
A;Accession: B44017
A;Molecule type: DNA
A;Residues: 687-718 <KAM2>
A;Cross-references: GB:S45136; NID:G257379; PIDN:AAB23646.1; PID:G257380
A;Experimental source: Familial Alzheimer disease family LIT
A;Note: sequence extracted from NCBI backbone (NCBIP:115376)

A;Note: this sequence has a silent mutation
R;Kang, J.; Lemaire, H.G.; Unterbeck, A.; Salbaum, J.M.; Masters, C.L.; Grzeschik, K.H.;
Nature 325, 733-736, 1987
A;Title: The precursor of Alzheimer's disease amyloid A4 protein resembles a cell-surface
A;Reference number: A03134; MUID:87144572; PMID:2881207
A;Accession: A03134
A;Molecule type: mRNA
A;Residues: 1-288, 'V', 365-770 <KAN>
A;Cross-references: GB:Y00264; NID:G28525; PIDN:CAA68374.1; PID:G28526
A;Note: alternative splice form APP(695)
R;Robakis, N.K.; Ramakrishna, N.; Wolfe, G.; Wisniewski, H.M.
Proc. Natl. Acad. Sci. U.S.A. 84, 4190-4194, 1987
A;Title: Molecular cloning and characterization of a cDNA encoding the cerebrovascular a
A;Reference number: A29030; MUID:87231971; PMID:3035574
A;Accession: A29030
A;Molecule type: mRNA
A;Residues: 284-288, 'V', 365-646, 'E', 648-770 <ROB>
A;Cross-references: GB:M16765; NID:G178539; PIDN:AAAS1722.1; PID:G178540
A;Note: the authors translated the codon GAG for residue 647 as Asp
R;Goldgaber, D.; Lerman, M.I.; McBride, O.W.; Saffiotti, U.; Gajdusek, D.C.
Science 235, 877-880, 1987
A;Title: Characterization and chromosomal localization of a cDNA encoding brain amyloid
A;Reference number: A47584; MUID:87120328; PMID:3810169
A;Accession: A47584
A;Molecule type: mRNA
A;Residues: 674-756, 'S', 758-770 <GOL>
A;Cross-references: GB:M15533; NID:G178706; PIDN:AAAS5540.1; PID:G178707
R;Tanzi, R.E.; Guealla, J.F.; Watkins, P.C.; Bruns, G.A.P.; St George-Hyslop, P.; Van Ke
Science 235, 880-884, 1987
A;Title: Amyloid beta protein gene: cDNA, mRNA distribution, and genetic linkage near th
A;Reference number: A47585; MUID:87120329; PMID:2949367
A;Accession: A47585
A;Molecule type: mRNA
A;Residues: 674-703 <TANI>
A;Cross-references: GB:M15533; NID:G177957; PIDN:AAAS1564.1; PID:G177958
R;Dyrks, T.; Weidemann, A.; Mulchaup, G.; Salbaum, J.M.; Lemaire, H.G.; Kang, J.; Muelle
EMBO J. 7, 949-957, 1988
A;Title: Identification, transmembrane orientation and biogenesis of the amyloid A4 prec
A;Reference number: S02638; MUID:88296437; PMID:2900137
A;Accession: S02638
A;Molecule type: mRNA
A;Residues: 672-678 <DYR>
R;Tanzi, R.E.; McClatchey, A.I.; Lamperti, E.D.; Villa-Komaroff, L.; Guealla, J.F.; Neve
Nature 331, 528-530, 1988
A;Title: Protease inhibitor domain encoded by an amyloid protein precursor mRNA associat
A;Reference number: S00707; MUID:88122640; PMID:2893290
A;Accession: S00707
A;Molecule type: mRNA
A;Residues: 286-344, 'I', 365-366 <TAN2>
A;Cross-references: EMBL:X06982; NID:G28817; PIDN:CAA30042.1; PID:G929612
A;Experimental source: promyelocytic leukemia cell line HL60
A;Note: alternative splice form APP(751)
R;Ponté, P.; Gonzalez-Dewhitt, P.; Schilling, J.; Miller, J.; Hsu, D.; Greenberg, B.; Dr
Nature 331, 525-527, 1988
A;Title: A new A4 amyloid mRNA contains a domain homologous to serine proteinase inhibit
A;Reference number: S00925; MUID:88122639; PMID:2893289
A;Accession: S00925
A;Molecule type: mRNA
A;Residues: 1-344, 'I', 365-770 <PO2>
A;Cross-references: GB:X06989; EMBL:Y00297; NID:G28720; PIDN:CAA30050.1; PID:G28721
A;Note: alternative splice form APP(751)
R;Kitaguchi, N.; Takahashi, Y.; Tokushima, Y.; Shiojiri, S.; Ito, H.
Nature 331, 530-532, 1988
A;Title: Novel precursor of Alzheimer's disease amyloid protein shows protease inhibito
A;Reference number: A38949; MUID:88122641; PMID:2893291
A;Accession: A38949
A;Molecule type: mRNA
A;Residues: 287-367 <KIT>
A;Cross-references: GB:X06981; NID:G28816; PIDN:CAA30041.1; PID:G929611
A;Experimental source: glioblastoma cell line
A;Note: alternative splice form APP(770)
R;Vitek, M.P.; Rasool, C.G.; de Sauvage, F.; Vitek, S.M.; Bartus, R.T.; Beer, B.; Ashtot

Brain Res. Mol. Brain Res. 4, 121-131, 1988
A:Title: Absence of mutation in the beta-amyloid cDNAs cloned from the brains of three p
A:Reference number: A30320
A:Accession: A30320
A>Status: not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 284-288, 'V', 365-770 <VIT1>
A:Accession: B30320
A>Status: not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 122-288, 'V', 365-770 <VIT2>
A:Accession: C30320
A>Status: not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 606-770 <VIT3>
R:Zain, S.B.; Salim, M.; Chou, W.G.; Sajdel-Sulkowska, E.M.; Majocha, R.E.; Marotta, C.A
Proc. Natl. Acad. Sci. U.S.A. 85, 929-933, 1988
A:Title: Molecular cloning of amyloid cDNA derived from mRNA of the Alzheimer disease br
A:Reference number: A31087; MUID:88124954; PMID:2893379
A:Accession: A31087
A:Molecule type: mRNA
A:Residues: 507-770 <ZAI>
A:Cross-references: GB:M18734; NID:g178572; PIDN:AAA51726.1; PID:g178573
A:Note: the authors translated the codon GAA for residue 599 as Gly, ACC for residue 603
8 as Val, GTG for residue 609 as Asn, AAT for residue 610 as Gly, and GGT for residue 65
A:Note: the cited Genbank accession number, J03594, is not in release 101.0
R:Masters, C.L.; Multhaup, G.; Simms, G.; Potgiesser, J.; Martins, R.N.; Beyreuther, K.

Query Match 20.5%; Score 154; DB 1; Length 770;
Best Local Similarity 44.4%; Pred. No. 6e-06;
Matches 24; Conservative 8; Mismatches 22; Indels 0; Gaps 0;

Qy 74 KDICMPQEAGPCLASIPHHWYNNKTKICSEFIYGGCGGNNNFQTEAICLVTC 127
Db 288 REVCSQAETGTCRAMISRWFVDVTEGKCAFFYGGCGGNRRNFDTEYCMAVC 341

RESULT 23
S19327
venom basic proteinase inhibitor - leaf-nosed viper
N:Alternate names: trypsin inhibitor (kunitz-type)
C:Species: Eristocophis macmahoni (leaf-nosed viper)
C:Date: 22-Nov-1993 #sequence_revision 03-Nov-1995 #text_change 09-Jul-2004
C:Accession: S19327
R:Siddiqi, A.R.; Zaidi, Z.H.; Joernvall, H.
FEBS Lett. 294, 141-143, 1991
A:Title: Purification and characterization of a Kunitz-type trypsin inhibitor from Leaf-
A:Reference number: S19327; MUID:92077130; PMID:1743283
A:Accession: S19327
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-62 <SID>
A:Cross-references: UNIPROT:P24541
C:Superfamily: basic proteinase inhibitor; animal Kunitz-type proteinase inhibitor homol
C:Keywords: serine proteinase inhibitor; venom
F:2-52/Domain: animal Kunitz-type proteinase inhibitor homology <BPI>

Query Match 20.3%; Score 153; DB 2; Length 62;
Best Local Similarity 51.0%; Pred. No. 9.5e-07;
Matches 26; Conservative 6; Mismatches 19; Indels 0; Gaps 0;

Qy 77 CSMPOEAGPCLASIPHHWYNNKTKICSEFIYGGCGGNNNFQTEAICLVTC 127
Db 2 CYLDDPQVCXKHIPFRFYNPASNKCKNFIYGGCGGNANFETRAECRHTC 52

RESULT 24
S07451
proteinase inhibitor 5.II - snake-locks sea anemone
C:Species: Anemonia sulcata (snake-locks sea anemone)
C:Date: 31-Dec-1990 #sequence_revision 09-May-1997 #text_change 09-Jul-2004
C:Accession: S07451; B27222
R:Wunderer, G.; Machleidt, W.; Fritz, H.

Meth. Enzymol. 80, 816-820, 1981
A:Title: The broad-specificity proteinase inhibitor 5 II from the sea anemone Anemonia su
A:Reference number: S07451
A:Accession: S07451
A:Molecule type: protein
A:Residues: 1-59 <WUN>
A:Cross-references: UNIPROT:P10280
A:Note: 13-Arg, 16-Gly, 17-Gly, 25-Leu, 28-Arg, and 39-Arg were also found
R:Krebs, H.C.; Habermehl, G.G.
Naturwissenschaften 74, 395-396, 1987
A:Title: Isolierung und strukturaufklaerung eines haemolytisch aktiven peptids aus der se
A:Reference number: A94700
A:Accession: B27222
A:Molecule type: protein
A:Residues: 1-38, 'R', 40, 'BB', 45-48, 'ZZ', 51, 'Z', 53-62 <KRE>
C:Superfamily: basic proteinase inhibitor; animal Kunitz-type proteinase inhibitor homol
C:Keywords: serine proteinase inhibitor
F:5-55/Domain: animal Kunitz-type proteinase inhibitor homology <BPI>

Query Match 20.2%; Score 152; DB 2; Length 62;
Best Local Similarity 49.0%; Pred. No. 1.2e-06;
Matches 25; Conservative 6; Mismatches 20; Indels 0; Gaps 0;

Qy 77 CSMPOEAGPCLASIPHHWYNNKTKICSEFIYGGCGGNNNFQTEAICLVTC 127
Db 5 CELPKVVGPCRARPPRYVYNNSSKRCBKFIYGGCGGNANFHTLECEKVC 55

RESULT 25
S06678
Alzheimer's disease amyloid beta protein - rhesus macaque (fragment)
C:Species: Macaca mulatta (rhesus macaque)
C:Date: 28-Feb-1990 #sequence_revision 28-Feb-1990 #text_change 09-Jul-2004
C:Accession: S06678
R:Koo, E.H.; Sisodia, S.S.; Price, D.L.
submitted to the EMBL Data Library, July 1989
A:Reference number: S06678
A:Accession: S06678
A:Molecule type: mRNA
A:Residues: 1-76 <KOO>
A:Cross-references: UNIPROT:P29216; EMBL:X15985; NID:g38080; PIDN:CAA34116.1; PID:g93013;
C:Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase in
C:Keywords: alternative splicing; serine proteinase inhibitor
F:3-53/Domain: animal Kunitz-type proteinase inhibitor homology <BPI>

Query Match 20.2%; Score 152; DB 2; Length 76;
Best Local Similarity 45.3%; Pred. No. 1.4e-06;
Matches 24; Conservative 7; Mismatches 22; Indels 0; Gaps 0;

Qy 75 DICSMPOEAGPCLASIPHHWYNNKTKICSEFIYGGCGGNNNFQTEAICLVTC 127
Db 1 EVCSEQAETGTCRAMISRWFVDVTEGKCAFFYGGCGGNRRNFDTEYCMAVC 53

RESULT 26
S03607
Alzheimer's disease amyloid A4 protein - rat (fragment)
C:Species: Rattus norvegicus (Norway rat)
C:Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 09-Jul-2004
C:Accession: S03607
R:Kang, J.; Mueller-Hill, B.
Nucleic Acids Res. 17, 2130, 1989
A:Title: The sequence of the two extra exons in rat preA4.
A:Reference number: S03607; MUID:89183625; PMID:2648331
A:Accession: S03607
A:Molecule type: mRNA
A:Residues: 1-76 <KAN>
A:Cross-references: UNIPROT:P08592; EMBL:X14066; NID:g56957; PIDN:CAA32229.1; PID:g93026;
C:Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase in
C:Keywords: alternative splicing; serine proteinase inhibitor; transmembrane protein
F:3-53/Domain: animal Kunitz-type proteinase inhibitor homology <BPI>

Query Match 20.2%; Score 152; DB 2; Length 76;

Best Local Similarity 45.3%; Pred. No. 1.4e-06;
Matches 24; Conservative 7; Mismatches 22; Indels 0; Gaps 0;

QY 75 DICSMPEACPGCLASIPHWNNKTKICSEFIYGGCGGNNNNPQTAEIACLVTCT 127
::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||:
Db 1 EVCSEQRGTGFCRAMISRWYFDVTEGKCAFFFYGGCGGNRNDFDIEYCMAVC 53

RESULT 27

HCHU

alpha-1-microglobulin/inter-alpha-trypsin inhibitor precursor [validated] - human N; Alternate names: bikunin; complex-forming glycoprotein heterogeneous in charge (HC) rich protein
N; Contains: alpha-1-microglobulin (protein HC); inter-alpha-trypsin inhibitor N; Species: Homo sapiens (man)
C; Date: 15-Oct-1982 #sequence revision 30-Jun-1987 #text change 09-Jul-2004 C; Accession: S13433, S10778, A93642; A90074; A90225; A90686; PNO450; B39079; A61580; B253217
R; Vetr, H.; Gebhard, W.
Biol. Chem. Hoppe-Seyler 371, 1185-1196, 1990
A; Title: Structure of the human alpha(1)-microglobulin-bikunin gene.
A; Reference number: S13433; UID: 91214554; PMID: 1708673
A; Accession: S13433
A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-352 <NET>
A; Cross-references: UNIPROT:P02760; EMBL:X54816; NID:g24475; PIDN:CAA38585.1; PID:g82561 R; Diarra-Mehrpour, M.; Bourguignon, J.; Sesboue, R.; Salier, J.P.; Leveillard, T.; Mart Eur. J. Biochem. 191, 131-139, 1990
A; Title: Structural analysis of the human inter-alpha-trypsin inhibitor light-chain gene
A; Reference number: S10778; UID: 90336621; PMID: 1696200
A; Accession: S10778
A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-202 <DIA>
R; Kaumeyer, J.F.; Polazzi, J.O.; Kotick, M.P.
Nucleic Acids Res. 14, 7839-7850, 1986
A; Title: The mRNA for a proteinase inhibitor related to the HI-30 domain of inter-alpha-N; Reference number: A93642; UID: 87040757; PMID: 2430261
A; Accession: A93642
A; Molecule type: mRNA
A; Residues: 1-352 <KAU>
A; Cross-references: GB:X04494; NID:g24478; PIDN:CAA28182.1; PID:g24479 R; Lopez Otin, C.; Grubb, A.O.; Mendez, E.
Arch. Biochem. Biophys. 228, 544-554, 1984
A; Title: The complete amino acid sequence of human complex-forming glycoprotein heteroge A; Reference number: A90074; UID: 84126849; PMID: 6198962
A; Accession: A90074
A; Molecule type: protein
A; Residues: 20-56, 58-202 <LOP>
A; Experimental source: individual with tubular proteinuria
A; Note: no evidence of sequence heterogeneity could be found, in spite of persistent het R; Takagi, T.; Takagi, K.; Kawai, T.
Biochem. Biophys. Res. Commun. 98, 997-1001, 1991
A; Title: Complete amino acid sequence of human alpha--1-microglobulin.
A; Reference number: A90225; UID: 81184038; PMID: 6164372
A; Accession: A90225
A; Molecule type: protein
A; Residues: 20-47, 58-136, 138-141, 'T', 143-144, 146-198 <TAK>
A; Experimental source: pooled urine of patients with tubular proteinuria
R; Reisinger, P.; Hochstrasser, K.; Albrecht, G.J.; Lempert, K.; Salier, J.P.
Biol. Chem. Hoppe-Seyler 366, 479-483, 1985
A; Title: Human inter-alpha-trypsin inhibitor: localization of the kunitz-type domains in A; Reference number: A90686; UID: 85225968; PMID: 2408638
A; Accession: A90686
A; Molecule type: protein
A; Residues: 20-230, 'VI', 293-342, 'E', 344-350 <REI>
R; Atmani, F.; Lacour, B.; Strecker, G.; Parvy, P.; Drueeke, T.; Daudon, M.
Biochem. Biophys. Res. Commun. 191, 1158-1165, 1993
A; Title: Molecular characteristics of uronic-acid-rich protein, a strong inhibitor of ca A; Reference number: PNO450; UID: 93221481; PMID: 8466493
A; Accession: PNO450
A; Molecule type: protein

[illegible]

C:Species: Bombyx mori (silkworm)
C:Date: 30-Sep-1989 #sequence_revision 30-Sep-1989 #text_change 09-Jul-2004
C:Accession: S01803
R:Sasaaki, T.
Biol. Chem. Hoppe-Seyler 369, 1235-1241, 1988
A:Title: Amino-acid sequences of two basic chymotrypsin inhibitors from silkworm larval
A:Reference number: S01802; MUID:89228538; PMID:3072972
A:Accession: S01803
A:Molecule type: protein
A:Residues: 1-62 <SAS>
A:Cross-references: UNIPROT:P10832
C:Superfamily: basic proteinase inhibitor
F:9-60/Domain: animal Kunitz-type proteinase inhibitor homology <BPI>
Query Match 19.7%; Score 148.5; DB 2; Length 62;
Best Local Similarity 52.6%; Pred. No. 2.3e-06;
Matches 30; Conservative 5; Mismatches 21; Indels 1; Gaps 1;
QY 74 KDICSM-P-QEAGPCLASIPHWYNNKTKICSEFYGGCGNNNFQTEAICLVTCCK 129
Db 6 KPICFQAFGNSGPCFAYIKLYSNQTKKCEBFYGGCKGNDNRFDTLAECQKCIK 62
RESULT 39
I46937
tissue factor pathway inhibitor - rabbit
C:Species: Oryctolagus cuniculus (domestic rabbit)
C:Date: 04-Sep-1997 #sequence_revision 04-Sep-1997 #text_change 09-Jul-2004
C:Accession: I46937
R:Belaouaj, A.; Kuppuswamy, M.N.; Birktoft, J.J.; Bajaj, S.P.
Thromb. Res. 69, 547-553, 1993
A:Title: Revised cDNA sequence of rabbit tissue factor pathway inhibitor.
A:Reference number: I46937; MUID:93276427; PMID:8503123
A:Accession: I46937
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-299 <BEL>
C:Cross-references: UNIPROT:P19761; GB:S61902; NID:G386015; PIDN:AAB26836.1; PID:G386016
C:Superfamily: tissue factor pathway inhibitor; animal Kunitz-type proteinase inhibitor
F:49-99/Domain: animal Kunitz-type proteinase inhibitor homology <BPI1>
F:120-170/Domain: animal Kunitz-type proteinase inhibitor homology <BPI>
F:212-262/Domain: animal Kunitz-type proteinase inhibitor homology <BPI2>
Query Match 19.7%; Score 148; DB 2; Length 299;
Best Local Similarity 29.3%; Pred. No. 9.3e-06;
Matches 48; Conservative 21; Mismatches 51; Indels 44; Gaps 8;
QY 3 LSLGLPILV-----PFILGLD---QEFGHA-----EG-----ILGKP 32
Db 14 LLLGLVPAPVSSAAEDEFNTIDIKPPLQKPTHSFCMKVDDGPCRAYIKRFFFNILTHQ 73
QY 33 CPK-IKVEE-----VEEDQCTK--PRDCPENMKCCPSCGKKCLDFKDKICSMPEAG 84
Db 74 CBEFYGGCGENRPFESLECKEKCARDYPKMTKLTQKQK-----PDFCFLEEDRG 127
QY 85 PCLASIPHWYNNKTKICSEFYGGCGNNNFQTEAICLVTCCK 128
Db 128 ICRGYITRIFYNNQSKQCFKRYGGCLGLNLFESLECKNTCE 171
RESULT 40
TIHOBI
alpha-1-microglobulin/inter-alpha-trypsin inhibitor - horse (fragment)
N:Alternate names: EI-14 (inhibitory fragment of ITI); ITI; trypsin inhibitor, E-UTI
C:Species: Equus caballus (domestic horse)
C:Date: 30-Jun-1987 #sequence_revision 04-Feb-2000 #text_change 09-Jul-2004
C:Accession: A01210; A45653
R:Hochrassner, K.; Wachter, E.; Albrecht, G.J.; Reisinger, P.
Biol. Chem. Hoppe-Seyler 366, 473-478, 1985
A:Title: Kunitz-type proteinase inhibitors derived by limited proteolysis of the inter-a
A:Reference number: A90685; MUID:85225967; PMID:2408637
A:Accession: A01210

A:Molecule type: protein
A:Residues: 3-125 <HOC>
A:Cross-references: UNIPROT:P04365
R:Veeraragavan, K.; Singh, K.; Wachter, E.; Hochrassner, K.
Biochem. Int. 26, 405-413, 1992
A:Title: Characterization of a trypsin inhibitor from equine urine.
A:Reference number: A45653; MUID:92328813; PMID:1627153
A:Accession: A45653
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-12, 'E', 14-33 <VEE>
A:Cross-references: PIDN:AAB22430.1; PID:G250858
A:Experimental source: urine
A:Note: sequence extracted from NCBI backbone (NCBP:107966)
C:Comment: This inhibitory fragment, released from native ITI after limited proteolysis
first domain interacts weakly with PMN-granulocytic elastase and not at all with pancrea
C:Comment: The amino acid at position P2' (19-Met) appears to determine the specificity
d elastase; those with leucine interact strongly.
C:Superfamily: alpha-1-microglobulin and inter-alpha-trypsin inhibitor light chain precu
C:Keywords: duplication; glycoprotein; plasma; serine proteinase inhibitor
F:7-57/Domain: animal Kunitz-type proteinase inhibitor homology <BPI>
F:63-113/Domain: animal Kunitz-type proteinase inhibitor homology <BP2>
F:7-57,16-40,32-53,63-113,72-96,88-109/Disulfide bonds: #status predicted
F:17/Inhibitory site: Leu (chymotrypsin, elastase) #status predicted
F:26/Binding site: carbohydrate (Asn) (covalent) #status experimental
F:73/Inhibitory site: Arg (trypsin) #status predicted
Query Match 19.5%; Score 147; DB 1; Length 125;
Best Local Similarity 42.9%; Pred. No. 5.6e-06;
Matches 24; Conservative 9; Mismatches 23; Indels 0; Gaps 0;
QY 73 RKDICSMPEQAGPCLASIPHWYNNKTKICSEFYGGCGNNNFQTEAICLVTCCK 128
Db 3 KEDSQDLHAQGPCLGMISRYFYNGTSMACETFOYGGCLGNGNPNFASQKCLQTCR 58
RESULT 41
TIHO
basic proteinase inhibitor precursor - bovine
N:Alternate names: aprotinin; basic pancreatic trypsin inhibitor; BPTI; cationic kallik
C:Species: Bos primigenius taurus (cattle)
C:Date: 24-Apr-1984 #sequence_revision 22-Jul-1994 #text_change 09-Jul-2004
C:Accession: S00277; A30333; S10546; S02486; S28197; A90162; A90203; A90736; A90927; A34
R:Creighton, T.E.; Charles, I.G.
J. Mol. Biol. 194, 11-22, 1987
A:Title: Sequences of the genes and polypeptide precursors for two bovine protease inhib
A:Reference number: S00274; MUID:87283304; PMID:2441071
A:Accession: S00277
A:Molecule type: DNA; mRNA
A:Residues: 1-100 <CR2>
A:Cross-references: UNIPROT:P00974; GB:M20934; GB:X05274; NID:G162767; PIDN:AAD13685.1;
R:Creighton, T.E.; Charles, I.G.
Cold Spring Harb. Symp. Quant. Biol. 52, 511-519, 1987
A:Title: Biosynthesis, processing, and evolution of bovine pancreatic trypsin inhibitor
A:Reference number: A90926; MUID:88295740; PMID:2456884
A:Accession: A30333
A:Molecule type: DNA
A:Residues: 1-100 <CR3>
A:Cross-references: GB:M20934; GB:X05274; NID:G162767; PIDN:AAD13685.1; PID:G162769
R:Kingston, I.B.; Anderson, S.
Biochem. J. 233, 443-450, 1986
A:Title: Sequences encoding two trypsin inhibitors occur in strikingly similar genomic
A:Reference number: S10546; MUID:86158754; PMID:2420326
A:Accession: S10546
A:Molecule type: DNA
A:Residues: 34-97 <KIN>
R:Piorretti, E.; Angeletti, M.; Fiorucci, L.; Barra, D.; Bossa, F.; Ascoli, F.
Biol. Chem. Hoppe-Seyler 369 (Suppl.), 37-42, 1988
A:Title: Aprotinin-like isoinhibitors in bovine organs.
A:Reference number: S02485; MUID:89076531; PMID:2462435
A:Accession: S02486
A:Molecule type: protein
A:Residues: 36-93 <FIO>

Search completed: September 21, 2005, 16:41:09
Job time : 30.9351 secs

Query Match 19.1%; Score 144; DB 2; Length 59;
Best Local Similarity 48.1%; Pred. No. 5.5e-06;
Matches 26: Conservative 5; Mismatches 23; Indels 0; Gaps 0;

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 21, 2005, 15:41:33 ; Search time 72.2625 Seconds
(without alignments)
928.315 Million cell updates/sec

Title: US-10-807-204-1
Perfect score: 753
Sequence: 1 MGLSGLLPILVPFILLGDIQ.....GNNNFQTEALCVTCCKYH 131

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 50 summaries

Database : UniProt_03.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	574	76.2	131	1 WFD6 HUMAN	Q9bqy6 homo sapien
2	526	69.9	137	2 Q9BDL0	Q9bd10 oryctolagus
3	467	62.0	133	1 EPII HUMAN	Q95925 homo sapien
4	467	62.0	143	2 Q8GT9	Q86tp9 homo sapien
5	462	61.4	182	2 Q6IE19	Q6ie19 rattus norv
6	461	61.2	133	2 Q8HZ45	Q8nz45 papio papio
7	453	60.2	133	1 EPII MACMU	Q9bd11 macaca mula
8	398	52.9	134	1 EPII MOUSE	Q9da01 mus musculus
9	231	30.7	77	2 Q8HZ44	Q8hz44 papio hamad
10	217	28.8	241	1 WFD8 HUMAN	Q8iua0 homo sapien
11	197	26.2	759	2 Q8IT91	Q8it91 ancylostoma
12	187	24.8	2772	2 Q9VAV4	Q9vav4 drosophila
13	187	24.8	2776	2 Q869A0	Q869a0 drosophila
14	187	24.8	2894	2 Q7KRX2	Q7krx2 drosophila
15	187	24.8	2898	2 Q868Z9	Q868z9 drosophila
16	186	24.7	110	1 IBP CARCR	P00993 caretta car
17	184.5	24.5	988	2 Q22685	Q22685 caenorhabdi
18	182.5	24.2	571	2 Q7TQNZ	Q7tqn3 mus musculus
19	182	24.2	2419	2 Q7PFX21	Q7pxz1 anopheles g
20	175	23.2	3198	2 Q9UG8	Q9u988 manduca sex
21	174	23.1	515	2 Q6DRJ1	Q6drj1 brachydanio
22	173.5	23.0	576	2 Q8TEU8	Q8teu8 homo sapien
23	173.5	23.0	576	2 Q6UXZ9	Q6uxz9 homo sapien
24	173	23.0	587	2 Q6AX20	Q6ax20 xenopus lae
25	173	23.0	751	2 Q708Z0	Q708z0 xenopus lae
26	172.5	22.9	1599	2 Q09983	Q09983 caenorhabdi
27	172	22.8	67	1 IBPC BOVIN	P00976 bos taurus
28	172	22.8	516	2 Q7F363	Q7f363 brachydanio
29	172	22.8	750	2 Q6DUB6	Q6dub6 xenopus tro
30	171	22.7	1416	1 YN81 CABEL	Q03610 caenorhabdi
31	170.5	22.6	122	1 BTA1_BOOMI	P83609 boophilus m

ALIGNMENTS

RESULT 1

ID	WFD6 HUMAN	STANDARD;	PRT;	131 AA.
AC	Q9BQY6; Q8NFV6;			
DT	10-OCT-2003 (Rel. 42, Created)			
DT	10-OCT-2003 (Rel. 42, Last sequence update)			
DT	05-JUL-2004 (Rel. 44, Last annotation update)			
DE	WAP four-disulfide core domain protein 6 precursor (Putative protease inhibitor WAP6).			
GN	Name=WPD6; Synonyms=C20orf171, WAP6;			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A. (ISOFORM 2).			
RX	MEDLINE=23304654; PubMed=12206714; DOI=10.1042/BJ20020869;			
RA	Clausen A., Lilja H., Lundwall A.;			
RT	"A locus on human chromosome 20 contains several genes expressing protease inhibitor domains with homology to whey acidic protein.";			
RL	Biochem. J. 368:233-242(2002).			
RN	[2]			
RP	SEQUENCE FROM N.A. (ISOFORM 1).			
RX	MEDLINE=21638749; PubMed=11780052; DOI=10.1038/414865a;			
RA	Deloukas P., Matthews L.H., Ashurst J.L., Burton J., Gilbert J.G.R.,			
RA	Jones M., Stavrides G., Almeida J.P., Babbage A.K., Begguley C.L.,			
RA	Bailey J., Barlow K.F., Bates K.N., Beard L.M., Beare D.M.,			
RA	Beasley O.P., Bird C.P., Blakey S.E., Bridgeman A.M., Brown A.J.,			
RA	Buck D., Burrill W.D., Butler A.P., Carder C., Carter N.P.,			
RA	Chapman J.C., Clamp M., Clark G., Clark L.N., Clark S.V., Clee C.M.,			
RA	Clegg S., Cobley V.E., Collier R.E., Connor R.E., Corby N.R.,			
RA	Coulson A., Coville G.J., Deadman R., Dhani P.D., Dunn M.,			
RA	Ellington A.G., Frankland J.A., Fraser A., French L., Garner P.,			
RA	Graham D.V., Griffiths C., Griffiths M.N.D., Gwilliam R., Hall R.E.,			
RA	Hammond S., Harley J.L., Heath P.D., Ho S., Holden J.L., Howden P.J.,			
RA	Huckle E., Hunt A.R., Hunt S.E., Jekosch K., Johnson C.M., Johnson D.,			
RA	Kay M.P., Kimberley A.M., King A., Knights A., Laird G.K., Lawlor S.,			
RA	Lehvaeslahti M.H., Leversha M.A., Lloyd C., Lloyd D.M., Lovell J.D.,			
RA	Marsh V.L., Martin S.L., McConachie L.J., McClay K., McMurray A.A.,			
RA	Milne S.A., Mistry D., Moore M.J.F., Mullikin J.C., Nickerson T.,			
RA	Oliver K., Parker A., Patel R., Pearce T.A.V., Peck A.I.,			
RA	Phillimore B.J.C.T., Prathalingam S.R., Plumb R.W., Ramsay H.,			
RA	Rice C.M., Ross M.T., Scott C.E., Sehra H.K., Shownkeen R., Sims S.,			
RA	Skuce C.D., Smith M.L., Soderlund C., Steward C.A., Sulston J.E.,			
RA	Swann R.M., Symamore N., Taylor R., Tee L., Thomas D.W., Thorpe A.,			
RA	Tracey A., Tromans A.C., Vaudin M., Wall M., Wallis J.M.,			
RA	Whitehead S.L., Whittaker P., Willey D.L., Williams L., Williams S.A.,			
RA	Wilming L., Wray P.W., Hubbard T., Durbin R.M., Bentley D.R., Beck S.,			
RA	Rogers J.;			

RT "The DNA sequence and comparative analysis of human chromosome 20.";
RL Nature 414:865-871(2001).
CC -1- SUBCELLULAR LOCATION: Secreted (Potential).
CC -1- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=1;
CC IsoId=Q9BQY6-1; Sequence=Displayed;
CC Name=2;
CC IsoId=Q9BOY6-2; Sequence=VSP_007550, VSP_007551;
CC -1- TISSUE SPECIFICITY: Ubiquitously expressed, but the highest levels
CC are found in epididymis, testis and trachea.
CC -1- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.
CC -1- SIMILARITY: Contains 1 WAP-type domain.
CC -----
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CC -----
CC EMBL; AF411861; AAN03684.1; -;
CC EMBL; AL031663; CAC36264.1; -;
CC HSSP; P02760; 1BIK.
CC Genew; HGNC:16164; WFD6.
CC InterPro; IPR002223; Prot_Inh_Kunz-m.
CC InterPro; IPR008197; WAP_Inh_Kunz-m.
CC Pfam; PF00014; Kunitz_BPTI; 1.
CC Pfam; PF00095; WAP; 1.
CC PRINTS; PR00759; BASICTPASE.
CC ProDom; PD000222; Prot_Inh_Kunz-m; 1.
CC SMART; SM00131; KU; 1.
CC SMART; SM00217; WAP; 1.
CC PROSITE; PS00317; 4_DISULFIDE_CORE; FALSE NEG.
CC PROSITE; PS00280; BPTI_KUNITZ_1; FALSE NEG.
CC PROSITE; PS0279; BPTI_KUNITZ_2; 1.
CC KW Alternative splicing; Serine protease inhibitor; Signal.
CC SIGNAL 1 25 Potential.
CC CHAIN 26 131 WAP four-disulfide core domain protein 6.
CC DOMAIN 31 69 WAP.
CC DOMAIN 70 128 BPTI/Kunitz inhibitor.
CC DISULFID 33 61 By similarity.
CC DISULFID 48 60 By similarity.
CC DISULFID 54 69 By similarity.
CC VARSPLIC 75 86 IYAVCHRRLLAPA -> VSLTYHKEELE (in isoform
CC 2).
CC FTid=VSP_007550.
CC VARSPLIC 87 131 Missing (in isoform 2).
CC FTid=VSP_007551.
CC SEQUENCE 131 AA; 14626 MW; 2F6D06EF43EB7564 CRC64;

Query Match 76.2%; Score 574; DB 1; Length 131;
Best Local Similarity 82.4%; Pred. No. 4.1e-47;
Matches 108; Conservative 1; Mismatches 22; Indels 0; Gaps 0;
SQ SEQUENCE 131 AA; 14626 MW; 2F6D06EF43EB7564 CRC64;

Qy 1 MGLSGLLPILVPFILLGDIQPGHAEGLGKPCPKIKVECEVEEIDQCTKPRDCPENMKC 60
Db 1 MGLSGLLPILVPFILLGDIQPGHAEGLGKPCPKIKVECEVEEIDQCTKPRDCPENMKC 60
Qy 61 CPFGSGKKCLDFRKIDCSMPQEAQPCLASIPHWYNNKTKICSEFIYGGCGGNNNNFQTE 120
Db 61 CPFGSGKKCLDFRKIDCSMPQEAQPCLASIPHWYNNKTKICSEFIYGGCGGNNNNFQTE 120
Qy 121 AICLVTKCKYH 131
Db 121 AICLVTKCKYH 131

RESULT 2

Q9BDL0
ID Q9BDL0 PRELIMINARY; PRT; 137 AA.
AC Q9BDL0;

DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Eppin.
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Testis;
RX MEDLINE=22791380; PubMed=12909348; DOI=10.1016/S0378-1119(03)00608-5;
RA Sivashanmugam P., Hall S.H., Hamil K.G., French F.S., O'Rand M.G.,
Richardson R.T.;
RT "Characterization of mouse Eppin and a gene cluster of similar
RT protease inhibitors on mouse chromosome 2.";
RL Gene 312:125-134(2003).
CC -1- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.
CC EMBL; AF346415; AAK31337.1; -;
CC HSSP; Q16019; IAAp.
CC GO; GO:0004867; F:serine-type endopeptidase inhibitor activity; IEA.
CC InterPro; IPR002223; Prot_Inh_Kunz-m.
CC InterPro; IPR008197; WAP.
CC Pfam; PF00014; Kunitz_BPTI; 1.
CC Pfam; PF00095; WAP; 1.
CC PRINTS; PR00003; 4DISULPHCORE.
CC PRINTS; PR00759; BASICTPASE.
CC ProDom; PD000222; Prot_Inh_Kunz-m; 1.
CC SMART; SM00131; KU; 1.
CC SMART; SM00217; WAP; 1.
CC PROSITE; PS00280; BPTI_KUNITZ_1; 1.
CC PROSITE; PS0279; BPTI_KUNITZ_2; 1.
SQ SEQUENCE 137 AA; 15773 MW; F397AF4E065D626B CRC64;

Query Match 69.9%; Score 526; DB 2; Length 137;
Best Local Similarity 71.1%; Pred. No. 1.6e-42;
Matches 91; Conservative 14; Mismatches 23; Indels 0; Gaps 0;
Qy 1 MGLSGLLPILVPFILLGDIQPGHAEGLGKPCPKIKVECEVEEIDQCTKPRDCPENMKC 60
Db 1 MRLSRLLPILLPILLGDIQPGHAEGLGKPCPKIKVECEVEEIDQCTKPRDCPENMKC 60
Qy 61 CPFGSGKKCLDFRKIDCSMPQEAQPCLASIPHWYNNKTKICSEFIYGGCGGNNNNFQTE 120
Db 61 CLFNGCGKKCLDRKVCMPKETGPCLAIFPRWYDKEREICTEFTYGGCGGNNNNFQTE 120
Qy 121 AICLVTKCK 128
Db 121 AICLVTKCK 128

RESULT 3
EPPI_HUMAN
ID EPPI_HUMAN STANDARD; PRT; 133 AA.
AC O95925; Q96SD7; Q9HD30;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Eppin precursor (Spididymal protease inhibitor) (Serine protease
DE inhibitor-like with Kunitz and WAP domains 1) (WAP four-disulfide core
DE domain protein 7) (Protease inhibitor WAP7).
GN Name=SPINLW1; Synonyms=WAP7, WFD67;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
RC TISSUE=Epididymis, and Testis;
RX MEDLINE=21297183; PubMed=11404006; DOI=10.1016/S0378-1119(01)00462-0;
RA Richardson R.T., Sivashanmugam P., Hall S.H., Hamil K.G., Moore P.A.,
Ruben S.M., French F.S., O'Rand M.G.;
RT "Cloning and sequencing of human Eppin: a novel family of protease

RT inhibitors expressed in the epididymis and testis.";

RL [2] Gene 270:93-102(2001).

RP SEQUENCE FROM N.A. (ISOFORM 1).

RA Stavrides G.S., Huckle E.J., Deloukas P.;

RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.

RN [3]

RP SEQUENCE FROM N.A.

RX MEDLINE=21638749; PubMed=11780052; DOI=10.1038/414865a;

RA Deloukas P., Matthews L.H., Aheurst J.L., Burton J., Gilbert J.G.R.,

RA Jones M., Stavrides G., Almeida J.P., Babbage A.K., Bagguley C.L.,

RA Bailey J., Barlow K.F., Bates K.N., Beard L.M., Beare D.M.,

RA Beasley O.P., Bird C.P., Blakey S.E., Bridgeman A.M., Brown A.J.,

RA Buck D., Burrill W.D., Butler A.P., Carder C., Carter N.P.,

RA Chapman J.C., Clamp M., Clark L.N., Clark S.Y., Clee C.M.,

RA Clegg S., Cobley V.E., Collier R.E., Connor R.E., Corby N.R.,

RA Coulson A., Coville G.J., Deadman R., Dhani P.D., Dunn M.,

RA Ellington A.G., Frankland J.A., Fraser A., French L., Garner P.,

RA Graham D.V., Griffiths C., Griffiths M.N.D., Gwilliam R., Hall R.E.,

RA Hammond S., Harley J.L., Heath P.D., Ho S., Holden J.L., Howden P.J.,

RA Huckle E., Hunt A.R., Hunt S.E., Jekosch K., Johnson C.M., Johnson D.,

RA Kay M.P., Kimberley A.M., King A., Koights A., Laird G.K., Lawlor S.,

RA Leivaeslhalo M.H., Leversha M.A., Lloyd C., Lloyd D.M., Lovell J.D.,

RA Marsh V.L., Martin S.L., McConachie L.J., McLeay K., McMurray A.A.,

RA Milne S.A., Mistry D., Moore M.J.F., Mullikin J.C., Nickerson T.,

RA Oliver K., Parker A., Patel R., Pearce T.A.V., Peck A.I.,

RA Phillimore B.J.C.T., Prathalingam S.R., Plumb R.W., Ramsay H.,

RA Rice C.M., Ross M.T., Scott C.E., Sehra H.K., Showkneen R., Sims S.,

RA Skuce C.D., Smith M.L., Soderlund C., Steward C.A., Sulston J.E.,

RA Swann R.M., Sycamore N., Taylor R., Tee L., Thomas D.W., Thorpe A.,

RA Tracey A., Tromans A.C., Vaudin M., Wall M., Wallis J.M.,

RA Whitehead S.L., Whittaker P., Willey D.L., Williams L., Williams S.A.,

RA Wilming L., Wray P.W., Hubbard T., Durbin R.M., Bentley D.R., Beck S.,

RA Rogers J.;

RT "The DNA sequence and comparative analysis of human chromosome 20.";

RL Nature 414:865-871(2001).

RN [4]

RP SEQUENCE FROM N.A. (ISOFORM 1).

RC TISSUE=Brain;

RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Schuler G.D.,

RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullány S.J.,

RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,

RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;

RT "Generation and initial analysis of more than 15,000 full-length human

RL and mouse cDNA sequences.";

RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

CC -!- SUBCELLULAR LOCATION: Secreted (Potential).

CC -!- ALTERNATIVE PRODUCTS:

CC Event=Alternative splicing; Named isoforms=2;

CC Name=1;

CC IsoId=O95925-1; Sequence=Displayed;

CC Name=2;

CC IsoId=O95925-2; Sequence=VSP_006755;

CC -!- TISSUE SPECIFICITY: Expressed in epididymis and testis.

CC -!- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.

CC -!- SIMILARITY: Contains 1 WAP-type domain.

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CC EMBL; AF286370; AAC00548.1; -

CC EMBL; AF286369; AAC00547.1; -

CC EMBL; AF286368; AAC00546.1; -

CC EMBL; AL118493; CAB56343.1; -

CC EMBL; AL031663; CAB37635.1; -

CC EMBL; AL031663; CAB36265.1; -

CC EMBL; BC053369; AAH53389.1; -

CC HSSP; P00974; 1BPI.

CC Genew; HGNC:15932; SPINLW1.

CC InterPro; IPR002223; Prot_Inh_Kunz-m.

CC InterPro; IPR00197; WAP.

CC Pfam; PF00014; Kunitz_BPTI; 1.

CC Pfam; PF00095; WAP; 1.

CC PRINTS; PR00003; 4DISULPHCORE.

CC PRINTS; PR00759; BASICPTASE.

CC ProDom; PD000222; Prot_Inh_Kunz-m; 1.

CC SMART; SM00131; KU; 1.

CC SMART; SM00217; WAP; 1.

CC PROSITE; PS00317; 4_DISULFIDE_CORE; 1.

CC PROSITE; PS00280; BPTI_KUNITZ_1; 1.

CC PROSITE; PS00279; BPTI_KUNITZ_2; 1.

CC KW Alternative splicing; Serine protease inhibitor; Signal.

CC SIGNAL 1 21 Potential.

CC CHAIN 22 133 Eppin.

CC DOMAIN 29 73 WAP.

CC FT BPTI/Kunitz inhibitor.

CC FT DISULFID 33 61 By similarity.

CC FT DISULFID 40 65 By similarity.

CC FT DISULFID 48 65 By similarity.

CC FT DISULFID 54 69 By similarity.

CC FT DISULFID 77 127 By similarity.

CC FT DISULFID 86 110 By similarity.

CC FT DISULFID 102 123 By similarity.

CC FT VARSPIC 1 31

CC

CC SEQUENCE 133 AA; 15284 MW; F7831B203366D9DC CRC64;

CC /FTId=VSP_006755.

CC

CC Query Match 62.0%; Score 467; DB 1; Length 133;

CC Best Local Similarity 60.9%; Pred. No. 6.8e-37;

CC Matches 78; Conservative 18; Mismatches 32; Indels 0; Gaps 0;

CC

CC QY 1 MGLSGLLPILVPFILLGDIQEPGHAEGILGKPCPKIYCEVEEIDCTKPRDCPENMKC 60

CC Db 1 MGSSGLLSLLVLLVLLANVQGLTDLWLFPRRCPKIRECECFQERDVCTKQCCDNKKC 60

CC

CC QY 61 CPFGCGKCLDPKDCSMPOBAGPLASIPHHWYNNKTKICSEFIYGCQGNNNNFOTE 120

CC Db 61 CVFGCGKCLDLKQDVCEMPKGTGCLAYFLHWWYDKKONTCSMFYGGCGQGNNNNFQSK 120

CC

CC QY 121 AICLVTK 128

CC Db 121 ANCLNTCK 128

CC

CC RESULT 4

CC Q86TP9 PRELIMINARY; PRT; 143 AA.

CC ID Q86TP9

CC AC Q86TP9

CC DT 01-JUN-2003 (TrEMBLrel. 24, Created)

CC DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)

CC DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)

CC DE SPINLW1 protein (Fragment).

CC GN Name=SPINLW1;

CC OS Homo sapiens (Human).

CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

CC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

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OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RA MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strauberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shermen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh P.,
RA Statchenko L., Maruina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek A.M., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahney J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smallos D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RA Strauberg R.;
RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.
DR EMBL; BC044829; AAH44829.1; -.
DR HSSP; P00974; IUUA.
DR GO; GO:0004867; F:serine-type endopeptidase inhibitor activity; IEA.
DR InterPro; IPR002223; Prot_Inh_Kunz-m.
DR InterPro; IPR008197; WAP.
DR Pfam; PF00095; WAP; 1.
DR PRINTS; PR00759; BASICPTASE.
DR PRODOM; PD000222; Prot_Inh_Kunz-m; 1.
DR SMART; SM00131; KU; 1.
DR SMART; SM00217; WAP; 1.
DR PROSITE; PS00317; 4_DISULFIDE_CORE; 1.
DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
DR PROSITE; PS0279; BPTI_KUNITZ_2; 1.
FT NON-TER 1
SQ SEQUENCE 143 AA; 16506 MW; 92BF56C2B7977508 CRC64;

Query Match 62.0%; Score 467; DB 2; Length 143;
Best Local Similarity 60.9%; Pred. No. 7,3e-37;
Matches 78; Conservative 18; Mismatches 32; Indels 0; Gaps 0;

Oy 1 MGLSGLPILVPFILLGDIQEPGHAEGILGKPCPKIKVECEVEIDQCTKPRDCPENMKC 60
Db 11 MGSGLLSLLVLLANVQEGFLTDWLFPRRCPKIRECECFQBRDVCTKQCDQDNKC 70

Oy 61 CPFGCGKCLDFRKDICSMPQEGAGCLASIPHHWYNNKTKICSEFIYGGCGGNNNFQTE 120
Db 71 CVFSGCKKLDLQDVCSEMPKETGCLAYFLHWWYDKNDTCSMFVYGGCGGNNNFQSK 130

Oy 121 AICLVTK 128
Db 131 ANCLNTCK 138

RESULT 5
Q6IE19 PRELIMINARY; PRT; 182 AA.
AC Q6IE19
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
```

```
DE WAP four-disulfide core 6-like 1.
GN Name=wfdc61;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Sprague-Dawley;
RA PubMed=15060002; DOI=10.1101/gr.1946304;
RA Puente X.S., Lopez-Otin C.;
RT "A genomic analysis of rat proteases and protease inhibitors.";
RL Genome Res. 14:609-622(2004).
CC -!- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.
CC -!- MISCELLANEOUS: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ third party annotation (TPA) entry.
DR EMBL; BN000374; CAB51900.1; -.
DR HSSP; P00974; 1K6U.
DR GO; GO:0004867; F:serine-type endopeptidase inhibitor activity; IEA.
DR InterPro; IPR002223; Prot_Inh_Kunz-m.
DR InterPro; IPR008197; WAP.
DR Pfam; PF00014; Kunitz_BPTI; 1.
DR Pfam; PF00095; WAP; 1.
DR PRINTS; PR00003; 4DISULPHCORE.
DR PRINTS; PR00759; BASICPTASE.
DR PRODOM; PD000222; Prot_Inh_Kunz-m; 1.
DR SMART; SM00131; KU; 1.
DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
DR PROSITE; PS0279; BPTI_KUNITZ_2; 1.
SQ SEQUENCE 182 AA; 21018 MW; EB12D7BFF756707E CRC64;

Query Match 61.4%; Score 462; DB 2; Length 182;
Best Local Similarity 58.3%; Pred. No. 2,8e-36;
Matches 74; Conservative 20; Mismatches 33; Indels 0; Gaps 0;

Oy 5 GLLPILVPFILLGDIQEPGHAEGILGKPCPKIKVECEVEIDQCTKPRDCPENMKCPFS 64
Db 5 GLLPFLVPLIFLWSIQKPLQGLFKTCPKYIKCDFEERSQCSRHKQCPKQRCQCMFA 64

Oy 65 CGKCKLDFRKDICSMPQEGAGCLASIPHHWYNNKTKICSEFIYGGCGGNNNFQTEAICL 124
Db 65 CGKCKLDELNEDICSLPQDAGPCLAYLPRFWYNNKTNLCQFIYGGCGGNTNNFLSKDICT 124

Oy 125 VTCKKYH 131
Db 125 SICTRKH 131

RESULT 6
Q8HZ45 PRELIMINARY; PRT; 133 AA.
AC Q8HZ45
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Epididymal protease inhibitor 1.
GN Name=Eppin;
OS Papio papio (Guinea baboon).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheidae;
OC Cercopitheinae; Papio.
OX NCBI_TaxID=100937;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Testis;
RA Sivashanmugam P., O'Rand M.G., Richardson R.T.;
RL Submitted (AUG-2002) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.
DR EMBL; AY141973; AAN08507.1; -.
DR HSSP; P00974; IUUA.
DR GO; GO:0008233; F:peptidase activity; IEA.
DR GO; GO:0004867; F:serine-type endopeptidase inhibitor activity; IEA.
DR InterPro; IPR002223; Prot_Inh_Kunz-m.
```

DR InterPro; IPR008197; WAP.
DR Pfam; PF00014; Kunitz BPTI; 1.
DR Pfam; PF00095; WAP; 1.
DR PRINTS; PR00759; BASICPTASE.
DR ProDom; PD000222; Prot_Inh_Kunz-m; 1.
DR SMART; SM00131; KU; 1.
DR SMART; SM00217; WAP; 1.
DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
DR PROSITE; PS0279; BPTI_KUNITZ_2; 1.
KW Protease.
SQ SEQUENCE 133 AA; 15277 MW; B33AE57ECBEBE84 CRC64;

Query Match 61.2%; Score 461; DB 2; Length 133;
Best Local Similarity 60.9%; Pred. No. 2.6e-36;
Matches 78; Conservative 15; Mismatches 35; Indels 0; Gaps 0;

QY 1 MGLSGLLPVIFLLGDIQBPQHAEGILGKPCPKIKVCEVEEIDQCTKPRDCPENMKC 60
DB 1 MGSSGLLSLLVLFILLANVQGFGLDWLFPFRCPTIRECEFRERDVCTHRQCPDNKKC 60

QY 61 CFFSGCKKCLDFRKDICSMPQAGPCLASIPHWYNNKTKICSEFIYGGCGQNNNFQTE 120
DB 61 CVFSGCKKCLDLKQDVCMPNETGCLAFFIRWYDKNNYCTSTFYGGCGQNNNFQSE 120

QY 121 AICLVTK 128
DB 121 ANCLNTCK 128

RESULT 7
EPII MACMU
ID EPII MACMU STANDARD; PRT; 133 AA.
AC Q9DA01;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Eppin precursor (Epididymal protease inhibitor) (Serine protease
DE inhibitor-like with Kunitz and WAP domains 1).
GN Name=SPINLW1;
OS Macaca mulatta (Rhesus macaque).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecoidea; Macaca.
OX NCBI_TaxID=9544;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Epithelium, and Testis;
RA Sivashanmugam P., Hall S.H., Hamil K.G., French F.S., O'Rand M.G.,
RA Richardson R.T.;
RT "Characterization of monkey and mouse Eppin, a protease inhibitor from
RT epididymis and testis."
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
CC -1- SUBCELLULAR LOCATION: Secreted (Potential).
CC -1- TISSUE SPECIFICITY: Expressed in epididymis and testis.
CC -1- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.
CC -1- SIMILARITY: Contains 1 WAP-type domain.
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CC or send an email to license@sib-sib.ch).
CC
CC EMBL; AF346414; AAK31336.1; -.
CC HSP; P00974; 1BPI.
DR InterPro; IPR002223; Prot_Inh_Kunz-m.
DR InterPro; IPR008197; WAP_Inh_Kunz-m.
DR Pfam; PF00014; Kunitz BPTI; 1.
DR Pfam; PF00095; WAP; 1.
DR PRINTS; PR00759; BASICPTASE.
DR ProDom; PD000222; Prot_Inh_Kunz-m; 1.

DR SMART; SM00131; KU; 1.
DR SMART; SM00217; WAP; 1.
DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
DR PROSITE; PS0279; BPTI_KUNITZ_2; 1.
KW Serine protease inhibitor; Signal.
FT SIGNAL 1 21 Potential.
FT CHAIN 22 133 Eppin.
FT DOMAIN 29 73 WAP.
FT DOMAIN 77 127 BPTI/Kunitz inhibitor.
FT DISULFID 33 61 By similarity.
FT DISULFID 40 65 By similarity.
FT DISULFID 48 60 By similarity.
FT DISULFID 54 69 By similarity.
FT DISULFID 77 127 By similarity.
FT DISULFID 86 110 By similarity.
FT DISULFID 102 123 By similarity.
SQ SEQUENCE 133 AA; 15277 MW; 433AE5946E39A35E9 CRC64;

Query Match 60.2%; Score 453; DB 1; Length 133;
Best Local Similarity 60.2%; Pred. No. 1.5e-35;
Matches 77; Conservative 16; Mismatches 35; Indels 0; Gaps 0;

QY 1 MGLSGLLPVIFLLGDIQBPQHAEGILGKPCPKIKVCEVEEIDQCTKPRDCPENMKC 60
DB 1 MGSSGLLSLLVLFILLANVQGFGLDWLFPFRCPTIRECEFRERDVCTHRQCPDNKKC 60

QY 61 CFFSGCKKCLDFRKDICSMPQAGPCLASIPHWYNNKTKICSEFIYGGCGQNNNFQTE 120
DB 61 CVFSGCKKCLDLKQDVCMPNETGCLAFFIRWYDKNNYCTSTFYGGCGQNNNFQSE 120

QY 121 AICLVTK 128
DB 121 ANCLNTCK 128

RESULT 8
EPII MOUSE
ID EPII MOUSE STANDARD; PRT; 134 AA.
AC Q9DA01;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Eppin precursor (Epididymal protease inhibitor) (Serine protease
DE inhibitor-like with Kunitz and WAP domains 1).
GN Name=Spinlwl;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/c; TISSUE=Epithelium, and Testis;
RA Sivashanmugam P., Hall S.H., Hamil K.G., French F.S., O'Rand M.G.,
RA Richardson R.T.;
RT "Characterization of monkey and mouse Eppin, a protease inhibitor from
RT epididymis and testis."
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Testis;
RX MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;
RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
RA Nikaido I., Oatso N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,
RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,
RA Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
RA Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,
RA Blake J.A., Bradt D., Bruscia V., Chochia C., Corbani L.E., Cousins S.,
RA Dalka E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,
RA Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,
RA Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,
RA Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,
RA Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
RA Maglott D.R., Maltais L., Marchionni L., Mckenzie L., Miki H.,

AC Q8TUA0; Q96A34;
 DT 10-OCT-2003 (Rel. 42, Created)
 DT 10-OCT-2003 (Rel. 42, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE WAP four-disulfide core domain protein 8 precursor (Putative protease
 DE inhibitor WAP8).
 GN Name=WAP8; Synonym=C20orf170, WAP8;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22304654; PubMed=12206714; DOI=10.1042/BJ20020869;
 RA Claus A., Lilja H., Lundwall A.;
 RT "A locus on human chromosome 20 contains several genes expressing
 RT protease inhibitor domains with homology to whey acidic protein.";
 RL Biochem. J. 368:233-242 (2002).
 [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21638749; PubMed=11780052; DOI=10.1038/414865a;
 RA Deloukas P., Matthews L.H., Aheuret J.L., Burton J., Gilbert J.G.R.,
 RA Jones M., Stavrides G., Almeida J.P., Babbage A.K., Bagguley C.L.,
 RA Bailey J., Barlow K.F., Bates K.N., Beard L.M., Beare D.M.,
 RA Beasley O.P., Bird C.P., Blakey S.E., Bridgeman A.M., Brown A.J.,
 RA Buck D., Burrill W.D., Butler A.P., Carder C., Carter N.P.,
 RA Chapman J.C., Clamp M., Clark G., Clark L.N., Clark S.Y., Clee C.M.,
 RA Clegg S., Cobley V.E., Collier R.E., Connor R.E., Corby N.R.,
 RA Coulson A., Coville G.J., Deadman R., Dhani P.D., Dunn M.,
 RA Ellington A.G., Frankland J.A., Fraser A., French L., Garner P.,
 RA Graham D.V., Griffiths C., Griffiths M.N.D., Gwilliam R., Hall R.E.,
 RA Hammond S., Harley J.L., Heath P.D., Ho S., Holden J.L., Howden P.J.,
 RA Huckle E., Hunt A.R., Hunt S.E., Jekosch K., Johnson C.M., Johnson D.,
 RA Kay M.P., Kimberley A.M., King A., Knights A., Laird G.K., Lawlor S.,
 RA Lehesvaara M.H., Leversha M.A., Lloyd C., Lloyd D.M., Lovell J.D.,
 RA Marsh V.L., Martin S.L., McConachie L.J., McLay K., McMurray A.A.,
 RA Milne S.A., Mistry D., Moore M.J.F., Mullikin J.C., Nickerson T.,
 RA Oliver K., Parker A., Patel R., Pearce T.A.V., Peck A.I.,
 RA Phillimore B.J.C.T., Prathalingam S.R., Plumb R.W., Ramsay H.,
 RA Rice C.M., Ross M.T., Scott C.E., Sehra H.K., Showkneen R., Sims S.,
 RA Skuce C.D., Smith M.L., Soderlund C., Steward C.A., Sulston J.E.,
 RA Swann R.M., Sycamore N., Taylor R., Tee L., Thomas D.W., Thorpe A.,
 RA Tracey A., Tromans A.C., Vaudin M., Wall M., Wallis J.M.,
 RA Whitehead S.L., Whittaker P., Willey D.L., Williams L., Williams S.A.,
 RA Wilming L., Wray P.W., Hubbard T., Durbin R.M., Bentley D.R., Beck S.,
 RA Rogers J.;
 RT "The DNA sequence and comparative analysis of human chromosome 20.";
 RL Nature 414:865-871 (2001).
 CC -1- SUBCELLULAR LOCATION: Secreted (Potential).
 CC -1- TISSUE SPECIFICITY: Expressed ubiquitously, the highest levels are
 CC found in the epididymis followed by testis and trachea.
 CC -1- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.
 CC -1- SIMILARITY: Contains 3 WAP-type domains.
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 DR EMBL; AF492015; AN70997.1; -;
 DR EMBL; AF492016; AN70998.1; -;
 DR EMBL; AL031663; CAB37634.2; -;
 DR EMBL; AL591715; CAC39449.1; -;
 DR HSSP; P31713; 1SHP.
 DR Genew; HGNC:16163; WPCD8.
 DR InterPro; IPR022223; Prot_Inh_Kunz-m.
 DR InterPro; IPR008197; WAP.
 DR Pfam; PF00014; Kunitz_BPTI; 1.
 DR Pfam; PF00095; WAP; 3.
 DR PRINTS; PR00003; 4DISULPHCORE.

DR PRINTS; PR00759; BASICPTASE.
 DR PRODOM; ED000222; Prot_Inh_Kunz-m; 1.
 DR SMART; SM00131; KU; 1.
 DR SMART; SM00217; WAP; 3.
 DR PROSITE; PS00317; 4 DISULFIDE CORE; 3.
 DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
 DR PROSITE; PS00279; BPTI_KUNITZ_2; 1.
 KW Repeat; Serine protease inhibitor; Signal.
 FT SIGNAL 1 38 Potential.
 FT CHAIN 39 241 WAP four-disulfide core domain protein 8.
 FT DOMAIN 47 90 WAP 1.
 FT DOMAIN 95 145 BPTI/Kunitz inhibitor.
 FT DOMAIN 150 193 WAP 2.
 FT DOMAIN 197 239 WAP 3.
 FT DISULFID 51 79 By similarity.
 FT DISULFID 58 83 By similarity.
 FT DISULFID 66 78 By similarity.
 FT DISULFID 95 145 By similarity.
 FT DISULFID 104 128 By similarity.
 FT DISULFID 120 141 By similarity.
 FT DISULFID 72 87 By similarity.
 FT DISULFID 154 182 By similarity.
 FT DISULFID 165 186 By similarity.
 FT DISULFID 169 181 By similarity.
 FT DISULFID 175 190 By similarity.
 FT DISULFID 201 229 By similarity.
 FT DISULFID 208 232 By similarity.
 FT DISULFID 216 228 By similarity.
 FT DISULFID 222 236 By similarity.
 SQ SEQUENCE 241 AA; 27797 MW; 2566B54AF4BDC57B CRC64;
 Query Match 28.8%; Score 217; DB 1; Length 241;
 Best Local Similarity 38.5%; Pred. No. 9.3e-13;
 Matches 40; Conservative 13; Mismatches 47; Indels 4; Gaps 1;
 QY 24 HAEGTLGKPCPKIKVECEVEIIDCTPRDCPENMKCCPFSCGKKCLDFRDKICSMPOEA 83
 DB 46 HKPGL-----CPKRLTCTTELPDSCNTDFDCKEYQKCCFFACQKCKMDFQSPCLPVRH 101
 QY 84 GPCLASIPHWYNNKTKICSEFIYGGCGGNNNNFQTEAICLVTC 127
 DB 102 GNCNHEAQRWHDFFKRYRCTPFKYRGCGGNANFLSEDACTAC 145
 RESULT 11
 Q8IT91
 ID Q8IT91 PRELIMINARY; PRT; 759 AA.
 AC Q8IT91;
 DT 01-MAR-2003 (TrEMBLrel. 23, Created)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Kunitz-like protease inhibitor precursor.
 OS Ancylostoma caninum (Dog hookworm).
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Strongylida;
 OC Ancylostomatidae; Ancylostomatidae; Ancylostominae; Ancylostoma.
 OX NCBI_TaxID=29170;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-Baltimore;
 RX MEDLINE=22645137; PubMed=12760667;
 RA Hawdon J.M., Datu B., Crowell M.;
 RT "Molecular cloning of a novel multidomain Kunitz-type proteinase
 RT inhibitor from the hookworm Ancylostoma caninum.";
 RL J. Parasitol. 89:402-407 (2003).
 CC -1- SIMILARITY: Contains 12 BPTI/Kunitz inhibitor domains.
 DR EMBL; AF533590; AANU0061.1; -;
 DR HSSP; P31713; 1SHP.
 DR GO; GO:0008233; F:peptidase activity; IEA.
 DR GO; GO:0004867; F:serine-type endopeptidase inhibitor activity; IEA.
 DR InterPro; IPR002223; Prot_Inh_Kunz-m.
 DR Pfam; PF00014; Kunitz_BPTI; 12.
 DR PRINTS; PR00759; BASICPTASE.
 DR SMART; SM00131; KU; 12.


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Name=agCG49342; ORFNames=ENSANGG00000019572;
OS Anopheles gambiae str. PEST.
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Nematocera; Culicoides; Anopheles.
OX NCBI_TaxID=180454;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=PEST;
RA Anopheles Genome Sequencing Consortium;
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Contains 9 BPTI/Kunitz inhibitor domains.
CC -1- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; AAAB01008987; EAA01339.1; -.
DR HSP; P10646; IIRH.
DR GO; GO:0004867; F:serine-type endopeptidase inhibitor activity; IEA.
DR InterPro; IPR010294; ADAM spacer1.
DR InterPro; IPR006209; EGF like.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR010909; PLAC.
DR InterPro; IPR002223; Prot_inh_Kunz-m.
DR InterPro; IPR000884; TSPI.
DR InterPro; IPR008197; WAP.
DR Pfam; PF05986; ADAM spacer1; 1.
DR Pfam; PF00014; Kunitz_BPTI; 9.
DR Pfam; PF00090; TSP_1; 7.
DR Pfam; PF00095; WAP; 1.
DR PRINTS; PR00003; 4DISULPHCORE.
DR PRINTS; PR00759; BASICPTASE.
DR ProDom; PD000222; Prot_inh_Kunz-m; 9.
DR PROSITE; PS00317; 4 DISULFIDE CORE; 1.
DR PROSITE; PS00280; BPTI_KUNITZ_1; 8.
DR PROSITE; PS02079; BPTI_KUNITZ_2; 9.
DR PROSITE; PS00022; EGF_1; UNKNOWN_1.
DR PROSITE; PS50835; IG LIKE; 2.
DR PROSITE; PS50900; PLAC; 1.
DR PROSITE; PS50092; TSPI; 5.
DR NON_TER
FT
SQ SEQUENCE 2419 AA; 260249 MW; 58B078660983C946 CRC64;

Query Match 24.2%; Score 182; DB 2; Length 571;
Best Local Similarity 31.8%; Pred. No. 4.3e-09;
Matches 35; Conservative 12; Mismatches 34; Indels 29; Gaps 3;

Qy 47 OCTKP---RDCEPNM-----KCCPF-----SCGKCLDFRKDIC 77
Dy 322 ECLKPPDSEDCGEGQTRWHFDAQNNCLTFTFGCHHNLNHFYEACMLACMSGPLATC 381
Qy 78 SMPQEAGPCLASIPHHWYKTKICSEFIYGCOCGNNNNFOTEICLVTC 127
Dy 382 SLPALQGFCKAYVRWYNSQTGLCQSFYGCCEGNGNFFSREACBESC 431

RESULT 19
ID Q7PXZ1 PRELIMINARY; PRT; 2419 AA.
AC Q7PXZ1.
DT 01-MAR-2004 (TrEMBLrel. 26, Created)
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE AgCP12609 (Fragment).

Name=agCG49342; ORFNames=ENSANGG00000019572;
OS Anopheles gambiae str. PEST.
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Nematocera; Culicoides; Anopheles.
OX NCBI_TaxID=180454;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=PEST;
RA Anopheles Genome Sequencing Consortium;
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Contains 9 BPTI/Kunitz inhibitor domains.
CC -1- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; AAAB01008987; EAA01339.1; -.
DR HSP; P10646; IIRH.
DR GO; GO:0004867; F:serine-type endopeptidase inhibitor activity; IEA.
DR InterPro; IPR010294; ADAM spacer1.
DR InterPro; IPR006209; EGF like.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR010909; PLAC.
DR InterPro; IPR002223; Prot_inh_Kunz-m.
DR InterPro; IPR000884; TSPI.
DR InterPro; IPR008197; WAP.
DR Pfam; PF05986; ADAM spacer1; 1.
DR Pfam; PF00014; Kunitz_BPTI; 9.
DR Pfam; PF00090; TSP_1; 7.
DR Pfam; PF00095; WAP; 1.
DR PRINTS; PR00003; 4DISULPHCORE.
DR PRINTS; PR00759; BASICPTASE.
DR ProDom; PD000222; Prot_inh_Kunz-m; 9.
DR PROSITE; PS00317; 4 DISULFIDE CORE; 1.
DR PROSITE; PS00280; BPTI_KUNITZ_1; 8.
DR PROSITE; PS02079; BPTI_KUNITZ_2; 9.
DR PROSITE; PS00022; EGF_1; UNKNOWN_1.
DR PROSITE; PS50835; IG LIKE; 2.
DR PROSITE; PS50900; PLAC; 1.
DR PROSITE; PS50092; TSPI; 5.
DR NON_TER
FT
SQ SEQUENCE 2419 AA; 260249 MW; 58B078660983C946 CRC64;

Query Match 24.2%; Score 182.5; DB 2; Length 571;
Best Local Similarity 31.8%; Pred. No. 4.3e-09;
Matches 35; Conservative 12; Mismatches 34; Indels 29; Gaps 3;

Qy 47 OCTKP---RDCEPNM-----KCCPF-----SCGKCLDFRKDIC 77
Dy 322 ECLKPPDSEDCGEGQTRWHFDAQNNCLTFTFGCHHNLNHFYEACMLACMSGPLATC 381
Qy 78 SMPQEAGPCLASIPHHWYKTKICSEFIYGCOCGNNNNFOTEICLVTC 127
Dy 382 SLPALQGFCKAYVRWYNSQTGLCQSFYGCCEGNGNFFSREACBESC 431

RESULT 19
ID Q7PXZ1 PRELIMINARY; PRT; 2419 AA.
AC Q7PXZ1.
DT 01-MAR-2004 (TrEMBLrel. 26, Created)
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE AgCP12609 (Fragment).

Name=agCG49342; ORFNames=ENSANGG00000019572;
OS Anopheles gambiae str. PEST.
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Nematocera; Culicoides; Anopheles.
OX NCBI_TaxID=180454;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=PEST;
RA Anopheles Genome Sequencing Consortium;
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Contains 9 BPTI/Kunitz inhibitor domains.
CC -1- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; AAAB01008987; EAA01339.1; -.
DR HSP; P10646; IIRH.
DR GO; GO:0004867; F:serine-type endopeptidase inhibitor activity; IEA.
DR InterPro; IPR010294; ADAM spacer1.
DR InterPro; IPR006209; EGF like.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR010909; PLAC.
DR InterPro; IPR002223; Prot_inh_Kunz-m.
DR InterPro; IPR000884; TSPI.
DR InterPro; IPR008197; WAP.
DR Pfam; PF05986; ADAM spacer1; 1.
DR Pfam; PF00014; Kunitz_BPTI; 9.
DR Pfam; PF00090; TSP_1; 7.
DR Pfam; PF00095; WAP; 1.
DR PRINTS; PR00003; 4DISULPHCORE.
DR PRINTS; PR00759; BASICPTASE.
DR ProDom; PD000222; Prot_inh_Kunz-m; 9.
DR PROSITE; PS00317; 4 DISULFIDE CORE; 1.
DR PROSITE; PS00280; BPTI_KUNITZ_1; 8.
DR PROSITE; PS02079; BPTI_KUNITZ_2; 9.
DR PROSITE; PS00022; EGF_1; UNKNOWN_1.
DR PROSITE; PS50835; IG LIKE; 2.
DR PROSITE; PS50900; PLAC; 1.
DR PROSITE; PS50092; TSPI; 5.
DR NON_TER
FT
SQ SEQUENCE 2419 AA; 260249 MW; 58B078660983C946 CRC64;

Query Match 24.2%; Score 182; DB 2; Length 571;
Best Local Similarity 33.9%; Pred. No. 1.9e-08;
Matches 39; Conservative 12; Mismatches 32; Indels 32; Gaps 4;

Qy 46 DQCTKPR-----DCPENMKCCPFSCG-----KKC-----LDPRK 74
Dy 1515 DVCHLPKISGPTCTGHYNNMYDAERNM-CAQFTYGGCLGNANRFESQEECKALCSVDDSK 1573
Qy 75 DICSMPOEAGPCLASIPHHWYKTKICSEFIYGCOCGNNNNFOTEICLVTC 129
Dy 1574 PCQEPNEAGPCNGTFFERWYDKETDACHPFYGGCKGNKNYPTASCGYHCK 1628

RESULT 20
ID Q9UG8 PRELIMINARY; PRT; 3198 AA.
AC Q9UG8.
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DB Lacunin precursor.
OS Manduca sexta (Tobacco hawkmoth) (Tobacco hornworm).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia; Sphingioidea;
OC Sphingidae; Sphinginae; Manduca.
OX NCBI_TaxID=7130;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99457716; PubMed=10528409; DOI=10.1016/S0965-1748(99)00064-8;
RA Nardi J.B., Martos R., Waiden K.K., Lampe D.J., Robertson H.M.;
RT "Expression of lacunin, a large multidomain extracellular matrix
protein, accompanies morphogenesis of epithelial monolayers in Manduca
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RESULT 21
Q6DRJ1 PRELIMINARY; PRT; 515 AA.
ID Q6DRJ1
AC Q6DRJ1;
DT 25-OCT-2004 (TREMBLrel. 28, Created)
DT 25-OCT-2004 (TREMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TREMBLrel. 28, Last annotation update)
DE Serine protease inhibitor HGFAL.
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Telostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RX PubMed=15256591; DOI=10.1073/pnas.0403929101;
RA Amsterdam A., Nissen R.M., Sun Z., Swindell E.C., Farrington S.,
RA Hopkins N.;
RT "Identification of 315 genes essential for early zebrafish
RT development.";
RL Proc. Natl. Acad. Sci. U.S.A. 101:12792-12797(2004).

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CC -!- SIMILARITY: Contains 2 BPTI/Kunitz inhibitor domains.
DR EMBL: AV648768; AT68086.1; -.
DR GO: GO:0008233; F:peptidase activity; IEA.
DR GO: GO:0004867; F:serine-type endopeptidase inhibitor activity; IEA.
DR InterPro: IPR002048; F:hand.
DR InterPro: IPR002172; LDL receptor_A.
DR InterPro: IPR011106; MANSC_N.
DR InterPro: IPR000601; PKD.
DR InterPro: IPR002223; Prot_Inh_Kunz-m.
DR Pfam: PF00014; Kunitz_BPTI; 2.
DR Pfam: PF00057; Ldl_recept_a; 1.
DR Pfam: PF07502; MANSC; 1.
DR PRINTS: PR00759; BASICPTASE.
DR ProDom: PD000222; Prot_Inh_Kunz-m; 2.
DR SMART: SM00131; KU; 2.
DR SMART: SM00192; LDLa; 1.
DR SMART: SM00089; PKD; 1.
DR PROSITE: PS00280; BPTI_KUNITZ_1; 2.
DR PROSITE: PS0279; BPTI_KUNITZ_2; 2.
DR PROSITE: PS00018; EF_HAND; UNKNOWN_1.
DR PROSITE: PS01209; LDLRA_1; 1.
DR PROSITE: PS00068; LDLRA_2; 1.
DR PROSITE: PS00093; PKD; 1.
KW Protease.
SQ SEQUENCE 515 AA; 57579 MW; AF948A7B0EE46DB4 CRC64;

Query Match 23.1%; Score 174; DB 2; Length 515;
Best Local Similarity 24.0%; Pred.No.2.Se-08;
Matches 42; Conservative 17; Mismatches 46; Indels 70; Gaps 5;

QY 5 GLLPILVPILLGDIQE-----PGHAEGILKPCPKIKVECEVEEIDQCTKP 51
DB 271 GCVPNRNNYALNECOSACNKVSVNIGSPPPHSGRIG-----PIDAVEQCRRP 320

QY 52 RDCPENMKCCP--FSCGKKCL-----DF 72
DB 321 -----CSPEFTCDKCCIGDLVCDKEKQSDGSEKCDKWDYDLKLGISPDV 372

QY 73 RKDICSMPQAGPCLASIPHWYNNKTKICSEFIYGCQCQGNNNNFQTEATCLVTC 127
DB 373 SKARCVKPPVTGTCPSGQTKWYNNPNKRLCYRNYGSGCEGNRFRTEAGCMTFC 427

RESULT 22
Q8TEU8 PRELIMINARY; PRT; 576 AA.
AC Q8TEU8; 2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Multivalent protease inhibitor protein.
GN Name=WFIKKRP;
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
[1]
RN_SEQUENCE FROM N.A.
RP MEDLINE=21173622; PubMed=11274388; DOI=10.1073/pnas.061028398;
RX Trexler M., Banyai L., Patthy L.;
RA "A human protein containing multiple types of protease-inhibitory
modules."
RL Proc. Natl. Acad. Sci. U.S.A. 98:3705-3709(2001).
RN [2]
RN_SEQUENCE FROM N.A.
RP Trexler M., Banyai L., Patthy L.;
RA "Distinct expression pattern of two related human proteins containing
multiple types of protease-inhibitory modules."
RL Biol. Chem. 383:0-0(2002)
CC -!- SIMILARITY: Contains 2 BPTI/Kunitz inhibitor domains.
DR EMBL: AF468657; AAL77058.1; -.
DR HSPSP: P00974; IK09.
DR GO: GO:0008233; F:peptidase activity; IEA.

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DR GO:0004867; F:serine-type endopeptidase inhibitor activity; IEA.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003598; IG c2.
DR InterPro; IPR001134; Netrin C.
DR InterPro; IPR002350; Prot_inh_Kazal.
DR InterPro; IPR011497; Prot_inh_Kazal_2.
DR InterPro; IPR002223; Prot_inh_Kunz-m.
DR InterPro; IPR008993; TIMP_like.
DR InterPro; IPR008197; WAP.
DR Pfam; PF07648; Kazal_2; 1.
DR Pfam; PF00014; Kunitz_BPTI; 2.
DR Pfam; PF00095; WAP; 1.
DR PRINTS; PR00003; 4DISULPHCORE.
DR PRINTS; PR00759; BASICPTASE.
DR ProDom; PD000222; Prot_inh_Kunz-m; 2.
DR SMART; SM00131; KU; 2.
DR SMART; SM00217; WAP; 1.
DR PROSITE; PS00317; 4 DISULFIDE CORE; 1.
DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
DR PROSITE; PS0279; BPTI_KUNITZ_2; 2.
DR PROSITE; PS0835; IG LIKE; 1.
DR PROSITE; PS0189; NTR; 1.
DR KW Protease.
SQ SEQUENCE 576 AA; 63941 MW; 08B4F2EDBE121F81 CRC64;

Query Match 23.0%; Score 173.5; DB 2; Length 576;
Best Local Similarity 31.8%; Pred. No. 3.1e-08;
Matches 35; Conservative 10; Mismatches 36; Indels 29; Gaps 3;

QY 47 QCTKP---RDCPENM-----KCCPF-----SGKKCLDFRKDIC 77
DQ 327 ECLAPPSEDCGEQTRWHFDAQNNCLTFTFGHCHRNLNHFYEACMLACMSGPLAAC 386

QY 78 SMPQAGPCLASIPHWYNNKTKICSEFIYGGCGGNNNFQTEAICLVTC 127
DQ 387 SLPALQGPCKAYAPRAYNSQTGCQSFYVGGCEGNGNFESREACEESC 436

RESULT 23
Q6UXZ9 PRELIMINARY; PRT; 576 AA.
AC Q6UXZ9
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Bikunin hlg.
GN ORFNames=UNQ9235;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22887296; PubMed=12975309; DOI=10.1101/gr.1293003;
RA Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D., Brush J.,
RA Chen J., Chow B., Chui C., Crowley C., Currell B., Deuel B., Dowd P.,
RA Eaton D., Foster J., Grimaldi C., Gu Q., Haas P.E., Heldens S.,
RA Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J.,
RA Lewis L., Liao D., Mark M., Robbie E., Sanchez C., Schoenfeld J.,
RA Seshagiri S., Simmons L., Singh J., Smith V., Stinson J., Vagts A.,
RA Vandlen R., Watanabe C., Wieand D., Woods K., Xie M.H., Yasnura D.,
RA Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A., Wood W.I.,
RA Godowski P.;
RT "The secreted protein discovery initiative (SPDI), a large-scale
RT effort to identify novel human secreted and transmembrane proteins: a
RT bioinformatics assessment.";
PL Genome Res. 13:2265-2270(2003).
CC -!- SIMILARITY: Contains 2 BPTI/Kunitz inhibitor domains.
DR EMBL; AY358142; AAQ88509.1; -.
DR HSSP; P00974; 1K09.
DR GO:0004867; F:serine-type endopeptidase inhibitor activity; IEA.
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DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003598; IG c2.
DR InterPro; IPR001134; Netrin C.
DR InterPro; IPR002223; Prot_inh_Kunz-m.
DR InterPro; IPR008993; TIMP_like.
DR InterPro; IPR008197; WAP.
DR Pfam; PF00014; Kunitz_BPTI; 2.
DR Pfam; PF00095; WAP; 1.
DR PRINTS; PR00003; 4DISULPHCORE.
DR PRINTS; PR00759; BASICPTASE.
DR ProDom; PD000222; Prot_inh_Kunz-m; 2.
DR SMART; SM00409; IG; 1.
DR SMART; SM00408; IGC2; 1.
DR SMART; SM00131; KU; 2.
DR SMART; SM00217; WAP; 1.
DR PROSITE; PS00317; 4 DISULFIDE CORE; 1.
DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
DR PROSITE; PS0279; BPTI_KUNITZ_2; 2.
DR PROSITE; PS0835; IG LIKE; 1.
DR PROSITE; PS0189; NTR; 1.
DR SQ SEQUENCE 576 AA; 63912 MW; 08B42DD50C3CF81 CRC64;

Query Match 23.0%; Score 173.5; DB 2; Length 576;
Best Local Similarity 31.8%; Pred. No. 3.1e-08;
Matches 35; Conservative 10; Mismatches 36; Indels 29; Gaps 3;

QY 47 QCTKP---RDCPENM-----KCCPF-----SCGKKCLDFRKDIC 77
DQ 327 ECLAPPSEDCGEQTRWHFDAQNNCLTFTFGHCHRNLNHFYEACMLACMSGPLAAC 386

QY 78 SMPQAGPCLASIPHWYNNKTKICSEFIYGGCGGNNNFQTEAICLVTC 127
DQ 387 SLPALQGPCKAYAPRAYNSQTGCQSFYVGGCEGNGNFESREACEESC 436

RESULT 24
Q6AX20 PRELIMINARY; PRT; 587 AA.
AC Q6AX20
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Afp2 A protein.
GN Name=afp2 A;
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RX TISSUE=Kidney;
RX MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;
RA Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
RA Richardson P.;
RT "Genetic and genomic tools for Xenopus research: The NIH Xenopus
RT initiative.";
RL Dev. Dyn. 225:384-391(2002).
RN [2]
RP SEQUENCE FROM N.A.
RX TISSUE=Kidney;
RX PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Rana S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
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RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smallus D.E., Schmerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Kidney;
RA Klein S., Gerhard D.S.;
RL Submitted (AUG-2004) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.
DR EMBL; BC079801; AAH79801.1; --
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0005488; F:binding; IEA.
DR GO; GO:0004867; F:serine-type endopeptidase inhibitor activity; IEA.
DR InterPro; IPR008155; A4_APP.
DR InterPro; IPR002223; Prot_Inh_Kunz-m.
DR Pfam; PF02177; A4_EXTRA; 1.
DR PRINTS; PR00203; AMYLOIDA4.
DR PRODOM; PD000222; Prot_Inh_Kunz-m.
DR SMART; SM00006; A4_EXTRA; 1.
DR SMART; SM00131; KU; 1.
DR PROSITE; PS00320; A4_INTRA; 1.
DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
DR PROSITE; PS0279; BPTI_KUNITZ_2; 1.
SQ SEQUENCE 587 AA; 66870 MW; 7DF224C2138B94BF CRC64;

Query Match 23.0%; Score 173; DB 2; Length 587;
Best Local Similarity 46.0%; Pred. No. 3.5e-08;
Matches 29; Conservative 8; Mismatches 26; Indels 0; Gaps 0;

QY 66 GKCLDFRDKICSMPEAGPCLASIPHWYNNKTKICSEFIYGGCGGNNNFQTEAICLV 125
DB 273 GKDITDVKSVCSEAITGPRAMPWRYFNLGQKCKFRFYGGCGGNNNFSESDYCWA 332

QY 126 TCK 128
DB 333 VCK 335

RESULT 25
Q708Z0 PRELIMINARY; PRT; 751 AA.
AC Q708Z0;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Amyloid-beta-like protein A precursor.
GN Name=ap1p2 A;
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RA Collin R.W.J., van Strien D., Leunissen J.A., Martens G.J.M.;
RL Submitted (NOV-2003) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.
DR EMBL; AJ360932; CAE75662.1; --
DR HSSP; Q16019; IAAp.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0005488; F:binding; IEA.
DR GO; GO:0004867; F:serine-type endopeptidase inhibitor activity; IEA.

DR InterPro; IPR008155; A4_APP.
DR InterPro; IPR008154; A4_extra.
DR InterPro; IPR002223; Prot_Inh_Kunz-m.
DR Pfam; PF02177; A4_EXTRA; 1.
DR Pfam; PF00014; Kunitz BPTI; 1.
DR PRINTS; PR00203; AMYLOIDA4.
DR PRINTS; PR00759; BASICPTASE.
DR PRODOM; PD000222; Prot_Inh_Kunz-m; 1.
DR SMART; SM00006; A4_EXTRA; 1.
DR SMART; SM00131; KU; 1.
DR PROSITE; PS00320; A4_INTRA; 1.
DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
DR PROSITE; PS0279; BPTI_KUNITZ_2; 1.
KW Signal.
FT SIGNAL 1 20 Potential.
FT CHAIN 21 751 amyloid-beta-like protein A.
SQ SEQUENCE 751 AA; 85200 MW; C5E8FE7302C36B58 CRC64;

Query Match 23.0%; Score 173; DB 2; Length 751;
Best Local Similarity 46.0%; Pred. No. 4.5e-08;
Matches 29; Conservative 8; Mismatches 26; Indels 0; Gaps 0;

QY 66 GKCLDFRDKICSMPEAGPCLASIPHWYNNKTKICSEFIYGGCGGNNNFQTEAICLV 125
DB 281 GKDITDVKSVCSEAITGPRAMPWRYFNLGQKCKFRFYGGCGGNNNFSESDYCWA 340

QY 126 TCK 128
DB 341 VCK 343

RESULT 26
Q09983 PRELIMINARY; PRT; 1599 AA.
AC Q09983;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Hypothetical protein F30H5.3.
GN Name=F30H5.3; ORFNames=F30H5.3;
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae;
OC Rhabditidae; Pelodierinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RX MEDLINE=99069613; PubMed=9851916;
RG WormBase Consortium;
RT "Genome sequence of the nematode C. elegans: a platform for
RT investigating biology. The C. elegans Sequencing Consortium.";
RL Science 282:2012-2018(1998).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RA Pauley A., Stellyes L.;
RT "The sequence of C. elegans cosmid F30H5.";
RL Submitted (JUN-1995) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RA Waterston R.;
RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RG WormBase Consortium;
RL Submitted (SEP-2004) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Contains 5 BPTI/Kunitz inhibitor domains.
DR EMBL; U29096; AAA68408.1; --
DR PIR; T16210; T16210.
DR HSSP; PI0646; IADZ.
DR IntAct; Q09983; --

-l- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.
EMBL; BC075266; AAH75266.1; --
GO; GO:0016021; C:integral co membrane; IEA.
GO; GO:0005488; F:binding; IEA.
GO; GO:0004867; F:serine-type endopeptidase inhibitor activity; IEA.
InterPro; IPR008155; A4 APP.
InterPro; IPR008154; A4 extra.
InterPro; IPR001255; Beta-APP.
InterPro; IFR002223; Prot_Inh_Kunz-m.
Pfam; PF02177; A4_EXTRA; 1.
Pfam; PF03494; Beta-APP; 1.
Pfam; PF00014; Kunitz_BPTI; 1.
PRINTS; PR00203; AMYLOIDA4.
PRINTS; PR00759; BASICPTASE.
PRINTS; PR00204; BETAMYLOID.
PRODom; PD000222; Prot_Inh_Kunz-m; 1.
SMART; SMOO006; A4 EXTRA; 1.
SMART; SMO0131; KU; 1.
PROSITE; PS00319; A4 EXTRA; 1.
PROSITE; PS00320; A4_INTRA; 1.
PROSITE; PS00280; BPTI_KUNITZ_1; 1.
PROSITE; PS00279; BPTI_KUNITZ_2; 1.
SEQUENCE 516 AA; 57695 MW; 20B0A4C5B270DE16 CRC64;

Query Match 22.8%; Score 172; DB 2; Length 516;
Best Local Similarity 24.8%; Pred.No. 3.9e-08;
Matches 41; Conservative 19; Mismatches 55; Indels 50; Gaps 5;

Qy 5 GLLPILVPIILLGDIOPGHAGSI--LGKPCPKIKVEC-EVEEIQCTKPDCPENMKCC 61
Db 271 GCVENNNVALNECOSACNKSUVSNIGSPAPHSRGIPDAVCQRDP-----CS 322

Qy 62 P-FSCGKKCL-----DFFRKDICMPQE 82
Db 323 PEHTCDNKCCIGKLVDCKEKQSDGSDEKDKWDYDLVKLRGISPDVSKARCVPVP 382

Qy 83 AGFCASLIPHWNKYTKICSEFIYGGCGGNNNNFOTEAILCVTC 127
Db 383 TGTCPGSGTQWYNPNKRCLCFRYNYGCCGNGNRPFETEGACTGC 427

RESULT 29
Q6DJB6 PRELIMINARY; PRT; 750 AA.

ID Q6DJB6 AC Q6DJB6 DT 25-OCT-2004 (T-EMBLrel. 28, Created) DT 25-OCT-2004 (T-EMBLrel. 28, Last sequence update) DT 25-OCT-2004 (T-EMBLrel. 28, Last annotation update) DE App-prov protein. OS Xenopus tropicalis (Western clawed frog) (Silurana tropicalis). OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae; OC Xenopodinae; Xenopus. NCBI_TaxID=8364; [1] SEQUENCE FROM N.A. RP TISSUE=whole body; RC MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899; RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D., Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., Datchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Spatletton M., Soares M.B., Bonaldo M.F., Casavant T.L., Schetz T.E., Brownstein M.J., Uadin T.B., Toshiyuki S., Carninci P., Prange C., Raja S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J., Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickinson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S., Krzywinski W.I., Skaleka U., Smallos D.E., Schnerch A., Schein J.E., Jones S.J., Marra M.A.; "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences." Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002). [2] SEQUENCE FROM N.A. RP TISSUE=whole body; RC Klein S., Gerhard D.S.; Submitted (JUN-2004) to the EMBL/GenBank/DBJP databases. RL

Pfam; PF00057; Ldl_recept_a; 1.
Pfam; PF07502; MANSC; 1.
PRODom; PD000222; Prot_Inh_Kunz-m; 2.
SMART; SMO0131; KU; 2.
SMART; SMO0192; LDLa; 1.
SMART; SMO0089; PKD; 1.
PROSITE; PS00280; BPTI_KUNITZ_1; 2.
PROSITE; PS00279; BPTI_KUNITZ_2; 2.
PROSITE; PS00018; EF_HAND; UNKNOWN_1.
PROSITE; PS01209; LDLRa_1; 1.
PROSITE; PS00068; LDLRa_2; 1.
SEQUENCE 516 AA; 57695 MW; 20B0A4C5B270DE16 CRC64;

Query Match 22.8%; Score 172; DB 2; Length 516;
Best Local Similarity 24.8%; Pred.No. 3.9e-08;
Matches 41; Conservative 19; Mismatches 55; Indels 50; Gaps 5;

Qy 5 GLLPILVPIILLGDIOPGHAGSI--LGKPCPKIKVEC-EVEEIQCTKPDCPENMKCC 61
Db 271 GCVENNNVALNECOSACNKSUVSNIGSPAPHSRGIPDAVCQRDP-----CS 322

Qy 62 P-FSCGKKCL-----DFFRKDICMPQE 82
Db 323 PEHTCDNKCCIGKLVDCKEKQSDGSDEKDKWDYDLVKLRGISPDVSKARCVPVP 382

Qy 83 AGFCASLIPHWNKYTKICSEFIYGGCGGNNNNFOTEAILCVTC 127
Db 383 TGTCPGSGTQWYNPNKRCLCFRYNYGCCGNGNRPFETEGACTGC 427

RESULT 29
Q6DJB6 PRELIMINARY; PRT; 750 AA.

ID Q6DJB6 AC Q6DJB6 DT 25-OCT-2004 (T-EMBLrel. 28, Created) DT 25-OCT-2004 (T-EMBLrel. 28, Last sequence update) DT 25-OCT-2004 (T-EMBLrel. 28, Last annotation update) DE App-prov protein. OS Xenopus tropicalis (Western clawed frog) (Silurana tropicalis). OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae; OC Xenopodinae; Xenopus. NCBI_TaxID=8364; [1] SEQUENCE FROM N.A. RP TISSUE=whole body; RC MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899; RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D., Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., Datchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Spatletton M., Soares M.B., Bonaldo M.F., Casavant T.L., Schetz T.E., Brownstein M.J., Uadin T.B., Toshiyuki S., Carninci P., Prange C., Raja S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J., Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villallon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickinson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S., Krzywinski W.I., Skaleka U., Smallos D.E., Schnerch A., Schein J.E., Jones S.J., Marra M.A.; "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences." Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002). [2] SEQUENCE FROM N.A. RP TISSUE=whole body; RC Klein S., Gerhard D.S.; Submitted (JUN-2004) to the EMBL/GenBank/DBJP databases. RL

CC -l- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.
DR EMBL; BC075266; AAH75266.1; --
DR GO; GO:0016021; C:integral co membrane; IEA.
DR GO; GO:0005488; F:binding; IEA.
DR GO; GO:0004867; F:serine-type endopeptidase inhibitor activity; IEA.
DR InterPro; IPR008155; A4 APP.
DR InterPro; IPR008154; A4 extra.
DR InterPro; IPR001255; Beta-APP.
DR InterPro; IFR002223; Prot_Inh_Kunz-m.
DR Pfam; PF02177; A4_EXTRA; 1.
DR Pfam; PF03494; Beta-APP; 1.
DR Pfam; PF00014; Kunitz_BPTI; 1.
DR PRINTS; PR00203; AMYLOIDA4.
DR PRINTS; PR00759; BASICPTASE.
DR PRINTS; PR00204; BETAMYLOID.
DR PRODom; PD000222; Prot_Inh_Kunz-m; 1.
DR SMART; SMOO006; A4 EXTRA; 1.
DR SMART; SMO0131; KU; 1.
DR PROSITE; PS00319; A4 EXTRA; 1.
DR PROSITE; PS00320; A4_INTRA; 1.
DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
DR PROSITE; PS00279; BPTI_KUNITZ_2; 1.
SQ SEQUENCE 750 AA; 84927 MW; 4222350843147CAF CRC64;

Query Match 22.8%; Score 172; DB 2; Length 750;
Best Local Similarity 48.1%; Pred.No. 5.6e-08;
Matches 26; Conservative 10; Mismatches 18; Indels 0; Gaps 0;

Qy 74 KDICSMPEAQGLASLPHWNKYTKICSEFIYGGCGGNNNNFOTEAILCVTC 127
Db 286 REVCEQAETGPCRAMIPRWYDVTERKCAQFIYGGCGGNRNFDSYCMAYC 339

RESULT 30
YN81 CAEBL ID_YN81 CAEBL STANDARD; PRT; 1416 AA.
AC Q03610; 1994 (Rel. 28, Created)
DT 01-FEB-1998 (Rel. 36, Last sequence update)
DT 15-JUL-1998 (Rel. 45, Last annotation update)
DT 25-OCT-2004 (REL. 45, Last annotation update)
DE Hypothetical protein 2C84.1 in chromosome III.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditiida; Rhabditoidea;
OC Rhabditiada; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239; [1] SEQUENCE FROM N.A. RN STRAIN=Bristol N2; RC MEDLINE=94150718; PubMed=7906398; DOI=10.1038/368032a0; RX Wilson R., Ainscough R., Anderson K., Baynes C., Berks M., Coxfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson A., Braxton M., Dear S., Du Z., Durbin R., Favetto A., Fraser A., Fultons L., Gardner A., Green P., Hawkins T., Hillier L., Jier M., Johnston L., Jones M., Kerhaw J., Kirsten J., Laister N., Latreille P., Lightning J., Lloyd C., Mortimore B., O'Callaghan M., Parsons J., Percy C., Rifkin L., Roopra A., Saunders D., Snowken R., Sims M., Smaldon N., Smith A., Smith M., Sonhammer E., Staden R., Sulston J., Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K., Waterston R., Watson A., Weinstock L., Wilkinson-Sproat J., Woildman P.; "2.2 Mb of contiguous nucleotide sequence from chromosome III of C. elegans." Nature 368:32-38(199

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RP REVISIONS.
RA Jones S.J.M.;
RL Submitted (NOV-1997) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Contains 5 BPTI/Kunitz inhibitor domains.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; Z19157; CAA79569.1; -.
DR PIR; E88550; E88550.
DR PIR; S28291; S28291.
DR HSSP; P00981; 1DTK.
DR WormBase; WBGene00013846; ZC84.1.
DR WormPep; ZC84.1; CE15020.
DR InterPro; IPR006149; EB region.
DR InterPro; IPR002223; Prot_Inh_Kunz-m.
DR InterPro; IPR006150; Worm_repeat_1.
DR Pfam; PF01683; EB; 3.
DR Pfam; PF00014; Kunitz BPTI; 5.
DR PRINTS; PR00759; BASICTPTASE.
DR ProDom; PD000222; Prot_Inh_Kunz-m; 5.
DR SMART; SM00131; KU; 5.
DR SMART; SM00289; WRI; 13.
DR PROSITE; PS00280; BPTI_KUNITZ_1; 3.
DR PROSITE; PS02079; BPTI_KUNITZ_2; 5.
KW Hypothetical protein; Repeat; Serine protease inhibitor.
FT DOMAIN 212 266 BPTI/Kunitz inhibitor 1.
FT DOMAIN 337 387 BPTI/Kunitz inhibitor 2.
FT DOMAIN 434 484 BPTI/Kunitz inhibitor 3.
FT DOMAIN 538 590 BPTI/Kunitz inhibitor 4.
FT DOMAIN 646 698 BPTI/Kunitz inhibitor 5.
SQ SEQUENCE 1416 AA; 152986 MW; 531CAC81CB222P70D CRC64;

Query Match 22.7%; Score 171; DB 1; Length 1416;
Best Local Similarity 30.4%; Pred. No. 1.3e-07;
Matches 35; Conservative 14; Mismatches 34; Indels 32; Gaps 3;

Qy 37 KVECEV-----EIDQCTKPRDCPENMK-----CPFSGCKKCLDFR 73
Db 380 KHECMYCARLCQERGSPLRGAEARQCNNAQCPSSHECKADQGVCCP-----RK 430
Qy 74 KDICSMFQEGAGPCLASIPHWYNNKTKICSEFIYGGCGNNNFQTEAICLVTCCK 128
Db 431 QTICAPLRIGDCTENVKRYWYNARTQCQMFVYTGCGNDNFDSDMDCQNFCK 485

RESULT 31
BTIA BOOMI
ID BTIA BOOMI STANDARD; PRT; 122 AA.
AC P83609;
DT 05-JUL-2004 (Rel. 44, Created)
DT 05-JUL-2004 (Rel. 44, Last sequence update)
DE Kunitz-type serine protease inhibitor BMTI-A (Fragments).
OS Boophilus microplus (Cattle tick).
OC Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Acari;
OC Parasitiformes; Ixodida; Ixodoidea; Ixodidae; Boophilus.
OX NCBI_TaxID=6941;
RN [1]
RP SEQUENCE, AND FUNCTION.
RC TISSUE=Larva;
RX PubMed=10615008; DOI=10.1016/S0162-3109(99)00074-0;
RA Tanaka A.S.; Andreotti R.; Gomes A.; Torquato R.J.S.; Sampaio M.U.;
RA Sampaio C.A.M.;
RT "A double headed serine proteinase inhibitor-human plasma kallikrein
and elastase inhibitor-from Boophilus microplus larvae."
RL Immunopharmacology 45:171-177(1999).
CC -1- FUNCTION: Inhibits bovine trypsin, human chymotrypsin, human
plasma kallikrein and human neutrophil elastase,
but not bovine thrombin, human factor Xa or porcine pancreatic
kallikrein. May play a role in blocking blood coagulation during
the larvae fixation on cattle.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: Contains 2 BPTI/Kunitz inhibitor domains.
DR InterPro; IPR002223; Kunitz BPTI.
DR PRINTS; PR00759; BASICTPTASE.
DR ProDom; PD000222; Prot_Inh_Kunz-m; 2.
DR SMART; SM00131; KU; 2.
DR PROSITE; PS00280; BPTI_KUNITZ_1; 2.
DR PROSITE; PS02079; BPTI_KUNITZ_2; 2.
KW Direct protein sequencing; Repeat; Serine protease inhibitor.
FT DOMAIN 10 60 BPTI/Kunitz inhibitor 1.
FT DOMAIN 62 112 BPTI/Kunitz inhibitor 2.
FT DISULFID 10 60 By similarity.
FT DISULFID 35 56 By similarity.
FT NON CONS 69 70 By similarity.
FT DISULFID 71 121 By similarity.
FT DISULFID 80 104 By similarity.
FT DISULFID 96 117 By similarity.
FT SITE 19 20 Reactive bond (By similarity).
FT SITE 71 72 Reactive bond (By similarity).
FT NON TER 122 122
SQ SEQUENCE 122 AA; 13736 MW; 8F5B1F48E10C566F CRC64;

Query Match 22.6%; Score 170.5; DB 1; Length 122;
Best Local Similarity 46.7%; Pred. No. 1.3e-08;
Matches 35; Conservative 7; Mismatches 18; Indels 15; Gaps 3;

Qy 61 CFPSC-----GKKCLDFRDKICSMFQEGAGPCLASIPHWYNNKTKICSEFIYGGCGN 113
Db 56 CKASCKPTEYEAKKCL-----ARP-ESGPCLAYPMWGYDSKLGQCQCFYIYGGCGDN 107
Qy 114 NNNFQTEAICLVTCCK 128
Db 108 DNKYTTEECCKSK 122

RESULT 32
Q6ITB9
ID Q6ITB9 PRELIMINARY; PRT; 83 AA.
AC Q6ITB9;
DT 05-JUL-2004 (T-EMBLrel. 27, Created)
DT 05-JUL-2004 (T-EMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (T-EMBLrel. 27, Last annotation update)
DE Malign-3.
OS Pseudechis australis (Mulga snake) (King brown snake).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC Elapidae; Acanthophiinae; Pseudechis.
OX NCBI_TaxID=8670;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Venom gland;
RA Filipovich I.V.; Sorokina N.I.;
RL Submitted (MAY-2004) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.
CC EMBL; AY626926; AAT45402.1; -.
DR HSSP; Q16019; 1AAP.
DR GO; GO:0004867; F:serine-type endopeptidase inhibitor activity; IEA.
DR InterPro; IPR002223; Prot_Inh_Kunz-m.
DR Pfam; PF00014; Kunitz BPTI; 1.
DR PRINTS; PR00759; BASICTPTASE.
DR ProDom; PD000222; Prot_Inh_Kunz-m; 1.
DR SMART; SM00131; KU; 1.
DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
DR PROSITE; PS02079; BPTI_KUNITZ_2; 1.
SQ SEQUENCE 83 AA; 9103 MW; 315C361D8EC89221 CRC64;

Query Match 22.6%; Score 170; DB 2; Length 83;
Best Local Similarity 52.7%; Pred. No. 1e-08;
Matches 29; Conservative 5; Mismatches 21; Indels 0; Gaps 0;

```


DE Hypothetical protein Y55F3BR.2.
GN Name=Y55F3BR.2; ORFNames=Y55F3BR.2;
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RX MEDLINE=99069613; PubMed=9851916;
RG WormBase Consortium;
RT "Genome sequence of the nematode C. elegans: a platform for
investigating biology. The C. elegans Sequencing Consortium.";
RL Science 282:2012-2018(1998).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RA Bradshaw-Cordum H., Leonard S., Graves T.;
RT "The sequence of C. elegans cosmid Y55F3BR.";
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RA Waterston R.;
RT Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RA Waterston R.;
RT Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
RN [5]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RA Waterston R.;
RT Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.
RN [6]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RA Waterston R.;
RT Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.
RN [7]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RA Waterston R.;
RT Submitted (AUG-2002) to the EMBL/GenBank/DBJ databases.
RN [8]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RA Waterston R.;
RT Submitted (AUG-2002) to the EMBL/GenBank/DBJ databases.
RN [9]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RA Waterston R.;
RT Submitted (NOV-2002) to the EMBL/GenBank/DBJ databases.
RN [10]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RA Waterston R.;
RT Submitted (NOV-2002) to the EMBL/GenBank/DBJ databases.
RN [11]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RA Waterston R.;
RT Submitted (NOV-2002) to the EMBL/GenBank/DBJ databases.
RN [12]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RA Waterston R.;
RT Submitted (DEC-2002) to the EMBL/GenBank/DBJ databases.
RN [13]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;

RA Waterston R.;
RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
RN [14]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RA Wilson R.;
RL Submitted (JUL-2003) to the EMBL/GenBank/DBJ databases.
RN [15]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RG WormBase Consortium;
RL Submitted (SEP-2004) to the EMBL/GenBank/DBJ databases.
RN [16]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RG WormBase Consortium;
RL Submitted (SEP-2004) to the EMBL/GenBank/DBJ databases.
CC -I- SIMILARITY: Contains 4 BPTI/Kunitz inhibitor domains.
DR EMBL; AC024830; AAF59608.3; -.
DR GO; GO:0004867; F:serine-type endopeptidase inhibitor activity; IEA.
KW Hypothetical protein.
SQ SEQUENCE 1297 AA; 142370 MW; 7C8FAA75CE07ED8C CRC64;

Query Match 22.2%; Score 167.5; DB 2; Length 1297;
Best Local Similarity 28.0%; Pred. No. 2.6e-07; Indels 43; Gaps 3;
Matches 35; Conservative 13; Mismatches 34;

QY 47 OCTPRDCP-----ENMKCCPFs-----CGKKCLDFR----- 73
DB 673 RARDTDCPSTHTCAMEHQVCCPTPPHREIQFYKYGDLVSSSLKIVGSRHENYRNPGRGV 732

QY 74 -----KDICSMPOEAGPCLASIPHHWYKTKICSEFIYGGCGGNNNNFOTEAIC 123
DB 733 ARPNIFLIEEKTLCTEPLRVGDCQSVRFQWYNAETKTCSFLYTGCQGNRRFNSLNEC 792

QY 124 LVTCK 128
DB 793 QSYCK 797

RESULT 39
OS2504 PRELIMINARY; PRT; 1474 AA.
AC O62504;
DT 01-AUG-1998 (TrEMBLrel. 07, Created)
DT 01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Hypothetical protein ZC84.6.
GN ORFNames=ZC84.6;
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RX MEDLINE=99069613; PubMed=9851916;
RA none;
RT "Genome sequence of the nematode C. elegans: A platform for
investigating biology.";
RL Science 282:2012-2018(1998).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RA Thomas K.;
RL Submitted (DEC-1992) to the EMBL/GenBank/DBJ databases.
CC -I- SIMILARITY: Contains 5 BPTI/Kunitz inhibitor domains.
DR EMBL; Z19157; CAA79570.1; -.
DR PIR; D88550; D88550.
DR HSP; P31713; 1SHP.
DR WormBase; WBGene00013849; ZC84.6.
DR WormPep; ZC84.6; CE15024.
DR GO; GO:0004867; F:serine-type endopeptidase inhibitor activity; IEA.

RESULT	41
Q6ITB4	PRELIMINARY; PRT; 83 AA.
AC	Q6ITB4;
DT	03-JUL-2004 (TrEMBLrel. 27, Created)
DT	05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT	05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE	Microlepidin-2.
OS	Oxyuranus microlepidotus (Inland taipan).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC	Elapidae; Acanthophinae; Oxyuranus.
OX	NCBI_TaxID=111177;
RN	[1]
RP	SEQUENCE FROM N.A.
RC	TISSUE=Venom gland;
RA	Filipovich I.V., Sorokina N.I.;
RL	Submitted (MAY-2004) to the EMBL/GenBank/DBJ databases.
CC	-1- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.
EMBL	AV626931; AAT45407.1; --
HSP	P10646; IADZ.
GO	GO:0004867; F:serine-type endopeptidase inhibitor activity; IEA;
DR	InterPro; IPRO02223; Prot_Inh_Kunzm-m.
DR	Pfam; PF00014; Kunitz_BPTI; 1.
DR	PRINTS; PR00759; BASICTPASE.
DR	ProDom; PD000222; Prot_Inh_Kunzm-m; 1.
DR	SMART; SM00131; KU; 1.
DR	PROSITE; PS00280; BPTI_KUNITZ_1; 1.
DR	PROSITE; PS0279; BPTI_KUNITZ_2; 1.
SQ	SEQUENCE 83 AA; 9074 MW; 3145E51757014221 CRC64;
Query Match	22.2%; Score 167; DB 2; Length 83;
Best Local Similarity	50.9%; Pred.No.1.9e-08;
Matches	28; Conservative 6; Mismatches 21; Indels 0; Gaps
QY	73 RXDICSMQEAGPCLASIPHWVNYKTKICSEFIYGGCGOANNNFOTEALCVTC 127
DB	27 RDFCFELADTGPCRVGFPSFYNPDKKCLEFIYGGCGGNANFNFKCECSTC 81
RESULT	42
Q6ITB6	PRELIMINARY; PRT; 83 AA.
AC	Q6ITB6;
DT	03-JUL-2004 (TrEMBLrel. 27, Created)
DT	05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT	05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE	Scutellin-2.
OS	Oxyuranus scutellatus.
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC	Elapidae; Acanthophinae; Oxyuranus.
OX	NCBI_TaxID=8668;
RN	[1]
RP	SEQUENCE FROM N.A.
RC	TISSUE=Venom gland;
RA	Filipovich I.V., Sorokina N.I.;
RL	Submitted (MAY-2004) to the EMBL/GenBank/DBJ databases.
CC	-1- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.
EMBL	AV626929; AAT45405.1; --
HSP	P10646; IADZ.
GO	GO:0004867; F:serine-type endopeptidase inhibitor activity; IEA;
DR	InterPro; IPRO02223; Prot_Inh_Kunzm-m.
DR	Pfam; PF00014; Kunitz_BPTI; 1.
DR	PRINTS; PR00759; BASICTPASE.
DR	ProDom; PD000222; Prot_Inh_Kunzm-m; 1.
DR	SMART; SM00131; KU; 1.
DR	PROSITE; PS00280; BPTI_KUNITZ_1; 1.
DR	PROSITE; PS0279; BPTI_KUNITZ_2; 1.
SQ	SEQUENCE 83 AA; 9074 MW; 3145E51757014221 CRC64;


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Query Match      22.2%; Score 167; DB 2; Length 83;
Best Local Similarity 50.9%; Pred. No. 1.9e-08;
Matches 28; Conservative 6; Mismatches 21; Indels 0; Gaps 0;

QY 73 RDXICSMPOEAGPCLASIPHHWYKTKICSFYIYGGCGNNNFOTBAICLVTC 127
DB 27 RPDFCLPADTGCVRGPFSPFYINDEKKCLCFIYGGCGNNNFITKECESTC 81

RESULT 43
Q6T6S5 PRELIMINARY; PRT; 90 AA.
ID Q6T6S5
AC Q6T6S5
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Kunitz protease inhibitor 2.
OS Bitis gabonica (Gaboon viper) (Gaboon viper).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidodonta; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC Viperidae; Viperinae; Bitis.
OX NCBI_TaxID=8694;
RN [1]
RP SEQUENCE FROM N.A.
RX PubMed=15276202; DOI=10.1016/j.gene.2004.03.024;
RA Francischetti I.M., My-Pham V., Harrison J., Garfield M.K.,
RA Ribeiro J.M.;
RT "Bitis gabonica (Gaboon viper) snake venom gland: toward a catalog for
RT the full-length transcripts (cDNA) and proteins.";
RL Gene 337:55-69(2004).
RN [2]
RP SEQUENCE FROM N.A.
RX Submitted (DEC-2003) to the EMBL/GenBank/DBJ databases.
RA Francischetti I.M.B., Pham V.M., Garfield M.K., Ribeiro J.M.C.;
RL Submitted (OCT-2003) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.
DR EMBL; AY430413; AAR24535.1; -.
DR HSP; Q16019; IAA.
DR GO; GO:0008233; F:peptidase activity; IEA.
DR GO; GO:0004867; F:serine-type endopeptidase inhibitor activity; IEA.
DR InterPro; IPR002223; Prot_Inh_Kunz-m.
DR Pfam; PF00014; Kunitz BPTI_1.
DR PRINTS; PR00759; BASICPTASE.
DR ProDom; PD000222; Prot_Inh_Kunz-m; 1.
DR SMART; SM00131; KU; 1.
DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
DR PROSITE; PS50279; BPTI_KUNITZ_2; 1.
KW Protease.
SQ SEQUENCE 90 AA; 10006 MW; 2BEDC1D2020852AF CRC64;

Query Match      22.2%; Score 167; DB 2; Length 90;
Best Local Similarity 45.2%; Pred. No. 2.1e-08;
Matches 28; Conservative 10; Mismatches 20; Indels 4; Gaps 1;

QY 66 GKXCLDFRDKICSMPOEAGPCLASIPHHWYKTKICSFYIYGGCGNNNFOTBAICLV 125
DB 24 GRK----RDFCYLPADTGCNANFRFYDSASKKCKFTYGGCHGNANFETRECKR 79

QY 126 TC 127
DB 80 KC 81

RESULT 44
Q6P2V8 PRELIMINARY; PRT; 342 AA.
ID Q6P2V8
AC Q6P2V8
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein MGC76314.
GN Name=MGC76314;
OS Xenopus tropicalis (Western clawed frog) (Silurana tropicalis).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8364;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Embryo;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.F., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.W., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max A.I., Wang J., Haiech F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.P., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udén T.B., Toshiyuki S., Carninci P., Prange C.,
RA Rana S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Embryo;
RA Klein S., Gerhardt D.S.;
RL Submitted (DEC-2003) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: Belongs to the lipocalin family.
CC -!- SIMILARITY: Contains 2 BPTI/Kunitz inhibitor domains.
DR EMBL; BC064278; AAH64278.1; -.
DR HSP; P10646; IADZ.
DR GO; GO:0004867; F:serine-type endopeptidase inhibitor activity; IEA.
DR GO; GO:0005215; F:transporter activity; IEA.
DR GO; GO:0006810; P:transport; IEA.
DR InterPro; IPR002968; AI-microglobin.
DR InterPro; IPR011038; Calycin.
DR InterPro; IPR002345; Lipocalin.
DR InterPro; IPR000566; Lipocalin_cytFABP.
DR InterPro; IPR002223; Prot_Inh_Kunz-m.
DR Pfam; PF00014; Kunitz BPTI_2.
DR Pfam; PF00061; Lipocalin; 1.
DR PRINTS; PR01215; ALMCGLOBULIN.
DR PRINTS; PR00759; BASICPTASE.
DR PRINTS; PR00179; LIPOCALIN.
DR ProDom; PD000222; Prot_Inh_Kunz-m; 2.
DR SMART; SM00131; KU; 2.
DR PROSITE; PS00280; BPTI_KUNITZ_1; 2.
DR PROSITE; PS50279; BPTI_KUNITZ_2; 2.
DR PROSITE; PS00213; LIPOCALIN; 1.
KW Hypothetical protein; Lipocalin.
SQ SEQUENCE 342 AA; 38191 MW; D9B95BE25C8CB5A CRC64;
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Query Match      22.1%; Score 166.5; DB 2; Length 342;
Best Local Similarity 32.9%; Pred. No. 8.7e-08;
Matches 47; Conservative 17; Mismatches 48; Indels 31; Gaps 7;

QY 3 LSGLLPILVPFILLGDIQEPGHAEGILGKPCPKIKV-----ECEVEIDQCTKPRD-- 53
DB 148 LVGRSPDLRP-VLIDFQOQFALAQGV-----PDSIFLTITNSGECAPGDIE--VRPRRTQ 199

QY 54 ---CPE-----NMKCCPFSCGKKKCLDFRDKICSMPOEAGPCLASIPHHWYKTKICSEF 105
DB 200 RAVLPEEEEGSGMNNPLSRNK-----GDSCLAPAFGPGCLGMHSRYFNSSTWACETF 253

QY 106 IYGGCGGNNNFOTBAICLVTC 128
DB 254 KYGGCLGNNNFHSEKELQTCR 276
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RESULT 45
Q90WA1 PRELIMINARY; PRT; 83 AA.
AC Q90WA1;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Textilin.
OS Pseudonaja textilis textilis.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroides;
OC Elapidae; Acanthophiinae; Pseudonaja.
OX NCBI_TaxID=169397;
[1]
RP SEQUENCE FROM N.A.
RC TISSUE=Venom gland;
RA Masci P.P., Lavin M.F., Gaffney P.J., Sorokina I.N., Flippovich I.V.;
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
[2]
RP SEQUENCE FROM N.A.
RC TISSUE=Venom gland;
RA Flippovich I.V., Sorokina N.I., Masci P.P., de Jersey J.,
RA Whitaker A.N., Gaffney P.J., Lavin M.F.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.
DR EMBL; AF402324; AAK95519.1; -.
DR HSPF; P25660; IUC6.
DR ProDom; PD000222; Prot_Inh_Kunz-m; 1.
DR SMART; SM00131; KU; 1_Kunz-m; 1.
DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
DR PROSITE; PS02079; BPTI_KUNITZ_2; 1.
SQ SEQUENCE 83 AA; 9173 MW; 2045E50657014221 CRC64;

Query Match 22.0%; Score 166; DB 2; Length 83;
Best Local Similarity 50.9%; Pred. No. 2.4e-08;
Matches 28; Conservative 6; Mismatches 21; Indels 0; Gaps 0;

Qy 73 RKDICSMQPEAGPCLASIPHWYKTKICSEFYGGCGGNNNFQTEAICLVTC 127
Db 27 RPDCFLPADTGPCRVFPFVYNDPKKCLEFYGGCGGNANNFITKECESIC 81

RESULT 46
Q6I750 PRELIMINARY; PRT; 507 AA.
AC Q6I750;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hepatocyte growth factor activator inhibitor-1.
GN Name=HAI-1;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
[1]
RP SEQUENCE FROM N.A.
RA Tezuka S.;
RL Submitted (DEC-2003) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Contains 2 BPTI/Kunitz inhibitor domains.
DR EMBL; AB154834; BAD33971.1; -.
DR GO; GO:0004867; F:serine-type endopeptidase inhibitor activity; IEA.
DR InterPro; IPR002172; LDL receptor_A.
DR InterPro; IPR011106; MAN5C_N.
DR InterPro; IPR002223; Prot_Inh_Kunz-m.
DR Pfam; PF00014; Kunitz_BPTI; 2.
DR Pfam; PF00057; Ldl_recept_a; 1.
DR Pfam; PF07502; MAN5C; 1.
DR PRINTS; PR00759; BASICPTASE.
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DR ProDom; PD000222; Prot_Inh_Kunz-m; 2.
DR SMART; SM00131; KU; 2.
DR SMART; SM00192; LDLa; 1.
DR PROSITE; PS00280; BPTI_KUNITZ_1; 2.
DR PROSITE; PS02079; BPTI_KUNITZ_2; 2.
DR PROSITE; PS01209; LDLRA_1; 1.
DR PROSITE; PS00068; LDLRA_2; 1.
SQ SEQUENCE 507 AA; 56469 MW; 810043AE28C47AF3 CRC64;

Query Match 22.0%; Score 166; DB 2; Length 507;
Best Local Similarity 34.0%; Pred. No. 1.4e-07;
Matches 33; Conservative 17; Mismatches 39; Indels 8; Gaps 3;

Qy 40 CEVEEIDQCTKPRDCP---ENMKCCPFSCG---KKCLDFRKD--ICSMQPEAGPCLASIP 91
Db 324 CCTDGFLECDTDCPDGSDTEATCEKYSSGFDELQSHFLSDKGYCAELPDTGCKENIP 383

Qy 92 HWYNNKTKICSEFYGGCGGNNNFQTEAICLVTC 128
Db 384 RWTYNPFSCARFTYGGCYGNKNFKEQQCLESCE 420

RESULT 47
Q9GQRO PRELIMINARY; PRT; 2174 AA.
AC Q9GQRO;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Extracellular matrix protein papilin precursor.
GN Name=Ppn;
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
[1]
RP SEQUENCE FROM N.A.
RC STRAIN=dp cn bw;
RX MEDLINE=20530499; PubMed=11076767;
RA Kramerova A.A., Kawaguchi N., Nelson R.E., Fessler L.I., Chen Y.,
RA Sieron A.L., Prockop D.J., Fessler J.H.;
RT "Papilin in development; a pericellular protein with a homology to the
RT ADAMTS metalloproteinases."
RL Development 127:5475-5485 (2000).
CC -1- SIMILARITY: Contains 3 BPTI/Kunitz inhibitor domains.
DR EMBL; AF205357; AAG37995.1; -.
DR HSPF; P12111; 1KTH.
DR FlyBase; FBgn0003137; Ppn.
DR GO; GO:0005604; C:basement membrane; IDA.
DR InterPro; IPR010294; ADAM_spacer1.
DR InterPro; IPR006209; EGF_like.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003598; Ig_c2.
DR InterPro; IPR010909; PLAC.
DR InterPro; IPR002223; Prot_Inh_Kunz-m.
DR InterPro; IPR000884; TSPI.
DR InterPro; IPR008197; WAP.
DR Pfam; PF05986; ADAM_spacer1; 1.
DR Pfam; PF00047; ig; 1.
DR Pfam; PF00014; Kunitz_BPTI; 3.
DR Pfam; PF00090; TSP_1; 5.
DR Pfam; PF00095; WAP_1.
DR PRINTS; PR00003; 4DISULPHCORE.
DR PRINTS; PR00759; BASICPTASE.
DR SMART; SM00408; IGC2; 2.
DR SMART; SM00131; KU; 3.
DR SMART; SM00209; TSP1; 7.
DR SMART; SM00217; WAP; 1.
DR PROSITE; PS00317; 4DISULFIDE CORE; 1.
DR PROSITE; PS00280; BPTI_KUNITZ_1; 3.
DR PROSITE; PS02079; BPTI_KUNITZ_2; 3.
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DR PROSITE; PS00022; EGF_1; UNKNOWN_1.
DR PROSITE; PS0835; IG LIKE; 2.
DR PROSITE; PS0900; PLAC; 1.
DR PROSITE; PS0092; TSP1; 5.
KW Matrix protein; Signal.
FT SIGNAL 1 26 Potential.
SQ SEQUENCE 2174 AA; 231935 MW; 038F707952623120 CRC64;

Query Match      22.0%; Score 165.5; DB 2; Length 2174;
Best Local Similarity 32.2%; Pred. No. 6.6e-07;
Matches 29; Conservative 16; Mismatches 42; Indels 3; Gaps 1;

QY 40 CEVEIDQKTRDPCPNKCCPFSGCKKCLDFRDKDICSMPQEAQCLASIPHWYNNKT 99
Db 1696 CEFQYGGCYGYNRFDLSLEQCGTC---AASENLPTCEQPVESGFCAGNFERWYDNET 1752
QY 100 KICSEFIYGGCGNNNNQTEALCLVTCK 129
Db 1753 DICRPFYGGCKGNKNYPTEHACYNCRQ 1782

RESULT 48
QYRQ8
ID Q7YRQ8 PRELIMINARY; PRT; 234 AA.
AC Q7YRQ8
DT 01-OCT-2003 (TREMBLrel. 25, Created)
DT 01-OCT-2003 (TREMBLrel. 25, Last sequence update)
DT 01-WAR-2004 (TREMBLrel. 26, Last annotation update)
DE Tissue factor pathway inhibitor-2.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovinae; Bos.
OX NCBI_TaxID=9913;
RN
RP SEQUENCE FROM N.A.
RX MEDLINE=22802738; PubMed=12921785; DOI=10.1016/S0003-9861(03)00332-1;
RA Du X., Deng F.M., Chand H.S., Kisiel W.;
RT "Molecular cloning, expression, and characterization of bovine tissue
RT factor pathway inhibitor-2";
RL Arch. Biochem. Biophys. 417:96-104(2003).
RN [2]
RP SEQUENCE FROM N.A.
RA Deng F.-M., Kisiel W., Sun T.-T.;
RL Submitted (FEB-2003) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: Contains 3 BPTI/Kunitz inhibitor domains.
DR EMBL; AY234861; A084035.1; -.
DR HSSP; P00981; 1DTK.
DR GO; GO:0004867; F:serine-type endopeptidase inhibitor activity; IEA.
DR InterPro; IPR002223; Prot_Inh_Kunz-m.
DR Pfam; PF00014; Kunitz_BPTI; 3.
DR ProDom; PD000222; Prot_Inh_Kunz-m; 3.
DR SMART; SM00131; KU; 3.
DR PROSITE; PS00280; BPTI_KUNITZ_1; 3.
DR PROSITE; PS0279; BPTI_KUNITZ_2; 3.
SQ SEQUENCE 234 AA; 26675 MW; 401BEC84D589B422 CRC64;

Query Match      21.9%; Score 165; DB 2; Length 234;
Best Local Similarity 49.1%; Pred. No. 8.3e-08;
Matches 27; Conservative 11; Mismatches 17; Indels 0; Gaps 0;

QY 75 DICMPQEAQCLASIPHWYNNKTICSEFIYGGCGNNNNFQTEALCLVTCK 129
Db 34 EICLLPDDGPCARIPSYDYRYTQSCREFFYGGCGGNANFETLEACNEACWK 88

RESULT 49
Q6ZNI4
ID Q6ZNI4 PRELIMINARY; PRT; 283 AA.
AC Q6ZNI4
DT 05-JUL-2004 (TREMBLrel. 27, Created)
DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)

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DE Hypothetical protein FLJ16032.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Tongue;
RA Ninomiya K., Wagatsuma M., Kanda K., Kondo H., Yokoi T., Kodaira H.,
RA Furuya T., Takahashi M., Kikkawa E., Omura Y., Abe K., Kamihara K.,
RA Katsuta N., Sato K., Tanikawa M., Yamazaki M., Sugiyama T., Irie R.,
RA Otsuki T., Sato H., Wakamatsu A., Ishii S., Yamamoto J., Isono Y.,
RA Kawai-Hio Y., Saito K., Nishikawa T., Kimura K., Yamashita H.,
RA Matsuo K., Nakamura Y., Sekine M., Kikuchi H., Murakawa K.,
RA Kanehori K., Takahashi-Fujii A., Oshima A., Sugiyama A., Kawakami B.,
RA Suzuki Y., Sugano S., Nagahari K., Masuho Y., Nagai K., Isogai T.;
RL Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.
DR EMBL; AK131196; BAD18391.1; -.
DR HSSP; P00974; 1K09.
DR GO; GO:0004867; F:serine-type endopeptidase inhibitor activity; IEA.
DR InterPro; IPR001134; Netrin C.
DR InterPro; IPR002223; Prot_Inh_Kunz-m.
DR InterPro; IPR008993; TIMP_like.
DR Pfam; PF00014; Kunitz_BPTI; 2.
DR PRINTS; PR00759; BASICPTASE.
DR ProDom; PD000222; Prot_Inh_Kunz-m; 2.
DR SMART; SM00131; KU; 1.
DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
DR PROSITE; PS0279; BPTI_KUNITZ_2; 1.
DR PROSITE; PS0189; NTR; 1.
SQ SEQUENCE 283 AA; 31291 MW; 8620657309866D30 CRC64;

Query Match      21.9%; Score 165; DB 2; Length 283;
Best Local Similarity 42.2%; Pred. No. 1e-07;
Matches 27; Conservative 9; Mismatches 28; Indels 0; Gaps 0;

QY 64 SCGKCLDFRDKDICSMPQEAQCLASIPHWYNNKTICSEFIYGGCGNNNNFQTEAIC 123
Db 80 ACLACMSGLAACLSPALQGPCKAYAPWAYNSQTQCQSFVYGGCGNGNPFESBAC 139
QY 124 LVTC 127
Db 140 EESC 143

RESULT 50
SPTI_MOUSE
ID SPTI_MOUSE STANDARD; PRT; 507 AA.
AC Q9R097;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Kunitz-type protease inhibitor 1 precursor (Hepatocyte growth factor
DE activator inhibitor type 1) (HAI-1).
GN Name=Spint1; Synonyms=Hail;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALE/c;
RX MEDLINE=21299055; PubMed=11406276; DOI=10.1016/S0167-4781(01)00216-0;
RA Itoh H., Kataoka H., Meng J.Y., Hamasuna R., Kitamura N., Koono M.;
RT "Mouse hepatocyte growth factor activator inhibitor type 1 (HAI-1) and
RT type 2 (HAI-2)/placental bikunin genes and their promoters.";
RL Biochim. Biophys. Acta 1519:92-95(2001).
CC -!- FUNCTION: Inhibitor of HGF activator (By similarity).
CC -!- SURCELLULAR LOCATION: Secreted (By similarity).
CC -!- DOMAIN: This inhibitor contains two inhibitory domains.
CC -!- SIMILARITY: Contains 2 BPTI/Kunitz inhibitor domains.
CC -!- SIMILARITY: Contains 1 LDL-receptor class A domain.

```

```
CC CC -!- SIMILARITY: Contains 1 MANSO domain.
CC CC -----
CC CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC CC the European Bioinformatics Institute. There are no restrictions on its
CC CC use by non-profit institutions as long as its content is in no way
CC CC modified and this statement is not removed. Usage by and for commercial
CC CC entities requires a license agreement (See http://www.ebi.ac.uk/announcements/
CC CC or send an email to license@ebi.ac.uk).
CC CC -----
CC DR EMBL; AF099018; AAF02490.1; -
CC DR HSSP; P31713; 1SHP.
CC DR MGD; MGI:1338033; Spint1.
CC DR InterPro; IPR002172; LDL_receptor_A.
CC DR InterPro; IPR011106; MANSO_N.
CC DR InterPro; IPR002223; Prot_Inh_Kunz-m.
CC DR Pfam; PF00014; Kunitz_BPTI; 2.
CC DR Pfam; PF00057; Ldl_recept_a; 1.
CC DR Pfam; PF07502; MANSO; 1.
CC DR PRINTS; PR00759; BASICPTASE.
CC DR ProDom; PD000222; Prot_Inh_Kunz-m; 2.
CC DR SMART; SM00131; KU; 2.
CC DR SMART; SM00192; LDLA; 1.
CC DR PROSITE; PS00280; BPTI_KUNITZ_1; 2.
CC DR PROSITE; PS0279; BPTI_KUNITZ_2; 2.
CC DR PROSITE; PS01209; LDLA_1; FALSE_NEG.
CC DR PROSITE; PS0068; LDLA_2; 1.
CC DR PROSITE; PS0986; MANSO; 1.
CC KW Glycoprotein; Repeat; Serine protease inhibitor; Signal.
FT SIGNAL 1 29 Potential.
FT CHAIN 30 507 Kunitz-type protease inhibitor 1.
FT DOMAIN 51 134 MANSO.
FT DOMAIN 244 294 BPTI/Kunitz inhibitor 1.
FT DOMAIN 312 348 LDL-receptor class A.
FT DOMAIN 369 419 BPTI/Kunitz inhibitor 2.
FT SITE 254 255 Reactive bond (By similarity).
FT SITE 379 380 Reactive bond (By similarity).
FT DISULFID 244 294 By similarity.
FT DISULFID 253 277 By similarity.
FT DISULFID 269 290 By similarity.
FT DISULFID 369 419 By similarity.
FT DISULFID 378 402 By similarity.
FT DISULFID 394 415 By similarity.
FT CARBOHYD 229 229 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 501 501 N-linked (GlcNAc...) (Potential).
SQ SEQUENCE 507 AA; 56676 MW; 20CB5DEDCF46AA7 CRC64;

Query Match 21.9%; Score 165; DB 1; Length 507;
Best Local Similarity 32.3%; Pred. No. 1.8e-07;
Matches 32; Conservative 15; Mismatches 40; Indels 12; Gaps 2;

Qy 40 CEVEIIOCTKPRDCPENMKCPSCGKKCLDF-----RKDTCMPQEAQGLAS 89
Db 324 CSIDGFLECDTDPDPCGSD--EATCEKYTSFGDELQNIHFLSDKGYCAELPDTGFCKEN 381

Qy 90 IPHWYNNKTKICSEFYGGCGGNNNFQTEAICLVCK 128
Db 382 IPRWYNPFSERCARFTYGGCYGNKNFEEQQCLESCR 420
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Search completed: September 21, 2005, 16:40:08
Job time : 83.2625 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 21, 2005, 14:52:13 ; Search time 66.2891 Seconds
(without alignments)
618.452 Million cell updates/sec

Title: US-10-807-204-2
Perfect score: 625
Sequence: 1 EGILGKPCPKIKVEBEI.....GNNNFQTEAICLVTCCKYH 106

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 50 summaries

Database : A_Geneseq_16Dec04: *
1: Genesep1980s: *
2: Genesep1990s: *
3: Genesep2000s: *
4: Genesep2001s: *
5: Genesep2002s: *
6: Genesep2003as: *
7: Genesep2003bs: *
8: Genesep2004s: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	625	100.0	106	7	ADAI19801 Mature fo
2	625	100.0	131	7	ADAI19800 Engineere
3	625	100.0	131	7	ADAI19811 Engineere
4	603	96.5	131	7	ADAI19814 Human DJL
5	423	67.7	98	7	ADAI19808 Engineere
6	416	66.6	136	7	ADAI19815 Mouse DJL
7	401.5	64.2	117	5	Aae27094 Human sec
8	401.5	64.2	117	5	Aae27165 Human gen
9	401.5	64.2	117	6	ABU65038 Human sec
10	401.5	64.2	117	8	ADG89847 Human sec
11	400	64.0	102	5	Aae27095 Human sec
12	400	64.0	102	5	Aae28009 Human gen
13	400	64.0	102	6	ABU65039 Human sec
14	400	64.0	102	8	ADG89848 Human sec
15	400	64.0	102	2	Aaw75219 Human sec
16	400	64.0	133	5	Aae26982 Human gen
17	400	64.0	133	5	Aae27120 Human gen
18	400	64.0	133	6	ABU64993 Human sec
19	400	64.0	133	7	ADAI19812 Human EPP
20	400	64.0	133	8	ADG89802 Human pro
21	400	64.0	164	3	Aay70010 Human pro
22	400	64.0	179	8	ABM85103 Human dia
23	352	56.3	134	7	ADAI19813 Mouse EPP
24	276	44.2	86	5	ABP69809 Human pol
25	276	44.2	86	6	ABJ26667 Human pro

26	276	44.2	101	4	ABB12236 Human epp
27	246	39.4	43	7	ADAI19804 Engineere
28	242	38.7	64	4	AAE13093 Human ser
29	236	37.8	58	4	AAE13084 Human ser
30	236	37.8	58	4	AAE13084 Human ser
31	236	37.8	58	7	ADAI1997 Human CAB
32	236	37.8	58	8	ADL16838 Human Kun
33	236	37.8	58	8	ADL16838 Human CAB
34	219	35.0	51	2	AAW75257 Fragment
35	219	35.0	51	5	AAE27025 Human gen
36	219	35.0	51	5	AAE27163 Human gen
37	219	35.0	51	8	ADG89845 Human sec
38	187	29.9	560	2	AAE2523 Hookworm
39	187	29.9	2858	4	ABB71150 Drosophil
40	187	29.9	3060	4	ABB58064 Drosophil
41	182.5	29.2	571	7	AAE39498 Cloned mo
42	182.5	29.2	571	7	AAE39498 Mouse GDF
43	182.5	29.2	571	7	ADG93670 Mouse GDF
44	181.5	29.0	101	8	ADQ66734 Novel hum
45	180	28.8	33	7	ADAI19806 Engineere
46	180	28.8	33	7	ADAI19809 Engineere
47	177	28.3	58	2	AAE99146 Aprotinin
48	175	28.0	43	4	AAE13096 Human ser
49	175	28.0	54	4	AAE13092 Trypsin i
50	173.5	27.8	503	5	ABJ01150 Ovary cel

ALIGNMENTS

RESULT 1
ADAI19801
ID ADAI19801 standard; protein; 106 AA.
XX
AC ADAI19801;
XX
DT 20-NOV-2003 (first entry)
XX
DE Mature form of engineered human DJL1 protein SEQ ID NO:2.

XX DJL1; Kunitz-type protease inhibitor domain; antiinflammatory;
KW antiallergic; thrombolytic; anticoagulant; cardiant; vasotropic;
KW antibacterial; immunosuppressive; antirheumatic; antiarthritic;
KW nephrotropic; antipsoriatic; vulnery; protease inhibitor; gene therapy;
KW acute pancreatitis; pulmonary injury; allergy-induced protease release;
KW deep vein thrombosis; myocardial infarction; shock; septic shock;
KW hyperfibrinolytic haemorrhage; inflammatory disorder; emphysema;
KW idiopathic pulmonary fibrosis; rheumatoid arthritis; glomerulonephritis;
KW chronic inflammatory bowel disease; psoriasis.

Key	Location/Qualifiers
Disulfide-bond	8..36 /note = predicted disulfide bond
Disulfide-bond	15..40 /note = predicted disulfide bond
Disulfide-bond	23..35 /note = predicted disulfide bond
Disulfide-bond	29..44 /note = predicted disulfide bond
Domain	52..102 /note = Kunitz domain predicted by pfscan
Disulfide-bond	52..102 /note = predicted disulfide bond
Disulfide-bond	61..85 /note = predicted disulfide bond
Disulfide-bond	77..98 /note = predicted disulfide bond

WO2003070770-A2.

PD 28-AUG-2003.
 XX
 XX 18-FEB-2003; 2003WO-EP001629.
 XX
 PR 21-FEB-2002; 2002US-0358683P.
 XX
 XX (GENE-) GENEPROT INC.
 XX
 XX Bougueleret L, Bairoch A, Niknejad A;
 XX WPI; 2003-663849/62.
 DR
 XX New engineered human Kunitz-type protease inhibitor for diagnosing,
 XX preventing or treating conditions associated with excessive proteinase
 PT activity, e.g. inflammation, pulmonary injuries, myocardial infarction or
 PT hemorrhage.
 XX
 XX Claim 5; Page 71; 87pp; English.
 PS
 XX The present invention describes an isolated, purified or recombinant DJ11
 CC polypeptide comprising a Kunitz-type protease inhibitor domain or its
 CC biologically active portion. The polypeptide comprises at least 98 %
 CC identity to residues 77-127 of a 131 amino acid sequence (S1, see
 CC ADA19800), or to residues 52-102 of a 106 amino acid sequence (S2, see
 CC ADA19801). DJ11 has antiinflammatory, anti-allergic, thrombolytic,
 CC anticoagulant, cardiant, vasotropic, antibacterial, immunosuppressive,
 CC antirheumatic, antiarthritic, nephrotropic, antipsoriatic and vulnary
 CC activities, and can be used as a protease inhibitor and in gene therapy.
 CC Composition and methods from the present invention can be used in
 CC diagnosing, preventing or treating conditions associated with excessive
 CC proteinase activity, such as acute pancreatitis, pulmonary injury,
 CC allergy-induced protease release, deep vein thrombosis, myocardial
 CC infarction, shock (including septic shock), hyperfibrinolytic
 CC haemorrhage, and especially, inflammatory disorders (e.g. emphysema,
 CC idiopathic pulmonary fibrosis, rheumatoid arthritis, glomerulonephritis,
 CC chronic inflammatory bowel disease or psoriasis). The DJ11 proteins may
 CC be used in preserving platelet function, organ preservation or in wound
 CC healing. The polynucleotide sequence encoding DJ11 may be used as
 CC hybridisation probes, in chromosome and gene mapping, in the generation
 CC of antisense RNA and DNA, and as targets for pharmaceutical intervention.
 CC The present sequence represents the mature form of an engineered human
 CC DJ11 protein from the present invention.
 XX
 XX Sequence 106 AA;
 SQ
 Query Match 100.0%; Score 625; DB 7; Length 106;
 Best Local Similarity 100.0%; Pred. No. 8.7e-47;
 Matches 106; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 EGILGKPCPKIKVECEVEEIDQCTKPRDCPENMKCCPFSCGKCLDFRDKICSMPOBAGP 60
 Db 1 EGILGKPCPKIKVECEVEEIDQCTKPRDCPENMKCCPFSCGKCLDFRDKICSMPOBAGP 60
 Qy 61 CLASIPHWYNNKTKICSEFIYGGCGQNNNNFQTEAICLVTCCKYH 106
 Db 61 CLASIPHWYNNKTKICSEFIYGGCGQNNNNFQTEAICLVTCCKYH 106
 RESULT 2
 ID ADA19800
 AC ADA19800 standard; protein; 131 AA.
 XX
 XX ADA19800;
 XX
 XX 20-NOV-2003 (first entry)
 DT
 XX Engineered human DJ11 protein SEQ ID NO:1.
 DE
 XX DJ11; Kunitz-type protease inhibitor domain; antiinflammatory;
 KW anti-allergic; thrombolytic; anticoagulant; cardiant; vasotropic;
 KW antibacterial; immunosuppressive; antirheumatic; antiarthritic;
 KW nephrotropic; antipsoriatic; vulnary; protease inhibitor; gene therapy;
 KW acute pancreatitis; pulmonary injury; allergy-induced protease release;

KW deep vein thrombosis; myocardial infarction; shock; septic shock;
 KW hyperfibrinolytic haemorrhage; inflammatory disorder; emphysema;
 KW idiopathic pulmonary fibrosis; rheumatoid arthritis; glomerulonephritis;
 KW chronic inflammatory bowel disease; psoriasis.
 XX
 OS Synthetic.
 OS Homo sapiens.
 XX
 XX Key Location/Qualifiers
 FT Misc-difference 1..131
 FT /note= "eppin-like precursor"
 FT Peptide 1..25
 FT /label= signal
 FT Protein 26..131
 FT /note= "mature DJ11 protein"
 FT Disulfide-bond 33..61
 FT /note = predicted disulfide bond
 FT Disulfide-bond 40..65
 FT /note = predicted disulfide bond
 FT Disulfide-bond 48..60
 FT /note = predicted disulfide bond
 FT Disulfide-bond 54..69
 FT /note = predicted disulfide bond
 FT Domain 77..127
 FT /note = Kunitz domain predicted by pfscan
 FT Disulfide-bond 77..127
 FT /note = predicted disulfide bond
 FT Disulfide-bond 86..110
 FT /note = predicted disulfide bond
 FT Disulfide-bond 102..123
 FT /note = predicted disulfide bond
 XX WO2003070770-A2.
 XX 28-AUG-2003.
 XX 18-FEB-2003; 2003WO-EP001629.
 XX 21-FEB-2002; 2002US-0358683P.
 XX (GENE-) GENEPROT INC.
 XX Bougueleret L, Bairoch A, Niknejad A;
 XX WPI; 2003-663849/62.
 XX N-PSDB; ADA19810.
 XX New engineered human Kunitz-type protease inhibitor for diagnosing,
 XX preventing or treating conditions associated with excessive proteinase
 PT activity, e.g. inflammation, pulmonary injuries, myocardial infarction or
 PT hemorrhage.
 XX
 PS Claim 5; Page 69-70; 87pp; English.
 XX
 XX The present invention describes an isolated, purified or recombinant DJ11
 CC polypeptide comprising a Kunitz-type protease inhibitor domain or its
 CC biologically active portion. The polypeptide comprises at least 98 %
 CC identity to residues 77-127 of a 131 amino acid sequence (S1, see
 CC ADA19800), or to residues 52-102 of a 106 amino acid sequence (S2, see
 CC ADA19801). DJ11 has antiinflammatory, anti-allergic, thrombolytic,
 CC anticoagulant, cardiant, vasotropic, antibacterial, immunosuppressive,
 CC antirheumatic, antiarthritic, nephrotropic, antipsoriatic and vulnary
 CC activities, and can be used as a protease inhibitor and in gene therapy.
 CC Composition and methods from the present invention can be used in
 CC diagnosing, preventing or treating conditions associated with excessive
 CC proteinase activity, such as acute pancreatitis, pulmonary injury,
 CC allergy-induced protease release, deep vein thrombosis, myocardial
 CC infarction, shock (including septic shock), hyperfibrinolytic
 CC haemorrhage, and especially, inflammatory disorders (e.g. emphysema,
 CC idiopathic pulmonary fibrosis, rheumatoid arthritis, glomerulonephritis,
 CC chronic inflammatory bowel disease or psoriasis). The DJ11 proteins may
 CC be used in preserving platelet function, organ preservation or in wound
 CC healing. The polynucleotide sequence encoding DJ11 may be used as

CC hybridisation probes, in chromosome and gene mapping, in the generation
 CC of antisense RNA and DNA, and as targets for pharmaceutical intervention.
 CC The present sequence represents an engineered human DJ11 protein from the
 CC present invention.

XX SQ Sequence 131 AA;

Query Match 100.0%; Score 625; DB 7; Length 131;
 Best Local Similarity 100.0%; Pred. No. 1.1e-46;
 Matches 106; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EGILGKPCPKIKVECEVEEIDQCTKPRDCPENMKCCPFSCGKKCLDFRDKICSMPEAGP 60
 Db 26 EGILGKPCPKIKVECEVEEIDQCTKPRDCPENMKCCPFSCGKKCLDFRDKICSMPEAGP 85

QY 61 CLASIPHHWYNNKTKICSEFIYGGCGQNNNNFQTEAICLVTCCKYH 106

Db 86 CLASIPHHWYNNKTKICSEFIYGGCGQNNNNFQTEAICLVTCCKYH 131

RESULT 3

ADA19811
 ID ADA19811 standard; protein; 131 AA.

XX AC ADA19811;

XX DT 20-NOV-2003 (first entry)

XX DE Engineered human DJ11 protein SEQ ID NO:12.

XX DJ11; Kunitz-type protease inhibitor domain; antiinflammatory;
 KW antiallergic; thrombolytic; anticoagulant; cardiant; vasotropic;
 KW antibacterial; immunosuppressive; antirheumatic; antiarthritic;
 KW nephrotropic; antipsoriatic; vulnary; protease inhibitor; gene therapy;
 KW acute pancreatitis; pulmonary injury; allergy-induced protease release;
 KW deep vein thrombosis; myocardial infarction; shock; septic shock;
 KW hyperfibrinolytic haemorrhage; inflammatory disorder; emphysema;
 KW idiopathic pulmonary fibrosis; rheumatoid arthritis; glomerulonephritis;
 KW chronic inflammatory bowel disease; psoriasis.

XX Synthetic.

OS Homo sapiens.

XX WO2003070770-A2.

XX PD 28-AUG-2003.

XX PF 18-FEB-2003; 2003WO-BF001629.

XX PR 21-FEB-2002; 2002US-0358683P.

XX PA (GENE-) GENEPROT INC.

XX PI Bougueleret L, Bairoch A, Niknejad A;

XX WPI; 2003-663849/62.

XX New engineered human Kunitz-type protease inhibitor for diagnosing,
 PT preventing or treating conditions associated with excessive proteinase
 PT activity, e.g. inflammation, pulmonary injuries, myocardial infarction or
 PT hemorrhage.

XX Disclosure; Page 84; 87pp; English.

XX The present invention describes an isolated, purified or recombinant DJ11
 CC polypeptide comprising a Kunitz-type protease inhibitor domain or its
 CC biologically active portion. The polypeptide comprises at least 98 %
 CC identity to residues 77-127 of a 131 amino acid sequence (S1, see
 CC ADA19800), or to residues 52-102 of a 106 amino acid sequence (S2, see
 CC ADA19801). DJ11 has antiinflammatory, antiallergic, thrombolytic,
 CC anticoagulant, cardiant, vasotropic, antibacterial, immunosuppressive,
 CC antirheumatic, antiarthritic, nephrotropic, antipsoriatic and vulnary
 CC activities, and can be used as a protease inhibitor and in gene therapy.

CC Composition and methods from the present invention can be used in
 CC diagnosing, preventing or treating conditions associated with excessive
 CC proteinase activity, such as acute pancreatitis, pulmonary injury,
 CC allergy-induced protease release, deep vein thrombosis, myocardial
 CC infarction, shock (including septic shock), hyperfibrinolytic
 CC haemorrhage, and especially, inflammatory disorders (e.g. emphysema,
 CC idiopathic pulmonary fibrosis, rheumatoid arthritis, glomerulonephritis,
 CC chronic inflammatory bowel disease or psoriasis). The DJ11 proteins may
 CC be used in preserving platelet function, organ preservation or in wound
 CC healing. The polynucleotide sequence encoding DJ11 may be used as
 CC hybridisation probes, in chromosome and gene mapping, in the generation
 CC of antisense RNA and DNA, and as targets for pharmaceutical intervention.
 CC The present sequence represents an engineered human DJ11 protein from the
 CC present invention.

XX SQ Sequence 131 AA;

Query Match 100.0%; Score 625; DB 7; Length 131;
 Best Local Similarity 100.0%; Pred. No. 1.1e-46;
 Matches 106; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EGILGKPCPKIKVECEVEEIDQCTKPRDCPENMKCCPFSCGKKCLDFRDKICSMPEAGP 60
 Db 26 EGILGKPCPKIKVECEVEEIDQCTKPRDCPENMKCCPFSCGKKCLDFRDKICSMPEAGP 85

QY 61 CLASIPHHWYNNKTKICSEFIYGGCGQNNNNFQTEAICLVTCCKYH 106

Db 86 CLASIPHHWYNNKTKICSEFIYGGCGQNNNNFQTEAICLVTCCKYH 131

RESULT 4

ADA19814
 ID ADA19814 standard; protein; 131 AA.

XX AC ADA19814;

XX DT 20-NOV-2003 (first entry)

XX DE Human DJ11 protein SEQ ID NO:15.

XX DJ11; Kunitz-type protease inhibitor domain; antiinflammatory;
 KW antiallergic; thrombolytic; anticoagulant; cardiant; vasotropic;
 KW antibacterial; immunosuppressive; antirheumatic; antiarthritic;
 KW nephrotropic; antipsoriatic; vulnary; protease inhibitor; gene therapy;
 KW acute pancreatitis; pulmonary injury; allergy-induced protease release;
 KW deep vein thrombosis; myocardial infarction; shock; septic shock;
 KW hyperfibrinolytic haemorrhage; inflammatory disorder; emphysema;
 KW idiopathic pulmonary fibrosis; rheumatoid arthritis; glomerulonephritis;
 KW chronic inflammatory bowel disease; psoriasis.

XX Homo sapiens.

XX WO2003070770-A2.

XX PD 28-AUG-2003.

XX PF 18-FEB-2003; 2003WO-BF001629.

XX PR 21-FEB-2002; 2002US-0358683P.

XX PA (GENE-) GENEPROT INC.

XX PI Bougueleret L, Bairoch A, Niknejad A;

XX WPI; 2003-663849/62.

XX New engineered human Kunitz-type protease inhibitor for diagnosing,
 PT preventing or treating conditions associated with excessive proteinase
 PT activity, e.g. inflammation, pulmonary injuries, myocardial infarction or
 PT hemorrhage.

XX Disclosure; Fig 1; 87pp; English.

XX

CC The present invention describes an isolated, purified or recombinant DJ11
 CC polypeptide comprising a Kunitz-type protease inhibitor domain or its
 CC biologically active portion. The polypeptide comprises at least 98 %
 CC identity to residues 77-127 of a 131 amino acid sequence (S1, see
 CC ADA19800), or to residues 52-102 of a 106 amino acid sequence (S2, see
 CC ADA19801). DJ11 has antiinflammatory, antiallergic, thrombolytic,
 CC anticoagulant, cardiant, vasotropic, antipapillary, immunosuppressive,
 CC antirheumatic, antiarthritic, nephrotropic, antibacterial, immunosuppressive,
 CC activities, and can be used as a protease inhibitor and in gene therapy.
 CC Composition and methods from the present invention can be used in
 CC diagnosing, preventing or treating conditions associated with excessive
 CC proteinase activity, such as acute pancreatitis, pulmonary injury,
 CC allergy-induced protease release, deep vein thrombosis, myocardial
 CC infarction, shock (including septic shock), hyperfibrinolytic
 CC haemorrhage, and especially, inflammatory disorders (e.g. emphysema,
 CC idiopathic pulmonary fibrosis, rheumatoid arthritis, glomerulonephritis,
 CC chronic inflammatory bowel disease or psoriasis). The DJ11 proteins may
 CC be used in preserving platelet function, organ preservation or in wound
 CC healing. The polynucleotide sequence encoding DJ11 may be used as
 CC hybridisation probes, in chromosome and gene mapping, in the generation
 CC of antisense RNA and DNA, and as targets for pharmaceutical intervention.
 CC The present sequence represents a human DJ11 protein given in comparison
 CC with DJ11 proteins in the exemplification of the present invention.
 XX
 SQ Sequence 131 AA;

Query Match 96.5%; Score 603; DB 7; Length 131;
 Best Local Similarity 98.1%; Pred. No. 8.6e-45;
 Matches 104; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 Qy 1 EGILGKPCPKIKVECEVEEIDQCTKPRDCPENMKCCPFSCGKKCLDFRDKICSMPOAGP 60
 Db 26 EGILGKPCPKIKVECEVEEIDQCTKPRDCPENMKCCPFSCGKKCLDFRDKICSMPOAGP 85
 Qy 61 CLASIPHHWYNNKTKICSEFYGGQGNNNNFQTEAICLVTCCKYH 106
 Db 86 CLASIPHHWYNNKTKICSEFYGGQGNNNNFQTEAICLVTCCKYH 131

RESULT 5
 ID ADA19808 standard; protein; 98 AA.
 XX
 AC ADA19808;
 XX
 DT 20-NOV-2003 (first entry)
 XX
 DE Engineered human DJ11 partial amino acid sequence SEQ ID NO:9.
 XX
 KW DJ11; Kunitz-type protease inhibitor domain; antiinflammatory;
 KW antiallergic; thrombolytic; anticoagulant; cardiant; vasotropic;
 KW antibacterial; immunosuppressive; antirheumatic; antiarthritic;
 KW nephrotropic; antipapillary; vulnary; protease inhibitor; gene therapy;
 KW acute pancreatitis; pulmonary injury; allergy-induced protease release;
 KW deep vein thrombosis; myocardial infarction; shock; septic shock;
 KW hyperfibrinolytic haemorrhage; inflammatory disorder; emphysema;
 KW idiopathic pulmonary fibrosis; rheumatoid arthritis; glomerulonephritis;
 KW Chronic inflammatory bowel disease; psoriasis.
 XX
 OS Synthetic.
 OS Homo sapiens.
 XX
 PN WO2003070770-A2.
 XX
 PD 28-AUG-2003.
 XX
 PF 18-FEB-2003; 2003WO-EP001629.
 XX
 PR 21-FEB-2002; 2002US-0358683P.
 XX
 PA (GENE-) GENEPROT INC.
 XX
 PI Bougueleret L, Bairoch A, Niknejad A;

XX WPI; 2003-663849/62.
 DR
 XX New engineered human Kunitz-type protease inhibitor for diagnosing,
 PT preventing or treating conditions associated with excessive proteinase
 PT activity, e.g. inflammation, pulmonary injuries, myocardial infarction or
 PT hemorrhage.
 XX
 PS Disclosure; Page 82; 87pp; English.
 XX
 CC The present invention describes an isolated, purified or recombinant DJ11
 CC polypeptide comprising a Kunitz-type protease inhibitor domain or its
 CC biologically active portion. The polypeptide comprises at least 98 %
 CC identity to residues 77-127 of a 131 amino acid sequence (S1, see
 CC ADA19800), or to residues 52-102 of a 106 amino acid sequence (S2, see
 CC ADA19801). DJ11 has antiinflammatory, antiallergic, thrombolytic,
 CC anticoagulant, cardiant, vasotropic, antibacterial, immunosuppressive,
 CC antirheumatic, antiarthritic, nephrotropic, antipapillary and vulnary
 CC activities, and can be used as a protease inhibitor and in gene therapy.
 CC Composition and methods from the present invention can be used in
 CC diagnosing, preventing or treating conditions associated with excessive
 CC proteinase activity, such as acute pancreatitis, pulmonary injury,
 CC allergy-induced protease release, deep vein thrombosis, myocardial
 CC infarction, shock (including septic shock), hyperfibrinolytic
 CC haemorrhage, and especially, inflammatory disorders (e.g. emphysema,
 CC idiopathic pulmonary fibrosis, rheumatoid arthritis, glomerulonephritis,
 CC chronic inflammatory bowel disease or psoriasis). The DJ11 proteins may
 CC be used in preserving platelet function, organ preservation or in wound
 CC healing. The polynucleotide sequence encoding DJ11 may be used as
 CC hybridisation probes, in chromosome and gene mapping, in the generation
 CC of antisense RNA and DNA, and as targets for pharmaceutical intervention.
 CC The present sequence represents a partial engineered human DJ11 protein
 CC amino acid sequence from the present invention.
 XX
 SQ Sequence 98 AA;
 Query Match 67.7%; Score 423; DB 7; Length 98;
 Best Local Similarity 98.6%; Pred. No. 2.8e-29;
 Matches 72; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Qy 1 EGILGKPCPKIKVECEVEEIDQCTKPRDCPENMKCCPFSCGKKCLDFRDKICSMPOAGP 60
 Db 26 EGILGKPCPKIKVECEVEEIDQCTKPRDCPENMKCCPFSCGKKCLDFRDKICSMPOAGP 85
 Qy 61 CLASIPHHWYNNK 73
 Db 86 CLASIPHHWYNNK 98
 RESULT 6
 ID ADA19815 standard; protein; 136 AA.
 XX
 AC ADA19815;
 XX
 DT 20-NOV-2003 (first entry)
 XX
 DE Mouse DJ11 protein SEQ ID NO:16.
 XX
 KW DJ11; Kunitz-type protease inhibitor domain; antiinflammatory;
 KW antiallergic; thrombolytic; anticoagulant; cardiant; vasotropic;
 KW antibacterial; immunosuppressive; antirheumatic; antiarthritic;
 KW nephrotropic; antipapillary; vulnary; protease inhibitor; gene therapy;
 KW acute pancreatitis; pulmonary injury; allergy-induced protease release;
 KW deep vein thrombosis; myocardial infarction; shock; septic shock;
 KW hyperfibrinolytic haemorrhage; inflammatory disorder; emphysema;
 KW idiopathic pulmonary fibrosis; rheumatoid arthritis; glomerulonephritis;
 KW Chronic inflammatory bowel disease; psoriasis.
 XX
 OS Mus musculus.
 XX
 PN WO2003070770-A2.
 XX

PA (SOPP/) SOPP D R.
PA (GENT/) GENTZ R L.
PA (WEIY/) WEI Y.
PA (MOOR/) MOORE P A.
PA (YOUN/) YOUNG P E.
PA (GREE/) GREENE J M.
PA (FERR/) FERRIE A M.
PA (HAST/) HASTINGS G A.
XX
PI Rosen CA, Ruben SM, Li Y, Zeng Z, Kyaw H, Fischer CL, Li H;
PI Soppet DR, Gentz RL, Wei Y, Moore PA, Young PE, Greene JM;
PI Ferrie AM, Hastings GA;
XX
DR WPI; 2004-042167/04.
XX
XX New polypeptides and nucleic acid molecules for diagnosing, preventing or
PT treating diseases associated with aberrant expression or activity of the
PT polypeptide, e.g. cancer, asthma, AIDS, Parkinson's disease or diabetes.
XX
PS Disclosure; SEQ ID NO 120; 320pp; English.
XX
CC The invention relates to an isolated nucleic acid molecule encoding a
CC secreted protein that is at least 95% identical to a polynucleotide
CC fragment of any of the nucleotide sequences listed in table 1A of the
CC specification, which is hybridisable to the nucleotide sequences, a
CC polynucleotide encoding a polypeptide (or a polypeptide fragment, domain
CC or epitope of any of the amino acid sequences) listed in table 1A of the
CC specification, a polynucleotide which is an (allelic) variant of the
CC nucleotide sequences listed in the specification, a polynucleotide which
CC encodes a species homologue of the above amino acid sequences, a
CC polynucleotide capable of hybridising under stringent conditions to any
CC of the above polynucleotides, where the polynucleotide does not hybridise
CC under stringent conditions to a nucleic acid molecule having a nucleotide
CC sequence of only A or T residues. Also included are a recombinant vector
CC comprising the above nucleic acid molecule, making a recombinant host
CC cell comprising the above nucleic acid molecule, an isolated polypeptide
CC comprising a sequence that is at least 95% identical to the polypeptide
CC (or its fragment, domain, epitope, secreted form, (allelic) variant or
CC homologue) encoded by the above nucleic acid molecule, an isolated
CC antibody that binds specifically to the above polypeptide, a recombinant
CC host cell produced by the above method and that expresses the above
CC polypeptide, making an isolated polypeptide, preventing, treating or
CC ameliorating a medical condition, diagnosing a pathological condition or
CC a susceptibility to a pathological condition in a subject, identifying a
CC binding partner to the above polypeptide, the gene corresponding to the
CC cDNA sequence given in the specification, and identifying an activity in
CC a biological assay. The nucleic acid molecule and polypeptide are useful
CC in diagnosing, preventing, prognosing or treating diseases or disorders
CC associated with aberrant expression and/or activity of the above
CC polypeptide, such as neural disorders, immune system disorders, muscular
CC disorders, reproductive disorders, gastrointestinal disorders, pulmonary
CC disorders, cardiovascular disorders, renal disorders, proliferative
CC disorders and/or cancers. In particular, these diseases are systemic
CC lupus erythematosus, rheumatoid arthritis, multiple sclerosis,
CC thyroditis, anaemia, Grave's disease, diabetes, hepatitis, asthma,
CC allergies, nephritis, Parkinson's disease, Alzheimer's disease,
CC atherosclerosis, myocardial infarction, AIDS and infections. The methods
CC may be used for identifying agonists and antagonists of the
CC polynucleotide and polypeptide. The present sequence is a protein from
CC one of the 28 disclosed secreted protein genes, it is not clear whether
CC this is an alternative expressed protein or a fragment of one of the
CC claimed proteins.
XX
SQ Sequence 117 AA;

Query Match 64.2%; Score 401.5; DB 8; Length 117;
Best Local Similarity 66.0%; Pred No. 2.4e-27;
Matches 66; Conservative 12; Mismatches 21; Indels 1; Gaps 1;
XX
Qy 4 LGKPCPKIKVECEVEIDCKPRDCPENMKCCPFSCGCKGLDFRDKTCSPQAGPCL 63
Db 14 LGR-CPKIRECEFEQERDVCTKRCQDNKCCVFCGCKGLDLKQDCEMPKGTGCL 72

Qy 64 SIPHWYNNKTKICSEFIYGGCGGNNNNNFQTEAICLVTK 103
Db 73 YFLHWYDKDNTCSMFYGGCGGNNNNNFQSKANCLNTCK 112

RESULT 11
AAE27095
ID AAE27095 standard; protein; 102 AA.
XX
AC AAE27095;
XX
DT 13-DEC-2002 (first entry)
XX
DE Human secreted protein #2.
XX
KW Human; immunodeficiency; X-linked agammaglobulinaemia; septic shock;
KW autoimmune disorder; rheumatoid arthritis; multiple sclerosis; cancer;
KW Grave's disease; diabetes mellitus; haematopoietic disorder; stroke;
KW respiratory disorder; asthma; allergy; gastrointestinal disorder;
KW inflammatory bowel disease; neurodegenerative disorder; hepatitis;
KW Parkinson's disease; Alzheimer's disease; cardiovascular disorder;
KW atherosclerosis; myocarditis; renal disorder; fungicide; virucide;
KW hyperproliferative disorder; acute glomerulonephritis; tonsillitis;
KW respiratory disorder; rhinitis; sinusitis; neurological disease;
KW endocrine disorder; Addison's disease; reproductive system disorder;
KW endometriosis; vasotropic; vulnary; cytostatic; nootropic; cardiant;
KW anti-HIV; tranquilliser; gout; antiparasitic.
XX
OS Homo sapiens.
XX
XX US2002077287-A1.
XX
XX 20-JUN-2002.
XX
XX 11-MAY-2001; 2001US-00852659.
XX
XX 11-SEP-1998; 98US-00152060.
XX
XX (RUBE/) RUBEN S M.
XX (ROSE/) ROSEN C A.
XX (LIYY/) LI Y.
XX (ZENG/) ZENG Z.
XX (KVAV/) KYAW H.
XX (FISC/) FISCHER C L.
XX (LIHH/) LI H.
XX (SOPP/) SOPP D R.
XX (GENT/) GENTZ R L.
XX (WEIY/) WEI Y.
XX (MOOR/) MOORE P A.
XX (YOUN/) YOUNG P E.
XX (GREE/) GREENE J M.
XX (FERR/) FERRIE A M.
XX
XX Ruben SM, Rosen CA, Li Y, Zeng Z, Kyaw H, Fischer CL, Li H;
XX Soppet DR, Gentz RL, Wei Y, Moore PA, Young PE, Greene JM;
XX Ferrie AM;
XX
XX WPI; 2002-598780/64.
XX
XX Novel human secreted polypeptides and polynucleotides for diagnosing,
XX preventing, treating immune, hyperproliferative, cardiovascular,
XX neurological, reproductive disorders and identifying modulators of
XX therapeutic use.
XX
PS Disclosure; Page 16; 209pp; English.
XX
XX AD44636-AD44676 represent cDNAs corresponding to 28 human secreted
XX protein genes, and AAE26959-AAE26999 represent the proteins they encode.
XX AAE27000-AAE27025 represent human secreted protein fragments or their
XX variants. The secreted proteins and genes are useful for preventing,
XX treating or ameliorating medical conditions, e.g., by protein or gene
XX therapy. Specific uses are described for each of the 28 genes, based on
XX the tissues in which they are most highly expressed and include

CC developing products for the diagnosis or treatment of immunodeficiencies,
 CC e.g., X-linked agammaglobulinaemia, B cell immunodeficiencies, severe
 CC combined immunodeficiencies, autoimmune disorders e.g., systemic lupus
 CC erythematosus, rheumatoid arthritis, multiple sclerosis, autoimmune
 CC thyroiditis, autoimmune haemolytic anaemia, Goodpasture's syndrome,
 CC Grave's disease, diabetes mellitus, dermatitis, inflammatory conditions
 CC including septic shock, sepsis, reperfusion injury, inflammatory bowel
 CC disease, Crohn's disease, haematopoietic disorders, respiratory disorders
 CC e.g., asthma and allergy, gastrointestinal disorders e.g., inflammatory
 CC bowel disease), cancers e.g., gastric, ovarian, lung, liver, bladder and
 CC breast), central nervous system (CNS) disorders e.g., ischaemic brain
 CC injury and/or stroke, neurodegenerative disorders e.g., Parkinson's
 CC disease and Alzheimer's disease, AIDS-related dementia and prion disease,
 CC cardiovascular disorders e.g., myocarditis, arrhythmias, atherosclerosis,
 CC inflammatory disorders e.g., hepatitis, gout, trauma, pancreatitis,
 CC sarcoidosis and allogeneic transplant rejection, blood-related disorder
 CC (thrombosis, arterial thrombosis, atherosclerosis), hyperproliferative
 CC disorders, respiratory disorders e.g. rhinitis, sinusitis, tonsillitis,
 CC lung cancer, allergic disorders, pneumonitis, renal disorders e.g. acute
 CC glomerulonephritis, neurological diseases, liver disorders, endocrine
 CC disorders e.g., hyperthyroidism, Addison's disease, hyperpituitarism,
 CC infectious diseases and reproductive system disorders e.g. endometriosis.
 CC The present sequence represents a human secreted protein of the invention
 XX
 SQ Sequence 102 AA;

Query Match 64.0%; Score 400; DB 5; Length 102;
 Best Local Similarity 66.7%; Pred. No. 2.9e-27;
 Matches 64; Conservative 11; Mismatches 21; Indels 0; Gaps 0;
 QY 8 CPKIKVECEVEIDQCTKPRDCPENMKCCPFCGKKCLDFRKIDICSMPOEAGPCLASIPH 67
 DB 2 CPKIRECECFQERDVCTKDRQCDNKKCCVFCGKKCLDLKQDVCMPKETGPCLAYFLH 61
 QY 68 WYNNKTKICSEFIYGGCGNNNNFQTEAICLVTK 103
 DB 62 WYDKDNTCSMFYGGCGNNNNFQSKANCLNTCK 97

RESULT 12

AAE28009
 ID AAE28009 standard; protein; 102 AA.

AC AAE28009;

XX 13-DEC-2002 (first entry)

XX Human gene 24 encoded secreted protein fragment #2.

XX Human; secreted protein; autoimmune disease; hyperproliferative disorder;
 KW rheumatoid arthritis; neoplasm; cerebrovascular disorder; angiogenesis;
 KW cerebral ischaemia; cardiovascular disorder; nervous system disorder;
 KW cardiac arrest; Alzheimer's disease; ocular disorder; wound healing;
 KW infection; corneal infection; skin aging; food additive; preservative;
 KW tissue regeneration; immunosuppressive; antiproliferative; cytostatic;
 KW cardiant; vasotropic; cerebroprotective; nootropic; neuroprotective;
 KW antibacterial; virucide; fungicide; ophthalmological; gene therapy;
 KW vulnery.

XX Homo sapiens.

OS US2002076756-A1.

XX 20-JUN-2002.

XX 11-MAY-2001; 2001US-00853161.

XX 02-FEB-2001; 2001US-0265583P.

XX (RUBE/) RUBEN S M.

PA (ROSE/) ROSEN C A.

PA (LIYY/) LI Y.

PA (ZENG/) ZENG Z.

PA (KYAW/) KYAW H.
 PA (FISC/) FISCHER C L.
 PA (LIHH/) LI H.
 PA (SOPP/) SOPPET D R.
 PA (GENT/) GENTZ R L.
 PA (WEIY/) WEI Y.
 PA (MOOR/) MOORE P A.
 PA (YOUN/) YOUNG P E.
 PA (GREE/) GREENE J M.
 PA (FERR/) FERRIE A M.

PI Ruben SM, Rosen CA, Li Y, Zeng Z, Kyaw H, Fischer CL, Li H;
 PI Soppet DR, Gentz RL, Wei Y, Moore PA, Young PE, Greene JM;
 PI Ferrie AM;

XX WPI; 2002-574454/61.

XX New nucleic acid molecules encoding 28 human secreted proteins, useful
 PT for diagnosing, preventing, treating or ameliorating medical conditions
 PT and as food additives or preservatives.

XX Disclosure; Page 17; 209pp; English.

XX AAD44854-AAD44984 represent cDNAs corresponding to 28 human secreted
 CC protein genes, and AAE27097-AAE27137 represent the proteins they encode.
 CC AAE27138-AAE27164 represent human secreted protein fragments. The genes
 CC and their corresponding secreted proteins are useful for preventing,
 CC treating or ameliorating medical conditions, e.g., by protein or gene
 CC therapy. Secreted protein sequences of the invention are useful for the
 CC diagnosis or treatment of disorders such as autoimmune diseases (e.g.
 CC rheumatoid arthritis), hyperproliferative disorders (e.g. neoplasms of
 CC the breast or liver), cerebrovascular disorders (e.g. cerebral ischaemia,
 CC anglogenesis), cardiovascular disorders (e.g. cardiac arrest), nervous
 CC system disorders (e.g. Alzheimer's disease), infections caused by fungi,
 CC bacteria and viruses and ocular disorders (e.g. corneal infection). The
 CC polypeptides can also be used to aid wound healing and epithelial cell
 CC proliferation, to prevent skin aging due to sunburn, to maintain organs
 CC before transplantation, for supporting cell culture of primary tissues,
 CC to regenerate tissues and in chemotaxis. They can also be used as food
 CC additives or preservative to increase or decrease storage capabilities,
 CC fat content, lipid, protein, carbohydrate, vitamins, minerals, cofactors
 CC and other nutritional components. The present sequence represents a human
 CC secreted protein fragment referred to in the disclosure of the invention

XX Sequence 102 AA;

Query Match 64.0%; Score 400; DB 5; Length 102;
 Best Local Similarity 66.7%; Pred. No. 2.9e-27;
 Matches 64; Conservative 11; Mismatches 21; Indels 0; Gaps 0;

QY 8 CPKIKVECEVEIDQCTKPRDCPENMKCCPFCGKKCLDFRKIDICSMPOEAGPCLASIPH 67
 DB 2 CPKIRECECFQERDVCTKDRQCDNKKCCVFCGKKCLDLKQDVCMPKETGPCLAYFLH 61
 QY 68 WYNNKTKICSEFIYGGCGNNNNFQTEAICLVTK 103
 DB 62 WYDKDNTCSMFYGGCGNNNNFQSKANCLNTCK 97

RESULT 13

ABU65039

ID ABU65039 standard; peptide; 102 AA.

XX AC ABU65039;

XX 15-MAY-2003 (first entry)

XX Human secreted protein gene 24, protein #3.

XX Secreted protein; immunodeficiency; multiple sclerosis;

XX severe combined immunodeficiency; autoimmune disorder; cancer;

XX rheumatoid arthritis; diabetes mellitus; haematopoietic disorder;

XX inflammatory condition; septic shock; inflammatory bowel disease;

30-MAY-1997; 97US-0048189P.
30-MAY-1997; 97US-0048357P.
30-MAY-1997; 97US-0050934P.
06-JUN-1997; 97US-0048970P.
05-SEP-1997; 97US-0057765P.
19-DEC-1997; 97US-0068368P.
12-MAR-1998; 98WO-US004858.
11-SEP-1998; 98US-00152060.
02-FEB-2001; 2001US-0265583P.
11-MAY-2001; 2001US-00852659.
11-MAY-2001; 2001US-00852797.
11-MAY-2001; 2001US-00853161.
(ROSE/) ROSEN C A.
(RUBE/) RUBEN S M.
(LIYV/) LI Y.
(ZENG/) ZENG Z.
(KYAW/) KYAW H.
(FISC/) FISCHER C L.
(LIHH/) LI H.
(SOPP/) SOPPET D R.
(GENT/) GENTZ R L.
(WEIY/) WEI Y.
(MOOR/) MOORE P A.
(YOUN/) YOUNG P E.
(GREE/) GREENE J M.
(FERR/) FERRIE A M.
(HAST/) HASTINGS G A.
XX
Rosen CA, Ruben SM, Li Y, Zeng Z, Kyaw H, Fischer CL, Li H;
PI Soppet DR, Gentz RL, Wei Y, Moore PA, Young PE, Greene JM;
PI Ferrie AM, Hastings GA;
XX WPI; 2004-042167/04.
XX
New polypeptides and nucleic acid molecules for diagnosing, preventing or
PT treating diseases associated with aberrant expression or activity of the
PT polypeptide, e.g. cancer, asthma, AIDS, Parkinson's disease or diabetes.
XX
Disclosure; SEQ ID NO 121; 320pp; English.
XX
The invention relates to an isolated nucleic acid molecule encoding a
CC secreted protein that is at least 95% identical to a polynucleotide
CC fragment of any of the nucleotide sequences listed in table 1A of the
CC specification, which is hybridisable to the nucleotide sequences, a
CC polynucleotide encoding a polypeptide (or a polypeptide fragment, domain
CC or epitope of any of the amino acid sequences) listed in table 1A of the
CC specification, a polynucleotide which is an (allelic) variant of the
CC nucleotide sequences listed in the specification, a polynucleotide which
CC encodes a species homologue of the above amino acid sequences, a
CC polynucleotide capable of hybridising under stringent conditions to any
CC of the above polynucleotides, where the polynucleotide does not hybridise
CC under stringent conditions to a nucleic acid molecule having a nucleotide
CC sequence of only A or T residues. Also included are a recombinant vector
CC comprising the above nucleic acid molecule, making a recombinant host
CC cell comprising the above nucleic acid molecule, an isolated polypeptide
CC comprising a sequence that is at least 95% identical to the polypeptide
CC (or its fragment, domain, epitope, secreted form, (allelic) variant or
CC homologue) encoded by the above nucleic acid molecule, an isolated
CC antibody that binds specifically to the above polypeptide, a recombinant
CC host cell produced by the above method and that expresses the above
CC polypeptide, making an isolated polypeptide, preventing, treating or
CC ameliorating a medical condition, diagnosing a pathological condition or
CC a susceptibility to a pathological condition in a subject, identifying a
CC binding partner to the above polypeptide, the gene corresponding to the
CC cDNA sequence given in the specification, and identifying an activity in
CC a biological assay. The nucleic acid molecule and polypeptide are useful
CC in diagnosing, preventing, prognosing or treating diseases or disorders
CC associated with aberrant expression and/or activity of the above
CC polypeptide, such as neural disorders, immune system disorders, muscular
CC disorders, reproductive disorders, gastrointestinal disorders, pulmonary
CC disorders, cardiovascular disorders, renal disorders, proliferative
CC disorders and/or cancers. In particular, these diseases are systemic

CC lupus erythematosus, rheumatoid arthritis, multiple sclerosis,
CC thyroiditis, anaemia, Grave's disease, diabetes, hepatitis, asthma,
CC allergies, nephritis, Parkinson's disease, Alzheimer's disease,
CC atherosclerosis, myocardial infarction, AIDS and infections. The methods
CC may be used for identifying agonists and antagonists of the
CC polynucleotide and polypeptide. The present sequence is a protein from
CC one of the 28 disclosed secreted protein genes, it is not clear whether
CC this is an alternative expressed protein or a fragment of one of the
CC claimed proteins.
XX
SQ Sequence 102 AA;
Query Match 64.0%; Score 400; DB 8; Length 102;
Best Local Similarity 66.7%; Pred. No. 2.9e-27;
Matches 64; Conservative 11; Mismatches 21; Indels 0; Gaps 0;
QY 8 CPKIKVECEVEEIDQCTKPRDCPENMKCCPSCGKKCLDFRDKICSMQPQAGPCLASIPH 67
DB 2 CPKIRECEFPQERDVCTKDRQCQDNKKCCVSCGKKCLDLKQDVCEMPKETGCLAYFLH 61
QY 68 WYNNKTKICSEFYGGCGGNNNNFQTEAICLVTK 103
DB 62 WYDKDKONTCSMFYVGGCGGNNNNFQSKANCLNTCK 97
RESULT 15
AAW75219
ID AAW75219 standard; protein; 133 AA.
XX
AC AAW75219;
XX
DT 29-JAN-1999 (first entry)
DE Human secreted protein encoded by gene 24 clone HTEBY11.
XX
KW Human; secreted protein; fusion protein; gene therapy; protein therapy;
KW diagnosis; tissue; cancer; tumour; neurodegenerative disorder; leukaemia;
KW developmental abnormality; foetal deficiency; blood; allergy; renal;
KW immune system; asthma; lymphocytic disease; brain; hepatitis; AIDS;
KW inflammation; ischaemic shock; Alzheimer's disease; restenosis; thymus;
KW cognitive disorder; schizophrenia; prostate; obesity; osteoclast; thymus;
KW osteoporosis; arthritis; testis; lung; thyroiditis; thyroid; digestion;
KW endocrine; metabolism; regulation; malabsorption; gastritis; neoplasm.
OS Homo sapiens.
XX
PN WO9840483-A2.
PD 17-SEP-1998.
XX
PF 12-MAR-1998; 98WO-US004858.
XX
PR 14-MAR-1997; 97US-0040710P.
PR 14-MAR-1997; 97US-0040762P.
PR 30-MAY-1997; 97US-0048100P.
PR 30-MAY-1997; 97US-0048189P.
PR 30-MAY-1997; 97US-0048357P.
PR 30-MAY-1997; 97US-0050934P.
PR 06-JUN-1997; 97US-0048970P.
PR 05-SEP-1997; 97US-0057765P.
PR 19-DEC-1997; 97US-0068368P.
XX
(HUMA-) HUMAN GENOME SCI INC.
XX
XX Ruben SM, Rosen CA, Li Y, Zeng Z, Kyaw H, Fischer CL, Li H;
PI Soppet DR, Gentz RL, Wei YF, Moore PA, Young PE, Greene JM;
PI Ferrie AM;
XX
XX WPI; 1998-520811/44.
DR N-PSDB; AAV34309.
XX
XX Isolated human polynucleotide(s) encoding secretory peptide(s) - used to
PT develop products for the diagnosis and treatment of e.g. inflammation,

CC be used in preserving platelet function, organ preservation or in wound
 CC healing. The polynucleotide sequence encoding DJ11 may be used as
 CC hybridisation probes, in chromosome and gene mapping, in the generation
 CC of antisense RNA and DNA, and as targets for pharmaceutical intervention.
 CC The present sequence represents a human EPPIN protein given in comparison
 CC with DJ11 proteins in the exemplification of the present invention.
 XX
 SQ Sequence 133 AA;

Query Match 64.0%; Score 400; DB 7; Length 133;
 Best Local Similarity 66.7%; Pred. No. 3.7e-27;
 Matches 64; Conservative 11; Mismatches 21; Indels 0; Gaps 0;
 QY 8 CPKIVEVEVEIDQCTPRDCPENMKCCPFSCGKKCLDFRDKICSMFQEAQPCIASIPH 67
 DB 33 CPKIRECEFEQERDVCTKDRQCQDNKCCVFCGKKCLDLKQDVCMPKGTGCLAYFLH 92
 QY 68 WMYNKKTKICSEFIYGGCGGNNNFQTEAICLVTK 103
 DB 93 WMYDKDNTCSMFVYGGCGGNNNFQSKANCLNTCK 128

RESULT 20
 ID ADG89802
 AC ADG89802 standard; protein; 133 AA.
 AC ADG89802;
 XX 11-MAR-2004 (first entry)
 XX Human protein from secreted protein gene 24 #1.
 XX
 KW Secreted protein; gene therapy; neural disorder; immune system disorders;
 KW muscular disorder; reproductive disorder; gastrointestinal disorder;
 KW pulmonary disorder; cardiovascular disorder; renal disorder;
 KW proliferative disorder; cancer; systemic lupus erythematosus;
 KW rheumatoid arthritis; multiple sclerosis; thyroiditis; anaemia;
 KW Grave's disease; diabetes; hepatitis; asthma; allergy; nephritis;
 KW Parkinson's disease; Alzheimer's disease; atherosclerosis;
 KW myocardial infarction; AIDS; infection; human.
 XX
 OS Homo sapiens.
 XX
 XX US2003225009-A1.
 XX 04-DEC-2003.
 XX
 XX 30-JAN-2002; 2002US-00058993.
 XX
 PR 14-MAR-1997; 97US-0040710P.
 PR 14-MAR-1997; 97US-0040762P.
 PR 30-MAY-1997; 97US-0048100P.
 PR 30-MAY-1997; 97US-0048189P.
 PR 30-MAY-1997; 97US-0048357P.
 PR 30-MAY-1997; 97US-0050934P.
 PR 06-JUN-1997; 97US-0048970P.
 PR 05-SEP-1997; 97US-0057765P.
 PR 19-DEC-1997; 97US-0068368P.
 PR 12-MAR-1998; 98WO-US004858.
 PR 11-SEP-1998; 98US-00152060.
 PR 02-FEB-2001; 2001US-0265583P.
 PR 11-MAY-2001; 2001US-00852659.
 PR 11-MAY-2001; 2001US-00852797.
 PR 11-MAY-2001; 2001US-00853161.
 XX
 XX (ROSE/) ROSEN C A.
 XX (RUBE/) RUBEN S M.
 XX (LIYV/) LI Y.
 XX (ZENG/) ZENG Z.
 XX (KIYAW/) KYAW H.
 XX (FISC/) FISCHER C L.
 XX (LIHH/) LI H.
 XX (SOPP/) SOPPET D R.

PA (GENTZ/) GENTZ R L.
 PA (WEIY/) WEI Y.
 PA (MOOR/) MOORE P A.
 PA (YOUN/) YOUNG P E.
 PA (GREE/) GREENE J M.
 PA (FERR/) FERRIE A M.
 PA (HAST/) HASTINGS G A.
 XX
 PI Rosen CA, Ruben SM, Li Y, Zeng Z, Kyaw H, Fischer CL, Li H;
 PI Soppet DR, Gentz RL, Wei Y, Moore PA, Young PE, Greene JM;
 PI Ferrie AM, Hastings GA;
 XX
 XX WPI; 2004-042167/04.
 DR N-PSDB; ADG89761.
 XX
 PT New polypeptides and nucleic acid molecules for diagnosing, preventing or
 PT treating diseases associated with aberrant expression or activity of the
 PT polypeptide, e.g. cancer, asthma, AIDS, Parkinson's disease or diabetes.
 XX
 PS Claim 11; SEQ ID NO 75; 320pp; English.
 XX
 CC The invention relates to an isolated nucleic acid molecule encoding a
 CC secreted protein that is at least 95% identical to a polynucleotide
 CC fragment of any of the nucleotide sequences listed in table 1A of the
 CC specification, which is hybridisable to the nucleotide sequences, a
 CC polynucleotide encoding a polypeptide (or a polypeptide fragment, domain
 CC or epitope of any of the amino acid sequences) listed in table 1A of the
 CC specification, a polynucleotide which is an (allelic) variant of the
 CC nucleotide sequences listed in the specification, a polynucleotide which
 CC encodes a species homologue of the above amino acid sequences, a
 CC polynucleotide capable of hybridising under stringent conditions to any
 CC of the above polynucleotides, where the polynucleotide does not hybridise
 CC under stringent conditions to a nucleic acid molecule having a nucleotide
 CC sequence of only A or T residues. Also included are a recombinant vector
 CC comprising the above nucleic acid molecule, making a recombinant host
 CC cell comprising the above nucleic acid molecule, an isolated polypeptide
 CC comprising a sequence that is at least 95% identical to the polypeptide
 CC (or its fragment, domain, epitope, secreted form, (allelic) variant or
 CC homologue) encoded by the above nucleic acid molecule, an isolated
 CC antibody that binds specifically to the above polypeptide, a recombinant
 CC host cell produced by the above method and that expresses the above
 CC polypeptide, making an isolated polypeptide, preventing, treating or
 CC ameliorating a medical condition, diagnosing a pathological condition or
 CC a susceptibility to a pathological condition in a subject, identifying a
 CC binding partner to the above polypeptide, the gene corresponding to the
 CC cDNA sequence given in the specification, and identifying an activity in
 CC a biological assay. The nucleic acid molecule and polypeptide are useful
 CC in diagnosing, preventing, prognosis or treating diseases or disorders
 CC associated with aberrant expression and/or activity of the above
 CC polypeptide, such as neural disorders, immune system disorders, muscular
 CC disorders, reproductive disorders, gastrointestinal disorders, pulmonary
 CC disorders, cardiovascular disorders, renal disorders, proliferative
 CC disorders and/or cancers. In particular, these diseases are systemic
 CC lupus erythematosus, rheumatoid arthritis, multiple sclerosis, asthma,
 CC thyroiditis, anaemia, Grave's disease, diabetes, hepatitis, asthma,
 CC allergies, nephritis, Parkinson's disease, Alzheimer's disease,
 CC atherosclerosis, myocardial infarction, AIDS and infections. The methods
 CC may be used for identifying agonists and antagonists of the
 CC polynucleotide and polypeptide. The present sequence is a protein from
 CC one of the 28 disclosed secreted protein genes.
 XX
 SQ Sequence 133 AA;
 Query Match 64.0%; Score 400; DB 8; Length 133;
 Best Local Similarity 66.7%; Pred. No. 3.7e-27;
 Matches 64; Conservative 11; Mismatches 21; Indels 0; Gaps 0;
 QY 8 CPKIVEVEVEIDQCTPRDCPENMKCCPFSCGKKCLDFRDKICSMFQEAQPCIASIPH 67
 DB 33 CPKIRECEFEQERDVCTKDRQCQDNKCCVFCGKKCLDLKQDVCMPKGTGCLAYFLH 92
 QY 68 WMYNKKTKICSEFIYGGCGGNNNFQTEAICLVTK 103

CC or Alzheimer's disease), autoimmune diseases (multiple sclerosis,
CC diabetes, lupus) genetic disorders, myeloid or lymphoid disorders,
CC platelet or coagulation disorders, wound, burns, incision, ulcers, liver
CC or lung fibrosis, infections (bacterial, viral, fungal, parasitic),
CC arthritis, etc. Note: The sequence data for this patent did not form part
CC of the printed specification, but was obtained in electronic format
CC directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 86 AA;

Query Match 44.2%; Score 276; DB 5; Length 86;
Best Local Similarity 98.0%; Pred. No. 1.4e-16;
Matches 48; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 EGILGKCPKIKVEVEEIDQCTKPRDCPENMKCCPFSGKCKCLDFRK 49

Db 26 EGILGKCPKIKVEVEEIDQCTKPRDCPENMKCCPFSGKCKCLDFRK 74

RESULT 25

ABJ26667

ID ABJ26667 standard; protein; 86 AA.

XX AC ABJ26667;

XX DT 01-MAY-2003 (first entry)

XX DE Human protein modification + maintenance molecule protein SEQ ID No 21.

XX KW Cytostatic; antiarteriosclerotic; anti-HIV; antiallergic; anticonvulsant;
KW cerebroprotective; antiparkinsonian; nootropic; antiinflammatory;
KW antiulcer; hepatotropic; gynaecological; antibacterial; virucide;
KW protozoacide; antiparasitic; cell proliferative disease; PMOD;
KW protein modification and maintenance molecule; immunogenic fragment;
KW cancer; autoimmune; inflammatory disease; neurological disorder;
KW gastrointestinal; developmental; vesicle trafficking disorder; infection;
KW protein-protein interaction; drug-target interaction;
KW gene expression profile; human.

XX OS Homo sapiens.

XX FN WO200300844-A2.

XX PD 03-JAN-2003.

XX PF 18-JUN-2002; 2002WO-US019360.

XX PR 22-JUN-2001; 2001US-0300508P.

PR 06-JUL-2001; 2001US-0303445P.

PR 13-JUL-2001; 2001US-0305405P.

PR 09-AUG-2001; 2001US-0311442P.

PR 24-AUG-2001; 2001US-0314821P.

PR 29-AUG-2001; 2001US-0315992P.

PR 03-MAY-2002; 2002US-0378205P.

XX (INCY-) INCYTE GENOMICS INC.

XX PI Gandhi AR, Kable AE, Swarnakar A, Hafalia AJA, Tran B, Duggan BM,
PI Warren BA, Ison CH, Honchell CD, Nguyen DB, Lu DAM, Lee EA, Yue H;
PI Forsythe IJ, Barroso I, Ramkumar J, Griffin JA, Li JX, Yang J;
PI Thangavelu K, Gietzen KJ, Ding L, Baughn MR, Borowsky ML, Yao MG;
PI Walia NK, Mason PM, Gururajan R, Lee S, Becha SD, Lee SY, Tran UK;
PI Elliott VS, Luo W, Sprague WW, Tang YT, Lu Y, Zebarradian Y;
XX WPI; 2003-184039/18.

DR N-PSDB; APT23220.

XX PT New isolated human PMOD polypeptide and polynucleotide, useful for
PT diagnosing, treating and preventing diseases or conditions associated
PT with the aberrant PMOD expression, e.g. cancer, AIDS, atherosclerosis and
PT infections.

XX PS Claim 76; Page 196; 225pp; English.

XX The invention relates to an isolated polypeptide comprising: any of 28
CC sequences of 48-1256 amino acids; a natural amino acid sequence at least
CC 90% identical to the 28 amino acid sequences, 94% identical to a sequence
CC of 703 or 277 amino acids, 96% identical to a sequence of 414 amino
CC acids, or 97% identical to a sequence of 242 amino acids, all given in
CC the specification; or a biologically active or immunogenic fragment of
CC the isolated polypeptide. The polypeptides and polynucleotides are useful
CC in diagnosing, treating and preventing diseases or conditions associated
CC with the decreased expression of protein modification and maintenance
CC molecules (PMOD), such as cell proliferative diseases (e.g. cancer,
CC atherosclerosis), autoimmune/inflammatory diseases (e.g. AIDS,
CC allergies), neurological disorders (e.g. stroke, Parkinson's disease,
CC epilepsy), gastrointestinal (e.g. ulcer, cirrhosis), reproductive (e.g.
CC endometriosis), developmental, vesicle trafficking disorders, and
CC infections (e.g. bacterial, viral, parasitic, protozoal). These are also
CC useful in assessing the effects of exogenous compounds on the expression
CC of nucleic acid and amino acid sequences of PMOD. The PMOD or its
CC fragments are useful in screening compounds for effectiveness as agonist
CC or antagonist of the polypeptides, or in altering the expression of the
CC target polynucleotide and compounds that specifically bind to or modulate
CC the activity of the polypeptide. The microarray is useful in monitoring
CC or measuring protein-protein interactions, drug-target interactions, and
CC gene expression profiles. This sequence represents a human PMOD protein
CC of the invention
XX
SQ Sequence 86 AA;

Query Match 44.2%; Score 276; DB 6; Length 86;

Best Local Similarity 98.0%; Pred. No. 1.4e-16;

Matches 48; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 EGILGKCPKIKVEVEEIDQCTKPRDCPENMKCCPFSGKCKCLDFRK 49

Db 26 EGILGKCPKIKVEVEEIDQCTKPRDCPENMKCCPFSGKCKCLDFRK 74

RESULT 26

ABJ12236

ID ABB12236 standard; peptide; 101 AA.

XX AC ABB12236;

XX DT 11-JAN-2002 (first entry)

XX DE Human eppin-1 homologue, SEQ ID NO:2606.

XX KW Human; cytokine; cell proliferation; cell differentiation; growth factor;
KW haematopoiesis regulation; tissue growth; immunomodulator; activin;
KW inhibin; chemotaxis; chemokines; thrombolysis; oncogenesis;
KW proliferation; metastasis; cancer; tumour; haematopoietic disorder;
KW myeloid cell disorder; lymphoid cell disorder; asthma; arthritis;
KW chronic inflammatory condition; proliferative retinopathy;
KW atherosclerosis; coronary heart disease; arterial ischaemia;
KW bone disorder; osteoporosis; vascular growth disorder;
KW tissue regeneration; wound healing; infection; immune disorder;
KW cell culture; drug screening; gene therapy; antiinflammatory;
KW antiasthmatic; antiarthritic; haemostatic; antiarteriosclerotic;
KW cytosstatic; osteopathic; vasotropic; cardiant; virucide; antibacterial;
KW antifungal; vulnery; antiulcer.

XX OS Homo sapiens.

XX FN WO200157188-A2.

XX PD 09-AUG-2001.

XX PF 05-FEB-2001; 2001WO-US003800.

XX PR 03-FEB-2000; 2000US-00496914.

XX PR 27-APR-2000; 2000US-00560875.

XX (HYSE-) HYSEQ INC.


```
DT 28-JAN-2002 (first entry)
DE Human serine proteinase inhibitor BTL.009 C-terminal peptide.
XX
KW Human; BTL.009 protein; serine proteinase inhibitor; cytostatic;
KW nephrotropic; idiopathic pulmonary fibrosis; cystic fibrosis; emphysema;
KW rheumatoid arthritis; adult respiratory distress syndrome; angiotensin;
KW blood coagulation; glomerulonephritis; prophylactic; platelet activation;
KW neutrophil; monocyte; granulocyte; organ failure; inflammatory disease;
KW elastase inhibitor; chymotrypsin inhibitor; lung injury; vascular injury;
KW therapeutic.
XX
OS Homo sapiens.
XX
PN US6294648-B1.
XX
PD 25-SEP-2001.
XX
PF 20-JUL-1999; 99US-00358569.
XX
PR 20-JUL-1999; 99US-00358569.
XX
PR (FARB ) BAYER CORP.
XX
PA Delaria K, Rocznia K, Davies C;
XX
PI WPI; 2001-662224/76.
XX
DR
XX
PT New isolated protein for inhibiting human serine proteinase activity in the
PT treatment of e.g. emphysema and adult respiratory distress syndrome.
XX
PS Disclosure; Col 6; 16pp; English.
XX
CC The invention relates to human BTL.009 protein, a serine proteinase
CC inhibitor of the Kunitz family that exhibits greater potency towards
CC neutral serine proteinases. BTL.009 protein is found to inhibit leukocyte
CC elastase, chymotrypsin-like protease and trypsin-like protease. BTL.009
CC protein is useful for treating emphysema, idiopathic pulmonary fibrosis,
CC adult respiratory distress syndrome, cystic fibrosis, rheumatoid
CC arthritis, organ failure, glomerulonephritis, other inflammatory diseases
CC and diseases involving lung and vascular injury. BTL.009 is also useful
CC for preventing neutrophil and monocyte activation and formation of active
CC oxygen species during the oxidative burst of stimulated granulocytes.
CC BTL.009 is useful for reducing platelet activation and blood coagulation
CC and for the prophylactic or therapeutic treatment of patients undergoing
CC angioplasty. The present sequence is human serine proteinase inhibitor
CC BTL.009 peptide corresponding to Kunitz domain used in the
CC exemplification of the invention. Note: The present sequence shown in
CC column 14 and sequence listing of the specification lacks 3 amino acid
CC residues at the C-terminal end
XX
SQ Sequence 64 AA;
Query Match 38.7%; Score 242; DB 4; Length 64;
Best Local Similarity 65.5%; Pred. No. 9.9e-14;
Matches 38; Conservative 8; Mismatches 12; Indels 0; Gaps 0;
QY 46 DFRKDCSMPQAGPCLASIPHWYNNKTKICSEFYGGCGGNNNNFQTEAICLVTK 103
Db 1 DLKQDVCEMPKETGTCPLAYFLHWYDKDNTCSMFVYGGCGGNNNNFQSKANCLNTCK 58
RESULT 29
AAE13084
ID AAE13084 standard; peptide; 58 AA.
XX
AC AAE13084;
XX
XX 28-JAN-2002 (first entry)
XX Human serine proteinase inhibitor BTL.009 peptide.
XX
KW Human; BTL.009 protein; serine proteinase inhibitor; cytostatic;
KW nephrotropic; idiopathic pulmonary fibrosis; cystic fibrosis; emphysema;
KW rheumatoid arthritis; adult respiratory distress syndrome; angiotensin;
KW blood coagulation; glomerulonephritis; prophylactic; platelet activation;
KW neutrophil; monocyte; granulocyte; organ failure; inflammatory disease;
KW elastase inhibitor; chymotrypsin inhibitor; lung injury; vascular injury;
KW therapeutic.
XX
OS Homo sapiens.
XX
PN US6294648-B1.
XX
PD 25-SEP-2001.
XX
PF 20-JUL-1999; 99US-00358569.
XX
PR 20-JUL-1999; 99US-00358569.
XX
PR (FARB ) BAYER CORP.
XX
PA Delaria K, Rocznia K, Davies C;
XX
PI WPI; 2001-662224/76.
XX
DR
XX
PT New isolated protein for inhibiting human serine proteinase activity in the
PT treatment of e.g. emphysema and adult respiratory distress syndrome.
XX
PS Disclosure; Col 6; 16pp; English.
XX
CC The invention relates to human BTL.009 protein, a serine proteinase
CC inhibitor of the Kunitz family that exhibits greater potency towards
CC neutral serine proteinases. BTL.009 protein is found to inhibit leukocyte
CC elastase, chymotrypsin-like protease and trypsin-like protease. BTL.009
CC protein is useful for treating emphysema, idiopathic pulmonary fibrosis,
CC adult respiratory distress syndrome, cystic fibrosis, rheumatoid
CC arthritis, organ failure, glomerulonephritis, other inflammatory diseases
CC and diseases involving lung and vascular injury. BTL.009 is also useful
CC for preventing neutrophil and monocyte activation and formation of active
CC oxygen species during the oxidative burst of stimulated granulocytes.
CC BTL.009 is useful for reducing platelet activation and blood coagulation
CC and for the prophylactic or therapeutic treatment of patients undergoing
CC angioplasty. The present sequence is human serine proteinase inhibitor
CC BTL.009 C-terminal peptide containing Kunitz domain which is used in the
CC exemplification of the invention
XX
SQ Sequence 64 AA;
Query Match 38.7%; Score 242; DB 4; Length 64;
Best Local Similarity 65.5%; Pred. No. 9.9e-14;
Matches 38; Conservative 8; Mismatches 12; Indels 0; Gaps 0;
QY 46 DFRKDCSMPQAGPCLASIPHWYNNKTKICSEFYGGCGGNNNNFQTEAICLVTK 103
Db 1 DLKQDVCEMPKETGTCPLAYFLHWYDKDNTCSMFVYGGCGGNNNNFQSKANCLNTCK 58
RESULT 29
AAE13084
ID AAE13084 standard; peptide; 58 AA.
XX
AC AAE13084;
XX
XX 28-JAN-2002 (first entry)
XX Human serine proteinase inhibitor BTL.009 peptide.
XX
KW Human; BTL.009 protein; serine proteinase inhibitor; cytostatic;
KW nephrotropic; idiopathic pulmonary fibrosis; cystic fibrosis; emphysema;
KW rheumatoid arthritis; adult respiratory distress syndrome; angiotensin;
KW blood coagulation; glomerulonephritis; prophylactic; platelet activation;
KW neutrophil; monocyte; granulocyte; organ failure; inflammatory disease;
KW elastase inhibitor; chymotrypsin inhibitor; lung injury; vascular injury;
KW therapeutic.
XX
OS Homo sapiens.
XX
PN US6294648-B1.
XX
PD 25-SEP-2001.
XX
PF 20-JUL-1999; 99US-00358569.
XX
PR 20-JUL-1999; 99US-00358569.
XX
PR (FARB ) BAYER CORP.
XX
PA Delaria K, Rocznia K, Davies C;
XX
PI WPI; 2001-662224/76.
XX
DR
XX
PT New isolated protein for inhibiting human serine proteinase activity in the
PT treatment of e.g. emphysema and adult respiratory distress syndrome.
XX
PS Disclosure; Col 6; 16pp; English.
XX
CC The invention relates to human BTL.009 protein, a serine proteinase
CC inhibitor of the Kunitz family that exhibits greater potency towards
CC neutral serine proteinases. BTL.009 protein is found to inhibit leukocyte
CC elastase, chymotrypsin-like protease and trypsin-like protease. BTL.009
CC protein is useful for treating emphysema, idiopathic pulmonary fibrosis,
CC adult respiratory distress syndrome, cystic fibrosis, rheumatoid
CC arthritis, organ failure, glomerulonephritis, other inflammatory diseases
CC and diseases involving lung and vascular injury. BTL.009 is also useful
CC for preventing neutrophil and monocyte activation and formation of active
CC oxygen species during the oxidative burst of stimulated granulocytes.
CC BTL.009 is useful for reducing platelet activation and blood coagulation
CC and for the prophylactic or therapeutic treatment of patients undergoing
CC angioplasty. The present sequence is human serine proteinase inhibitor
CC BTL.009 peptide corresponding to Kunitz domain used in the
CC exemplification of the invention. Note: The present sequence shown in
CC column 14 and sequence listing of the specification lacks 3 amino acid
CC residues at the C-terminal end
XX
SQ Sequence 58 AA;
Query Match 37.8%; Score 236; DB 4; Length 58;
Best Local Similarity 66.1%; Pred. No. 3e-13;
Matches 37; Conservative 8; Mismatches 11; Indels 0; Gaps 0;
QY 48 RKDTCSPQAGPCLASIPHWYNNKTKICSEFYGGCGGNNNNFQTEAICLVTK 103
Db 1 KQDVCEMPKETGTCPLAYFLHWYDKDNTCSMFVYGGCGGNNNNFQSKANCLNTCK 56
RESULT 30
AAE60630
ID AAE60630 standard; protein; 58 AA.
XX
XX AAE60630;
XX
XX 27-APR-2001 (first entry)
XX Kunitz domain, SEQ ID NO:8, used to identify BTL.010 protein.
XX
KW Human BTL.010; neutral serine proteinase inhibitor; elastase inhibitor;
KW proteinase-3 inhibitor; Kunitz domain; emphysema;
KW idiopathic pulmonary fibrosis; adult respiratory distress syndrome;
KW cystic fibrosis; rheumatoid arthritis; organ failure; glomerulonephritis;
KW platelet activation; blood coagulation; neutrophil activation;
KW monocyte activation; angioplasty; inflammatory disease; lung injury;
KW vascular injury; nephrotropic; antirheumatic; antiarthritic.
XX
```



```
XX 05-AUG-1999; 99US-00369494.
XX (FARB ) BAYER PHARM CORP.
XX
XX Davies C, Chen D, Roczniak S;
XX WPI; 2004-141424/14.
XX
XX New isolated polynucleotide encoding BTL010 serine proteinase, useful
XX for treating e.g. emphysema, idiopathic pulmonary fibrosis, adult
XX respiratory distress syndrome, cystic fibrosis, rheumatoid arthritis or
XX glomerulonephritis.
XX
XX Disclosure; SEQ ID NO 8; 17pp; English.
XX
XX The invention relates to BTL010, a human serine proteinase inhibitor of
XX the Kunitz family and its corresponding nucleic acid sequence. The
XX sequences of the invention are useful for treating diseases, e.g.
XX emphysema, idiopathic pulmonary fibrosis, adult respiratory distress
XX syndrome, cystic fibrosis, rheumatoid arthritis, organ failure,
XX glomerulonephritis or inflammatory diseases. The BTL010 protein is also
XX useful for preventing neutrophil and monocyte activation and formation of
XX active oxygen species during the oxidative burst of stimulated
XX granulocytes. It is also useful for reducing platelet activation and
XX blood coagulation. BTL010 DNA is useful in gene therapy. The present
XX sequence is human Kunitz domain (KD) peptide.
XX
XX Sequence 58 AA;
SQ
Query Match 37.8%; Score 236; DB 8; Length 58;
Best Local Similarity 66.1%; Pred. No. 3e-13;
Matches 37; Conservative 8; Mismatches 11; Indels 0; Gaps 0;
Oy 48 RKDTCSPQEPAGPCLASIPHWYNNKTKICSEFIYGGCGQNNNFQTEAICLVTK 103
Db :|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||
1 KQDVCMPKETGPGCLAYFLHWYDKDNTCSMFYGGCGQNNNFQSKANCLNTCK 56
RESULT 33
ADR89980
ID ADR89980 standard; peptide; 58 AA.
XX
XX ADR89980;
XX
XX 18-NOV-2004 (first entry)
XX
XX Human CAB37 protein kunitz domain peptide.
XX
XX Kunitz domain peptide; cystic fibrosis; cystic fibrosis related disease;
XX hereditary angioedema; cancer; chronic obstructive pulmonary disease;
XX asthma; bronchitis; acute respiratory syndrome; pneumonia; bleeding;
XX cytosstatic; haemostatic; CAB37 protein; human.
XX
XX Homo sapiens.
XX
XX US2004171794-A1.
XX
XX 02-SEP-2004.
XX
XX 07-FEB-2003; 2003US-00361997.
XX
XX 07-FEB-2003; 2003US-00361997.
XX (LADN/) LADNER R C.
XX PA (LEVA/) LEV A C.
XX
XX Ladner RC, Ley AC;
XX
XX WPI; 2004-625120/60.
XX
XX New kunitz domain peptide useful as human neutrophil elastase inhibitor
XX for the treatment of e.g. cystic fibrosis and related disease.
XX
XX
XX Disclosure; SEQ ID NO 5; 123pp; English.
XX
XX The invention relates to proteins comprising kunitz domain peptide,
XX designated DPI-14 for inhibiting human neutrophil elastase, fused to
XX albumin. The invention is useful for treating cystic fibrosis and related
XX diseases, hereditary angioedema, cancer and related diseases including
XX chronic obstructive pulmonary disease, asthma, bronchitis, acute
XX respiratory syndrome, pneumonia and bleeding. The invention acts as a
XX cytosstatic and haemostatic agent. The present sequence is the human CAB37
XX protein (A4) kunitz domain peptide. This sequence is used in the
XX invention.
XX
XX Sequence 58 AA;
SQ
Query Match 37.8%; Score 236; DB 8; Length 58;
Best Local Similarity 66.1%; Pred. No. 3e-13;
Matches 37; Conservative 8; Mismatches 11; Indels 0; Gaps 0;
Oy 48 RKDTCSPQEPAGPCLASIPHWYNNKTKICSEFIYGGCGQNNNFQTEAICLVTK 103
Db :|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||
1 KQDVCMPKETGPGCLAYFLHWYDKDNTCSMFYGGCGQNNNFQSKANCLNTCK 56
RESULT 34
AAW75257
ID AAW75257 standard; protein; 51 AA.
XX
XX AAW75257;
XX
XX 29-JAN-1999 (first entry)
XX
XX Fragment of human secreted protein encoded by gene 24.
XX
XX Human; secreted protein; fusion protein; gene therapy; protein therapy;
XX diagnosis; tissue; cancer; tumour; neurodegenerative disorder; leukaemia;
XX developmental abnormality; foetal deficiency; blood; allergy; renal;
XX immune system; asthma; lymphocytic disease; brain; hepatic; lymphoma;
XX inflammation; ischaemic shock; Alzheimer's disease; restenosis; AIDS;
XX cognitive disorder; schizophrenia; prostate; obesity; osteoclast; thymus;
XX osteoporosis; arthritis; testis; lung; thyroiditis; thyroid; digestion;
XX endocrine; metabolism; regulation; malabsorption; gastritis; neoplasm.
XX
XX Homo sapiens.
XX
XX WO98040483-A2.
XX
XX 17-SEP-1998.
XX
XX 12-MAR-1998; 98WO-US004858.
XX
XX 14-MAR-1997; 97US-0040710P.
XX 14-MAR-1997; 97US-0040762P.
XX 30-MAY-1997; 97US-0048100P.
XX 30-MAY-1997; 97US-0048189P.
XX 30-MAY-1997; 97US-0048357P.
XX 30-MAY-1997; 97US-0050934P.
XX 06-JUN-1997; 97US-0048970P.
XX 05-SEP-1997; 97US-0057765P.
XX 19-DEC-1997; 97US-0068368P.
XX
XX (HUMA-) HUMAN GENOME SCI INC.
XX
XX Ruben SM, Rosen CA, Li Y, Zeng Z, Kyaw H, Fischer CL, Li H;
XX Soppet DR, Gentz RL, Wei YF, Moore PA, Young PE, Greene JW;
XX Ferrie AM;
XX
XX WPI; 1998-520811/44.
XX N-PSDB; AAV34309.
XX
XX Isolated human polynucleotide(s) encoding secretory peptide(s) - used to
XX develop products for the diagnosis and treatment of e.g. inflammation,
XX cancers, CNS disorders or immune system disorders.
XX
```

XX PS Disclosure; Page 24; 201pp; English.

XX CC This sequence represents a fragment of a secreted human protein encoded

XX CC by the nucleic acid molecule designated Gene 24 (AAV34309). The gene can

XX CC be used to generate fusion proteins by linking to the gene to a human

XX CC immunoglobulin Fc portion (e.g. AAV34277) for increasing the stability of

XX CC the fused protein as compared to the human protein only. The invention

XX CC relates to 28 novel genes and their fragments (nucleic acid sequences:

XX CC AAV34286-V34325; amino acid sequences AAV75196-W75235) which are useful

XX CC for preventing, treating or ameliorating medical conditions e.g. by

XX CC protein or gene therapy. Also, pathological conditions can be diagnosed

XX CC by determining the amount of the new polypeptides in a sample or by

XX CC determining the presence of mutations in the 28 polynucleotides.

XX CC Specific uses are described for each of the 28 polynucleotides, based on

XX CC which tissues they are most highly expressed in (see AAV34286 for

XX CC described uses)

XX SQ Sequence 51 AA;

Query Match 35.0%; Score 219; DB 2; Length 51;

Best Local Similarity 68.6%; Pred. No. 7,9e-12;

Matches 35; Conservative 5; Mismatches 11; Indels 0; Gaps 0;

QY 52 CSMQOAGFCLASIPHWYNNKTKICSEPIYGGCGNNNNFOTEAICLVTC 102

DB 1 CEMPKEGTCLAYFLHWYDKDNTCSMFVYGGCGNNNNFQSKANCLNTC 51

RESULT 35

AAE27025

ID AAE27025 standard; protein; 51 AA.

AC AAE27025;

XX 13-DEC-2002 (first entry)

XX Human gene 24 encoded secreted protein variant, SEQ ID NO:118.

XX Human; immunodeficiency; X-linked agammaglobulinaemia; septic shock;

KW autoimmune disorder; rheumatoid arthritis; multiple sclerosis; cancer;

KW Grave's disease; diabetes mellitus; haematopoietic disorder; stroke;

KW respiratory disorder; asthma; allergy; gastrointestinal disorder;

KW inflammatory bowel disease; neurodegenerative disorder; hepatitis;

KW Parkinson's disease; Alzheimer's disease; cardiovascular disorder;

KW atherosclerosis; myocarditis; renal disorder; fungicide; virucide;

KW hyperproliferative disorder; acute glomerulonephritis; tonsillitis;

KW respiratory disorder; rhinitis; sinusitis; neurological disease;

KW endocrine disorder; Addison's disease; reproductive system disorder;

KW endometriosis; vasotropic; vulnery; cytotatic; nootropic; cardiant;

KW anti-HIV; tranquilliser; gout; antiparasitic.

XX Homo sapiens.

XX US2002077287-A1.

XX 20-JUN-2002.

XX 11-MAY-2001; 2001US-00852659.

XX 11-SEP-1998; 98US-00152060.

XX (RUBE/) RUBEN S M.

PA (ROSE/) ROSEN C A.

PA (LIY/) LI Y.

PA (ZENG/) ZENG Z.

PA (KYAW/) KYAW H.

PA (FISC/) FISCHER C L.

PA (LIH/) LI H.

PA (SOPP/) SOPPET D R.

PA (GENT/) GENTZ R L.

PA (WEI/) WEI Y.

PA (MOOR/) MOORE P A.

PA (YOUNG/) YOUNG P E.

PA (GREEN/) GREENE J M.

PA (FERR/) FERRIE A M.

XX Ruben SM, Rosen CA, Li Y, Zeng Z, Kyaw H, Fischer CL, Li H;

PI Soppet DR, Gentz RL, Wei Y, Moore PA, Young PE, Greene JM;

XX Ferrie AM;

XX WPI; 2002-598780/64.

XX Novel human secreted polypeptides and polynucleotides for diagnosing,

PT preventing, treating immune, hyperproliferative, cardiovascular,

PT neurological, reproductive disorders and identifying modulators of

PT therapeutic use.

XX Disclosure; Page 16; 209pp; English.

XX AAD44636-AAD44676 represent cDNAs corresponding to 28 human secreted

CC protein genes, and AAE26959-AAE26999 represent the proteins they encode.

CC AAE27000-AAE27025 represent human secreted protein fragments or their

CC variants. The secreted proteins and genes are useful for preventing,

CC treating or ameliorating medical conditions, e.g., by protein or gene

CC therapy. Specific uses are described for each of the 28 genes, based on

CC the tissues in which they are most highly expressed and include

CC developing products for the diagnosis or treatment of immunodeficiencies,

CC e.g., X-linked agammaglobulinaemia, B cell immunodeficiencies, severe

CC combined immunodeficiencies, autoimmune disorders e.g., systemic lupus

CC erythematosus, rheumatoid arthritis, multiple sclerosis, autoimmune

CC thyroiditis, autoimmune haemolytic anaemia, Goodpasture's syndrome,

CC Grave's disease, diabetes mellitus, dermatitis, inflammatory conditions

CC including septic shock, sepsis, reperfusion injury, inflammatory bowel

CC disease, Crohn's disease, haematopoietic disorders, respiratory disorders

CC e.g., asthma and allergy, gastrointestinal disorders e.g., inflammatory

CC bowel disease), cancers e.g., gastric, ovarian, lung, liver, bladder and

CC breast), central nervous system (CNS) disorders e.g., ischaemic brain

CC injury and/or stroke, neurodegenerative disorders e.g., Parkinson's

CC disease and Alzheimer's disease, AIDS-related dementia and prion disease,

CC cardiovascular disorders e.g., myocarditis, arrhythmias, atherosclerosis,

CC inflammatory disorders e.g., hepatitis, gout, trauma, pancreatitis,

CC sarcoidosis and allogenic transplant rejection, blood-related disorder

CC (thrombosis, arterial thrombosis, atherosclerosis), hyperproliferative

CC disorders, respiratory disorders e.g. rhinitis, sinusitis, tonsillitis,

CC lung cancer, allergic disorders, pneumonitis, renal disorders, endocrine

CC glomerulonephritis, neurological diseases, liver disorders, endocrine

CC disorders e.g., hyperthyroidism, Addison's disease, hyperpituitarism,

CC infectious diseases and reproductive system disorders e.g. endometriosis.

CC The present sequence represents a human secreted protein variant of the

CC invention

XX SQ Sequence 51 AA;

Query Match 35.0%; Score 219; DB 5; Length 51;

Best Local Similarity 68.6%; Pred. No. 7,9e-12;

Matches 35; Conservative 5; Mismatches 11; Indels 0; Gaps 0;

QY 52 CSMQOAGFCLASIPHWYNNKTKICSEPIYGGCGNNNNFOTEAICLVTC 102

DB 1 CEMPKEGTCLAYFLHWYDKDNTCSMFVYGGCGNNNNFQSKANCLNTC 51

RESULT 36

AAE27163

ID AAE27163 standard; protein; 51 AA.

XX AAE27163;

XX 13-DEC-2002 (first entry)

XX Human gene 24 encoded secreted protein fragment kunitz-type domain.

XX Human; secreted protein; autoimmune disease; hyperproliferative disorder;

KW rheumatoid arthritis; neoplasm; cerebrovascular disorder; angiogenesis;

KW cerebral ischaemia; cardiovascular disorder; nervous system disorder;

KW cardiac arrest; Alzheimer's disease; ocular disorder; wound healing;
KW infection; corneal infection; skin aging; food additive; preservative;
KW tissue regeneration; immunosuppressive; antiproliferative; cytostatic;
KW cardiant; vasotropic; cerebroprotective; nootropic; neuroprotective;
KW antibacterial; virucide; fungicide; ophthalmological; gene therapy;
KW vulneryary.
XX
XX Homo sapiens.
XX US2002076756-A1.
XX
XX 20-JUN-2002.
XX
XX 11-MAY-2001; 2001US-00853161.
XX
XX 02-FEB-2001; 2001US-0265583P.
XX
XX (RUBE/) RUBEN S M.
XX (ROSE/) ROSEN C A.
XX (LIYU/) LI Y.
XX (ZENG/) ZENG Z.
XX (KYAW/) KYAW H.
XX (FISC/) FISCHER C L.
XX (LIHH/) LI H.
XX (SOPP/) SOPPET D R.
XX (GENT/) GENTZ R L.
XX (WEIY/) WEI Y.
XX (MOOR/) MOORE P A.
XX (YOUN/) YOUNG P E.
XX (GREE/) GREENE J M.
XX (FERR/) FERRIE A M.
XX
XX Ruben SM, Rosen CA, Li Y, Zeng Z, Kyaw H, Fischer CL, Li H;
PI Soppet DR, Gentz RL, Wei Y, Moore PA, Young PE, Greene JM;
PI Ferrie AM;
XX
XX WPI; 2002-574454/61.
XX
XX New nucleic acid molecules encoding 28 human secreted proteins, useful
PT for diagnosing, preventing, treating or ameliorating medical conditions
PT and as food additives or preservatives.
XX
XX Disclosure; Page 16; 209pp; English.
XX
XX AAD44854-AAD44984 represent cDNAs corresponding to 28 human secreted
CC protein genes, and AAE27097-AAE27137 represent the proteins they encode.
CC AAE27138-AAE27164 represent human secreted protein fragments. The genes
CC and their corresponding secreted proteins are useful for preventing,
CC treating or ameliorating medical conditions, e.g., by protein or gene
CC therapy. Secreted protein sequences of the invention are useful for the
CC diagnosis or treatment of disorders such as autoimmune diseases (e.g.
CC rheumatoid arthritis), hyperproliferative disorders (e.g. neoplasms of
CC the breast or liver), cerebrovascular disorders (e.g. cerebral ischaemia,
CC angioneuosis), cardiovascular disorders (e.g. cardiac arrest), nervous
CC system disorders (e.g. Alzheimer's disease), infections caused by fungi,
CC bacteria and viruses and ocular disorders (e.g. corneal infection). The
CC polypeptides can also be used to aid wound healing and epithelial cell
CC proliferation, to prevent skin aging due to sunburn, to maintain organs
CC before transplantation, for supporting cell culture of primary tissues,
CC to regenerate tissues and in chemotaxis. They can also be used as food
CC additives or preservative to increase or decrease storage capabilities,
CC fat content, lipid, protein, carbohydrate, vitamins, minerals, cofactors
CC and other nutritional components. The present sequence represents a human
CC secreted protein fragment Kunitz-type domain referred to in the
XX disclosure of the invention
XX
XX Sequence 51 AA;
XX
XX Query Match 35.0%; Score 219; DB 5; Length 51;
XX Best Local Similarity 68.6%; Pred. No. 7.9e-12;
XX Matches 35; Conservative 5; Mismatches 11; Indels 0; Gaps 0;
XX
XX 52 CSMQEGAGPCLASIPHHWYKTKICSEFIYGGCGGNNNNFQTEAICLVTC 102

Db 1 CEMPKEGTGPCLAYFLHWYDKDNTCSMFYVGCGGNNNNFQSKANCLNTC 51
RESULT 37
ADG89845
XX ADG89845 standard; protein; 51 AA.
XX
XX ADG89845;
XX
XX 11-MAR-2004 (first entry)
XX
XX Human secreted protein gene 24 protein #3.
XX
XX Secreted protein; gene therapy; neural disorder; immune system disorders;
KW muscular disorder; reproductive disorder; gastrointestinal disorder;
KW pulmonary disorder; cardiovascular disorder; renal disorder;
KW proliferative disorder; cancer; systemic lupus erythematosus;
KW rheumatoid arthritis; multiple sclerosis; thyroiditis; anaemia;
KW Grave's disease; diabetes; hepatitis; asthma; allergy; nephritis;
KW Parkinson's disease; Alzheimer's disease; atherosclerosis;
KW myocardial infarction; AIDS; infection; human.
XX
XX Homo sapiens.
XX
XX US2003225009-A1.
XX
XX 04-DEC-2003.
XX
XX 30-JAN-2002; 2002US-00058993.
XX
XX 14-MAR-1997; 97US-0040710P.
XX 14-MAR-1997; 97US-0040762P.
XX 30-MAY-1997; 97US-0048100P.
XX 30-MAY-1997; 97US-0048189P.
XX 30-MAY-1997; 97US-0048357P.
XX 30-MAY-1997; 97US-0050934P.
XX 06-JUN-1997; 97US-0048970P.
XX 05-SEP-1997; 97US-0057765P.
XX 19-DEC-1997; 97US-0068368P.
XX 12-MAR-1998; 98WO-US0004858.
XX 11-SEP-1998; 98US-00152060.
XX 02-FEB-2001; 2001US-0265583P.
XX 11-MAY-2001; 2001US-00852659.
XX 11-MAY-2001; 2001US-00852797.
XX 11-MAY-2001; 2001US-00853161.
XX
XX (ROSE/) ROSEN C A.
XX (RUBE/) RUBEN S M.
XX (LIYU/) LI Y.
XX (ZENG/) ZENG Z.
XX (KYAW/) KYAW H.
XX (FISC/) FISCHER C L.
XX (LIHH/) LI H.
XX (SOPP/) SOPPET D R.
XX (GENT/) GENTZ R L.
XX (WEIY/) WEI Y.
XX (MOOR/) MOORE P A.
XX (YOUN/) YOUNG P E.
XX (GREE/) GREENE J M.
XX (FERR/) FERRIE A M.
XX (HAST/) HASTINGS G A.
XX
XX Rosen CA, Ruben SM, Li Y, Zeng Z, Kyaw H, Fischer CL, Li H;
PI Soppet DR, Gentz RL, Wei Y, Moore PA, Young PE, Greene JM;
PI Ferrie AM, Hastings GA;
XX
XX WPI; 2004-042167/04.
XX
XX New polypeptides and nucleic acid molecules for diagnosing, preventing or
PT treating diseases associated with aberrant expression or activity of the
PT polypeptide, e.g. cancer, asthma, AIDS, Parkinson's disease or diabetes.
XX

used to modulate GDF-8 for treatment of muscular disorders such as
 muscular dystrophy (benign X-linked, limb-girdle, facioscapulohumeral,
 myotonic, distal, oculopharyngeal, Duchenne or Fukuyama-type congenital),
 progressive dystrophic ophthalmoplegia, amyotrophic lateral sclerosis,
 congestive obstructive pulmonary disease, congenital myopathy (myotonia),
 familial periodic paralysis, paroxysmal myoglobinuria, myasthenia gravis,
 Eaton-Lambert syndrome, secondary myasthenia, organ atrophy, frailty,
 carpal tunnel syndrome, paroxysmal muscle atrophy, sarcopaenia, cachexia
 and other muscle wasting syndromes such as traumatic or chronic injury to
 muscle, metabolic disorders such as diabetes types 1 or 2, impaired
 glucose tolerance, hyperglycaemia, metabolic syndrome, insulin resistance
 induced by trauma and obesity, adipose tissue disorder such as obesity,
 and bone degenerative conditions such as osteoporosis, osteopaenia,
 osteoarthritis, low bone mass due to chronic glucocorticoid therapy,
 premature gonadal failure, vitamin D deficiency, androgen suppression,
 secondary hyperparathyroidism, nutritional deficiencies and anorexia
 nervosa. The present sequence is cloned mouse GDF (growth and
 differentiation factor)-associated serum protein (GASP)
 Sequence 571 AA;

Query Match 29.2%; Score 182.5; DB 7; Length 571;
 Best Local Similarity 31.8%; Pred. No. 1.1e-07;
 Matches 35; Conservative 12; Mismatches 34; Indels 29; Gaps 3;
 QY 22 QCTKP---RDCPENM-----KCCPF-----SCGKKCLDFRKC 52
 DB 322 ECLKPPDSEDCGEQTRWHFDAQANCLTFTGCHCHNLNHFETAEACLMACSGPLATC 381
 QY 53 SMPQAGPCLASIPHWYNNKTKICSEFYGGCGQNNNFQTEAICLVTC 102
 DB 382 SLPALGQPCKAYVPRWAYNSQTGLQCSFYVGGCEGNGNFFESREACEESC 431

RESULT 42

AAE39459
 ID AAE39459 standard; protein; 571 AA.

AC AAE39459;
 XX

DT 18-DEC-2003 (first entry)

XX Mouse GDF-associated serum protein (GASP)1 protein.

XX Mouse: GDF-associated serum protein; GASP; amyotrophic lateral sclerosis;
 growth and differentiation factor; GDF; chronic glucocorticoid therapy;
 familial periodic paralysis; paroxysmal myoglobinuria; muscular disorder;
 progressive dystrophic ophthalmoplegia; adipose tissue disorder; frailty;
 bone degenerative disorder; congenital myopathy; Eaton-Lambert syndrome;
 muscular dystrophy; congestive obstructive pulmonary disease; cachexia;
 carpal tunnel syndrome; premature gonadal failure; vitamin D deficiency;
 nutritional deficiency; osteoarthritis; hyperparathyroidism; sarcopaenia;
 androgen suppression; myasthenia gravis; hyperglycaemia; organ atrophy;
 metabolic disorder; metabolic syndrome; anorexia nervosa; osteoporosis;
 myotonia; neuroprotective; obesity; immunomodulator; diabetes.

OS Mus sp.

XX Key Location/Qualifiers
 FT Domain 105..170
 FT /note= "Follistatin domain"

XX US2003162714-A1.

XX 28-AUG-2003.

XX 21-FEB-2003; 2003US-00369736.

XX 21-FEB-2002; 2002US-0357845P.

XX 20-DEC-2002; 2002US-043644P.

XX (AMHP) WYETH.

XX

PI Hill JJ, Wolfman NM;

XX WPI; 2003-756055/71.
 DR N-PSDB; AAD59923.

XX Composition containing growth and differentiation factor-associated serum
 protein-1, useful for treating e.g. muscular dystrophy or diabetes, also
 for diagnosis.

PS Disclosure; Fig 6C; Opp; English.

XX The present invention relates to the use of a protein GDF (growth and
 differentiation factor)-associated serum protein (GASP) 1 comprising
 at least one follistatin domain to modulate the level or activity of
 growth and differentiation factor (GDF) -8. Administration of GASP1 is
 used to modulate GDF-8 for treatment of muscular disorders such as
 muscular dystrophy (benign X-linked, limb-girdle, facioscapulohumeral,
 myotonic, distal, oculopharyngeal, Duchenne or Fukuyama-type congenital),
 progressive dystrophic ophthalmoplegia, amyotrophic lateral sclerosis,
 congestive obstructive pulmonary disease, congenital myopathy (myotonia),
 familial periodic paralysis, paroxysmal myoglobinuria, myasthenia gravis,
 Eaton-Lambert syndrome, secondary myasthenia, organ atrophy, frailty,
 carpal tunnel syndrome, paroxysmal muscle atrophy, sarcopaenia, cachexia
 and other muscle wasting syndromes such as traumatic or chronic injury to
 muscle, metabolic disorders such as diabetes types 1 or 2, impaired
 glucose tolerance, hyperglycaemia, metabolic syndrome, insulin resistance
 induced by trauma and obesity, adipose tissue disorder such as obesity,
 and bone degenerative conditions such as osteoporosis, osteopaenia,
 osteoarthritis, low bone mass due to chronic glucocorticoid therapy,
 premature gonadal failure, vitamin D deficiency, androgen suppression,
 secondary hyperparathyroidism, nutritional deficiencies and anorexia
 nervosa. The present sequence is mouse GDF (growth and differentiation
 factor)-associated serum protein (GASP)
 Sequence 571 AA;

Query Match 29.2%; Score 182.5; DB 7; Length 571;

Best Local Similarity 31.8%; Pred. No. 1.1e-07;

Matches 35; Conservative 12; Mismatches 34; Indels 29; Gaps 3;

QY 22 QCTKP---RDCPENM-----KCCPF-----SCGKKCLDFRKC 52
 DB 322 ECLKPPDSEDCGEQTRWHFDAQANCLTFTGCHCHNLNHFETAEACLMACSGPLATC 381

QY 53 SMPQAGPCLASIPHWYNNKTKICSEFYGGCGQNNNFQTEAICLVTC 102

DB 382 SLPALGQPCKAYVPRWAYNSQTGLQCSFYVGGCEGNGNFFESREACEESC 431

RESULT 43

ADD93670

ID ADD93670 standard; protein; 571 AA.

XX ADD93670;

XX 29-JAN-2004 (first entry)

XX Mouse GDF-associated serum protein 1 (GASP1).

XX Mouse: GDF-associated serum protein 1; GASP1; antidiabetic; anorectic;
 osteopathic; gene therapy.

OS Mus sp.

XX Key Location/Qualifiers

FT Peptide 1..29
 FT /note= "Signal peptide"

FT Protein 30..571
 FT /note= "Mature protein"

FT Domain 105..170
 FT /note= "Follistatin domain"

FT Modified-site 313

FT /note= "potential N-glycosylation site"

FT

OS Synthetic.
OS Homo sapiens.
PN WO2003070770-A2.
XX
XX
PD 28-AUG-2003.
XX
XX
PF 18-FEB-2003; 2003WO-EP001629.
XX
XX
PR 21-FEB-2002; 2002US-0358683P.
XX
XX (GENE-) GENEPROT INC.
PA
PI Bougueleret L, Bairoch A, Niknejad A;
XX WPI; 2003-663849/62.
XX
XX New engineered human Kunitz-type protease inhibitor for diagnosing,
PT preventing or treating conditions associated with excessive proteinase
PT activity, e.g. inflammation, pulmonary injuries, myocardial infarction or
PT hemorrhage.
XX
XX Disclosure; Page 80; 87pp; English.
XX
XX The present invention describes an isolated, purified or recombinant DJ11
CC polypeptide comprising a Kunitz-type protease inhibitor domain or its
CC biologically active portion. The polypeptide comprises at least 98 %
CC identity to residues 77-127 of a 131 amino acid sequence (S1, see
CC ADA19800), or to residues 52-102 of a 106 amino acid sequence (S2, see
CC ADA19801). DJ11 has antiinflammatory, antiallergic, thrombolytic,
CC anticoagulant, cardiatic, vasotropic, antibacterial, immunosuppressive,
CC antirheumatic, antiarthritic, nephrotropic, antipsoriatic and vulnary
CC activities, and can be used as a protease inhibitor and in gene therapy.
CC Composition and methods from the present invention can be used in
CC diagnosing, preventing or treating conditions associated with excessive
CC proteinase activity, such as acute pancreatitis, pulmonary injury,
CC allergy-induced protease release, deep vein thrombosis, myocardial
CC infarction, shock (including septic shock), hyperfibrinolytic
CC haemorrhage, and especially, inflammatory disorders (e.g. emphysema,
CC idiopathic pulmonary fibrosis, rheumatoid arthritis, glomerulonephritis,
CC chronic inflammatory bowel disease or psoriasis). The DJ11 proteins may
CC be used in preserving platelet function, organ preservation or in wound
CC healing. The polynucleotide sequence encoding DJ11 may be used as
CC hybridisation probes, in chromosome and gene mapping, in the generation
CC of antisense RNA and DNA, and as targets for pharmaceutical intervention.
CC The present sequence represents a partial engineered human DJ11 protein
CC amino acid sequence from the present invention.
XX
XX Sequence 33 AA;
XX
Query Match 28.8%; Score 180; DB 7; Length 33;
Best Local Similarity 97.0%; Pred. No. 1.3e-08;
Matches 32; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 74 TKICSEFIYGGCGNNNNFQTEAICLVTCCKYH 106
Db 1 TKICSEFIYGGCGNNNNFQTEAICLVTCCKYH 33
RESULT 46
ADA19809
ID ADA19809 standard; peptide; 33 AA.
XX
AC ADA19809;
XX
XX 20-NOV-2003 (first entry)
DT
XX Engineered human DJ11 partial amino acid sequence SEQ ID NO:10.
DE
XX DJ11; Kunitz-type protease inhibitor domain; antiinflammatory;
KW antiallergic; thrombolytic; anticoagulant; cardiatic; vasotropic;
KW antibacterial; immunosuppressive; antirheumatic; antiarthritic;
KW nephrotropic; antipsoriatic; vulnary; protease inhibitor; gene therapy;
XX

KW acute pancreatitis; pulmonary injury; allergy-induced protease release;
KW deep vein thrombosis; myocardial infarction; shock; septic shock;
KW hyperfibrinolytic haemorrhage; inflammatory disorder; emphysema;
KW idiopathic pulmonary fibrosis; rheumatoid arthritis; glomerulonephritis;
KW chronic inflammatory bowel disease; psoriasis.
XX
XX Synthetic.
OS Homo sapiens.
XX
XX WO2003070770-A2.
XX
XX 28-AUG-2003.
XX
XX 18-FEB-2003; 2003WO-EP001629.
XX
XX 21-FEB-2002; 2002US-0358683P.
XX (GENE-) GENEPROT INC.
PA
PI Bougueleret L, Bairoch A, Niknejad A;
XX WPI; 2003-663849/62.
XX
XX New engineered human Kunitz-type protease inhibitor for diagnosing,
PT preventing or treating conditions associated with excessive proteinase
PT activity, e.g. inflammation, pulmonary injuries, myocardial infarction or
PT hemorrhage.
XX
XX Disclosure; Page 82-83; 87pp; English.
XX
XX The present invention describes an isolated, purified or recombinant DJ11
CC polypeptide comprising a Kunitz-type protease inhibitor domain or its
CC biologically active portion. The polypeptide comprises at least 98 %
CC identity to residues 77-127 of a 131 amino acid sequence (S1, see
CC ADA19800), or to residues 52-102 of a 106 amino acid sequence (S2, see
CC ADA19801). DJ11 has antiinflammatory, antiallergic, thrombolytic,
CC anticoagulant, cardiatic, vasotropic, antibacterial, immunosuppressive,
CC antirheumatic, antiarthritic, nephrotropic, antipsoriatic and vulnary
CC activities, and can be used as a protease inhibitor and in gene therapy.
CC Composition and methods from the present invention can be used in
CC diagnosing, preventing or treating conditions associated with excessive
CC proteinase activity, such as acute pancreatitis, pulmonary injury,
CC allergy-induced protease release, deep vein thrombosis, myocardial
CC infarction, shock (including septic shock), hyperfibrinolytic
CC haemorrhage, and especially, inflammatory disorders (e.g. emphysema,
CC idiopathic pulmonary fibrosis, rheumatoid arthritis, glomerulonephritis,
CC chronic inflammatory bowel disease or psoriasis). The DJ11 proteins may
CC be used in preserving platelet function, organ preservation or in wound
CC healing. The polynucleotide sequence encoding DJ11 may be used as
CC hybridisation probes, in chromosome and gene mapping, in the generation
CC of antisense RNA and DNA, and as targets for pharmaceutical intervention.
CC The present sequence represents a partial engineered human DJ11 protein
CC amino acid sequence from the present invention.
XX
XX Sequence 33 AA;
XX
Query Match 28.8%; Score 180; DB 7; Length 33;
Best Local Similarity 97.0%; Pred. No. 1.3e-08;
Matches 32; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 74 TKICSEFIYGGCGNNNNFQTEAICLVTCCKYH 106
Db 1 TKICSEFIYGGCGNNNNFQTEAICLVTCCKYH 33
RESULT 47
AAR99146
ID AAR99146 standard; protein; 58 AA.
XX
XX AAR99146;
XX
XX 12-FEB-1997 (first entry)
DT
XX

DE Aprotinin-like Kunitz domain.
 XX KW Aprotinin; Kunitz domain; human neutrophil elastase; hNE;
 KW connective tissue; alpha 1 protease inhibitor; API; neutrophil;
 KW alaphal antitrypsin; respiratory disorder; cystic fibrosis;
 KW smokers emphysema.
 XX OS Synthetic.
 XX WO9620278-A2.
 XX PD 04-JUL-1996.
 XX PF 15-DEC-1995; 95WO-US016349.
 XX PR 16-DEC-1994; 94US-00358160.
 XX PA (PROT-) PROTEIN ENG CORP.
 XX PI Ley AC, Ladner RC, Guterman SK, Roberts BL, Markland W, Kent RB;
 XX WPI; 1996-321851/32.
 XX New engineered inhibitors of human neutrophil elastase - contg. aprotinin
 PT -like Kunitz domain for treating, e.g. cystic fibrosis or other
 PT respiratory disorders.
 XX Example 23; Page 47; 105pp; English.
 CC Genetically engineered human derived Kunitz domains can be used to
 CC inhibit human neutrophil elastase, an enzyme involved in the elimination
 CC of pathogens and the restructuring of connective tissue. In cases of
 CC reduction of the circulating alpha-1-protease inhibitor (API or alaphal
 CC antitrypsin), or the inactivation of API by oxidation (smokers
 CC emphysema), extensive destruction of the lung tissue may result from
 CC uncontrolled elastolytic activity of human neutrophil elastase. Other
 CC respiratory disorders such as cystic fibrosis are thought to be caused by
 CC human neutrophil elastase release by neutrophils. The genetically
 CC engineered human derived Kunitz domains can be used to treat such
 CC respiratory disorders. See AAR99146-R99211
 XX Sequence 58 AA;
 SQ Query Match 28.3%; Score 177; DB 2; Length 58;
 Best Local Similarity 56.4%; Pred. No. 4e-08; Mismatches 19; Indels 0; Gaps 0;
 Matches 31; Conservative 5;
 QY 48 RKDICSMPQAGPCILASIPHWYNNKTKICSEFYGGCGGNNNFQTEAICLVTC 102
 DB 1 RPDFCLLPAGTGPCRAMIPRFYNNKSGKCEPFYGGCGGNNNFQTEECRCRTC 55
 RESULT 48
 AAE13096
 ID AAE13096 standard; peptide; 43 AA.
 AC AAE13096;
 XX 28-JAN-2002 (first entry)
 DE Human serine proteinase inhibitor BTL.009 peptide fragment #2.
 XX Human; BTL.009 protein; serine proteinase inhibitor; cystostatic;
 KW nephrotropic; idiopathic pulmonary fibrosis; cystic fibrosis; emphysema;
 KW rheumatoid arthritis; adult respiratory distress syndrome; angiotensin;
 KW blood coagulation; glomerulonephritis; prophylactic; platelet activation;
 KW neutrophil; monocyte; granulocyte; organ failure; inflammatory disease;
 KW elastase inhibitor; chymotrypsin inhibitor; lung injury; vascular injury;
 KW therapeutic.
 XX Homo sapiens.
 OS US6294648-B1.
 XX

XX 25-SEP-2001.
 PD 20-JUL-1999; 99US-00358569.
 PF 20-JUL-1999; 99US-00358569.
 PR (FARB) BAYER CORP.
 PA Delaria K, Rocznik S, Davies C;
 XX WPI; 2001-662224/76.
 XX New isolated protein for inhibiting human serine proteinase activity in the
 PT treatment of e.g. emphysema and adult respiratory distress syndrome.
 XX Disclosure; Col 5-6; 16pp; English.
 CC The invention relates to human BTL.009 protein, a serine proteinase
 CC inhibitor of the Kunitz family that exhibits greater potency towards
 CC neutral serine proteinases. BTL.009 protein is found to inhibit leukocyte
 CC elastase, chymotrypsin-like protease and trypsin-like protease. BTL.009
 CC protein is useful for treating emphysema, idiopathic pulmonary fibrosis,
 CC adult respiratory distress syndrome, cystic fibrosis, rheumatoid
 CC arthritis, organ failure, glomerulonephritis, other inflammatory diseases
 CC and diseases involving lung and vascular injury. BTL.009 is also useful
 CC for preventing neutrophil and monocyte activation and formation of active
 CC oxygen species during the oxidative burst of stimulated granulocytes.
 CC BTL.009 is useful for reducing platelet activation and blood coagulation
 CC and for the prophylactic or therapeutic treatment of patients undergoing
 CC angioplasty. The present sequence is human serine proteinase inhibitor
 CC BTL.009 peptide fragment related to the invention
 XX Sequence 43 AA;
 SQ Query Match 28.0%; Score 175; DB 4; Length 43;
 Best Local Similarity 69.0%; Pred. No. 4.5e-08;
 Matches 29; Conservative 4; Mismatches 9; Indels 0; Gaps 0;
 QY 62 LASIPHWYNNKTKICSEFYGGCGGNNNFQTEAICLVTC 103
 DB 1 LAYELHWYDKKONTCSMFYGGCGGNNNFQSKANCLNTCK 42
 RESULT 49
 AAE13092
 ID AAE13092 standard; peptide; 54 AA.
 AC AAE13092;
 XX 28-JAN-2002 (first entry)
 DE Trypsin inhibitor peptide.
 XX BTL.009 protein; serine proteinase inhibitor; cystostatic; therapeutic;
 KW nephrotropic; idiopathic pulmonary fibrosis; cystic fibrosis; emphysema;
 KW rheumatoid arthritis; adult respiratory distress syndrome; angiotensin;
 KW blood coagulation; glomerulonephritis; prophylactic; platelet activation;
 KW neutrophil; monocyte; granulocyte; organ failure; inflammatory disease;
 KW elastase inhibitor; chymotrypsin inhibitor; lung injury; vascular injury;
 KW trypsin inhibitor.
 XX Unidentified.
 OS US6294648-B1.
 XX 25-SEP-2001.
 PD 20-JUL-1999; 99US-00358569.
 PF 20-JUL-1999; 99US-00358569.
 PR (FARB) BAYER CORP.
 PA

XX Delaria K, Rocznik S, Davies C;
XX WPI; 2001-662224/76.
XX New isolated protein for inhibiting human serine protease activity in the
XX treatment of e.g. emphysema and adult respiratory distress syndrome.
XX
XX Disclosure; Col 5-6; 16pp; English.
XX
XX The invention relates to human BTL 009 protein, a serine proteinase
XX inhibitor of the Kunitz family that exhibits greater potency towards
XX neutral serine proteinases. BTL 009 protein is found to inhibit leukocyte
XX elastase, chymotrypsin-like protease and trypsin-like protease. BTL 009
XX protein is useful for treating emphysema, idiopathic pulmonary fibrosis,
XX adult respiratory distress syndrome, cystic fibrosis, rheumatoid
XX arthritis, organ failure, glomerulonephritis, other inflammatory diseases
XX and diseases involving lung and vascular injury. BTL 009 is also useful
XX for preventing neutrophil and monocyte activation and formation of active
XX oxygen species during the oxidative burst of stimulated granulocytes.
XX BTL 009 is useful for reducing platelet activation and blood coagulation
XX and for the prophylactic or therapeutic treatment of patients undergoing
XX angioplasty. The present sequence is trypsin inhibitor peptide related to
XX the invention
XX
XX Sequence 54 AA;

Query Match 28.0%; Score 175; DB 4; Length 54;
Best Local Similarity 50.0%; Pred. No. 5.5e-08;
Matches 27; Conservative 10; Mismatches 17; Indels 0; Gaps 0;
QY 50 DICSMPOEAGPCLASIPHWYNNKTKICSEFIYGGCGQNNNNFQTEAICLVTC 103
DB 1 DICLPQARGPCXKALLRYFNSTNACEPFTYGGCGQNNNNFETEMCLRICE 54

RESULT 50
ABJ01150
ID ABJ01150 standard; protein; 503 AA.
XX
XX AC ABJ01150;
XX
XX DT 28-NOV-2002 (first entry)
XX
XX DE Ovary cell-specific amino acid sequence 96.
XX
XX KW Ovary cell; neoplastic ovary cell; ovary specific nucleic acid;
XX KW ovary specific protein; ovarian cancer; breast cancer; vaccine;
XX KW gene therapy.
XX
XX OS Homo sapiens.
XX
XX PN WO200238606-A2.
XX
XX PD 16-MAY-2002.
XX
XX PF 07-NOV-2001; 2001WO-US046459.
XX
XX PR 08-NOV-2000; 2000US-0246640P.
XX
XX PA (DIAD-) DIADEXUS INC.
XX
XX PI Sun Y, Recipon H, Salceda S, Liu C;
XX
XX DR WPI; 2002-519297/55.
XX
XX Polypeptide and polynucleotides present in normal and neoplastic ovary
XX cells, useful for identifying, monitoring, staging, diagnosing,
XX PT preventing and treating ovarian cancer, and non-cancerous disease states
XX PT in the ovary.
XX
XX Claim 11; Page 244-245; 247pp; English.
XX
XX

CC The invention comprises amino acid and DNA sequences which are present in
CC normal and neoplastic ovary cells. The DNA and protein sequences of the
CC invention are useful for determining the presence of an ovary specific
CC nucleic acid or an ovary specific protein in a sample. The DNA and
CC protein sequences of the invention are useful for diagnosing and
CC monitoring the presence and metastasis of ovarian cancer and breast
CC cancer. Amino acids ABJ01055 - ABJ01155 represent the ovary cell specific
CC protein sequences of the invention
XX
XX Sequence 503 AA;

Query Match 27.8%; Score 173.5; DB 5; Length 503;
Best Local Similarity 31.8%; Pred. No. 6.1e-07;
Matches 35; Conservative 10; Mismatches 36; Indels 29; Gaps 3;
QY 22 QCTKP---RDCPENM-----KCCPF-----SCGKKCLDFRKCIC 52
DB 258 ECLKPPDSEDCGEGTQRWHFPAQANNCLTFTFGHCHRNLNHFETVEACMLACMSGPLAAC 317
QY 53 SMPQEAGPCLASIPHWYNNKTKICSEFIYGGCGQNNNNFQTEAICLVTC 102
DB 318 SLPALQGPCKAYAPRWAYNSQTQCQSFVYGGCGEGNGNPFESFACEESC 367

Search completed: September 21, 2005, 16:36:50
Job time : 67.2891 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 21, 2005, 16:27:13 ; Search time 19.3864 Seconds
(without alignments)
408.162 Million cell updates/sec

Title: US-10-807-204-2

Perfect score: 625

Sequence: 1 EGILGKPCPKIKVECEEI.....GNNNFQTEAICLVTCRKYH 106

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 50 summaries

Database : Issued Patents AA.*

- 1: /cgn2_6/prodata/1/iaa/5A_COMB.pep.*
- 2: /cgn2_6/prodata/1/iaa/5B_COMB.pep.*
- 3: /cgn2_6/prodata/1/iaa/6A_COMB.pep.*
- 4: /cgn2_6/prodata/1/iaa/6B_COMB.pep.*
- 5: /cgn2_6/prodata/1/iaa/PCTUS_COMB.pep.*
- 6: /cgn2_6/prodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	400	64.0	133	4	US-09-152-060-75
2	242	38.7	64	3	US-09-358-569D-10
3	236	37.8	58	3	US-09-369-494-8
4	236	37.8	58	4	US-09-569-670-8
5	233	37.3	54	3	US-09-358-569D-8
6	231	37.0	55	3	US-09-358-569D-1
7	186	29.8	66	1	US-08-358-160-113
8	186	29.8	79	6	5466783-7
9	186	29.8	79	6	5466783-7
10	177	28.3	58	1	US-08-358-160-71
11	175	28.0	43	3	US-09-358-569D-13
12	175	28.0	54	3	US-09-358-569D-9
13	175	28.0	67	1	US-08-358-160-123
14	173	27.7	58	1	US-08-358-160-17
15	173	27.7	58	1	US-08-358-160-18
16	169	27.0	77	6	5466783-4
17	169	27.0	77	6	5466783-4
18	168	26.9	86	4	US-09-910-430-8
19	167	26.7	58	1	US-08-358-160-10
20	167	26.7	58	1	US-08-358-160-11
21	166	26.6	58	1	US-07-664-989B-48
22	166	26.6	58	1	US-07-664-989B-51
23	166	26.6	58	1	US-08-358-160-1
24	166	26.6	58	1	US-08-358-160-15
25	166	26.6	58	1	US-08-358-160-26
26	166	26.6	62	1	US-08-358-160-27
27	166	26.6	107	4	US-09-270-767-46540

28	165	26.4	58	1	US-07-664-989B-49
29	165	26.4	58	1	US-08-358-160-24
30	164	26.2	58	1	US-08-358-160-9
31	164	26.2	61	2	US-08-829-876-211
32	164	26.2	61	2	US-08-829-876-214
33	164	26.2	61	3	US-09-234-874A-211
34	164	26.2	61	3	US-09-234-874A-214
35	164	26.2	61	4	US-09-234-873A-211
36	164	26.2	61	4	US-09-234-873A-214
37	163	26.1	58	1	US-07-664-989B-84
38	163	26.1	58	1	US-08-358-160-12
39	163	26.1	58	1	US-08-358-160-61
40	163	26.1	58	1	US-08-463-155A-56
41	163	26.1	58	1	US-08-463-432B-56
42	163	26.1	58	3	US-08-676-124-69
43	163	26.1	58	3	US-09-414-878-69
44	163	26.1	58	3	US-09-240-136-69
45	163	26.1	58	4	US-09-638-770A-69
46	163	26.1	61	2	US-08-829-876-180
47	163	26.1	61	2	US-08-829-876-218
48	163	26.1	61	3	US-09-234-874A-180
49	163	26.1	61	3	US-09-234-874A-218
50	163	26.1	61	4	US-09-234-873A-180

ALIGNMENTS

RESULT 1
US-09-152-060-75
; Sequence 75, Application US/09152060
; Patent No. 6448230
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 28 Human Secreted Proteins
; FILE REFERENCE: P2003P1.US
; CURRENT APPLICATION NUMBER: US/09152,060
; CURRENT FILING DATE: 1998-09-11
; EARLIER APPLICATION NUMBER: PCT/US98/04858
; EARLIER FILING DATE: 1998-03-12
; EARLIER APPLICATION NUMBER: 60/040,762
; EARLIER FILING DATE: 1997-03-14
; EARLIER APPLICATION NUMBER: 60/040,710
; EARLIER FILING DATE: 1997-03-14
; EARLIER APPLICATION NUMBER: 60/050,934
; EARLIER FILING DATE: 1997-05-30
; EARLIER APPLICATION NUMBER: 60/048,100
; EARLIER FILING DATE: 1997-05-30
; EARLIER APPLICATION NUMBER: 60/048,357
; EARLIER FILING DATE: 1997-05-30
; EARLIER APPLICATION NUMBER: 60/048,189
; EARLIER FILING DATE: 1997-05-30
; EARLIER APPLICATION NUMBER: 60/057,765
; EARLIER FILING DATE: 1997-09-05
; EARLIER APPLICATION NUMBER: 60/048,970
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/068,368
; EARLIER FILING DATE: 1997-12-19
; NUMBER OF SEQ ID NOS: 118
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 75
; LENGTH: 133
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-152-060-75

Query Match 64.0%; Score 400; DB 4; Length 133;
Best Local Similarity 66.7%; Pred. No. 1.7e-33;
Matches 64; Conservative 11; Mismatches 21; Indels 0; Gaps 0;
QY 8 CPKIKVECEEIDQCTKPCDENMKCCPFSCGKKCLDFRDKDICSMPQEGPCLASIPH 67
| | | | | : | | | | | : | | | | | : | | | | | : | | | | |
DB 33 CPKIRECBFQBRDVCTKRCQDNKKCVFCGKKCLDLKQDVCEMPKETGCLAYFLH 92


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; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 55
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:derived from
; OTHER INFORMATION: EST sequence database
US-09-358-569D-1

Query Match      37.0%; Score 231; DB 3; Length 55;
Best Local Similarity 65.5%; Pred. No. 1.1e-16;
Matches 36; Conservative 8; Mismatches 11; Indels 0; Gaps 0;

QY 48 RNDICSMPOEAGPCLASIPHHWYNNKTKICSEFIYGGCGGNNNNFOTEICLVTC 102
Db 1 KQDVCEMPKETGPCLAYFLHWYDKDNTCSMFVYGGCGGNNNNFOSKNCNLNTC 55

RESULT 7
US-08-358-160-113
; Sequence 113, Application US/08358160
; Patent No. 5663143
; GENERAL INFORMATION:
; APPLICANT: LEY, Arthur C.
; APPLICANT: LADNER, Robert C.
; APPLICANT: GUTERMAN, Sonia K.
; APPLICANT: ROBERTS, Bruce L.
; APPLICANT: MARKLAND, William
; APPLICANT: KENT, Rachel B.
; TITLE OF INVENTION: ENGINEERED HUMAN-DERIVED KUNITZ
; TITLE OF INVENTION: DOMAINS THAT INHIBIT HUMAN NEUTROPHIL ELASTASE
; NUMBER OF SEQUENCES: 234
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W. Suite 300
; CITY: Washington
; STATE: District of Columbia
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM: disk
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/358,160
; FILING DATE: 16-DEC-1994
; CLASSIFICATION: 514
; PRIOR APPLICATION NUMBER: US 08/133,031
; FILING DATE: 13-OCT-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/009,319
; FILING DATE: 26-JAN-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/664,989
; FILING DATE: 01-MAR-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/487,063
; FILING DATE: 02-MAR-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/240,160
; FILING DATE: 02-SEP-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Cooper, Iver P.
; REGISTRATION NUMBER: 28,005
; REFERENCE/DOCKET NUMBER: LEY=1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; TELEX: 248633
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; INFORMATION FOR SEQ ID NO: 113:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 66 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-358-160-113

Query Match      29.8%; Score 186; DB 1; Length 66;
Best Local Similarity 50.0%; Pred. No. 5.3e-12;
Matches 28; Conservative 13; Mismatches 15; Indels 0; Gaps 0;

QY 48 RNDICSMPOEAGPCLASIPHHWYNNKTKICSEFIYGGCGGNNNNFOTEICLVTC 103
Db 4 KRDCRLPPEQGPKGRIPRYFYFNPASRMCSFIYGGCKGNKNFKTKAECVRACR 59

RESULT 8
5466783-7
; Patent No. 5466783
; APPLICANT: Wun, Tze-Chain,;Kretzmer, Kuniko K.;Broze,
; George J. Jr.
; TITLE OF INVENTION: HUMAN TISSUE FACTOR INHIBITOR
; NUMBER OF SEQUENCES: 26
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/93,285
; FILING DATE: 15-JUL-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 566,280
; FILING DATE: 13-AUG-1990
; APPLICATION NUMBER: 123,753
; FILING DATE: 23-NOV-1987
; APPLICATION NUMBER: 77,366
; FILING DATE: 23-JUL-1987
; SEQ ID NO:7:
; LENGTH: 79
5466783-7

Query Match      29.8%; Score 186; DB 6; Length 79;
Best Local Similarity 50.0%; Pred. No. 6.3e-12;
Matches 28; Conservative 13; Mismatches 15; Indels 0; Gaps 0;

QY 48 RNDICSMPOEAGPCLASIPHHWYNNKTKICSEFIYGGCGGNNNNFOTEICLVTC 103
Db 4 KRDCRLPPEQGPKGRIPRYFYFNPASRMCSFIYGGCKGNKNFKTKAECVRACR 59

RESULT 9
5466783-7
; Patent No. 5466783
; APPLICANT: Wun, Tze-Chain,;Kretzmer, Kuniko K.;Broze,
; George J. Jr.
; TITLE OF INVENTION: HUMAN TISSUE FACTOR INHIBITOR
; NUMBER OF SEQUENCES: 26
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/93,285
; FILING DATE: 15-JUL-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 566,280
; FILING DATE: 13-AUG-1990
; APPLICATION NUMBER: 123,753
; FILING DATE: 23-NOV-1987
; APPLICATION NUMBER: 77,366
; FILING DATE: 23-JUL-1987
; SEQ ID NO:7:
; LENGTH: 79
5466783-7

Query Match      29.8%; Score 186; DB 6; Length 79;
Best Local Similarity 50.0%; Pred. No. 6.3e-12;
Matches 28; Conservative 13; Mismatches 15; Indels 0; Gaps 0;
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```
; APPLICANT: KENT, Rachel B.
; TITLE OF INVENTION: ENGINEERED HUMAN-DERIVED KUNITZ
; TITLE OF INVENTION: DOMAINS THAT INHIBIT HUMAN NEUTROPHIL ELASTASE
; NUMBER OF SEQUENCES: 234
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W. Suite 300
; CITY: Washington
; STATE: District of Columbia
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC Compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/358,160
; FILING DATE: 16-DEC-1994
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/133,031
; FILING DATE: 13-OCT-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/009,319
; FILING DATE: 26-JAN-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/664,989
; FILING DATE: 01-MAR-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/487,063
; FILING DATE: 02-MAR-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/240,160
; FILING DATE: 02-SEP-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Cooper, Iver P.
; REGISTRATION NUMBER: 28,005
; REFERENCE/DOCKET NUMBER: LEY=1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; TELEX: 248633
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 58 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-358-160-18

Query Match 27.7%; Score 173; DB 1; Length 58;
Best Local Similarity 50.0%; Pred. No. 9.8e-11;
Matches 28; Conservative 7; Mismatches 21; Indels 0; Gaps 0;

QY 48 RKDSCMPOEAGPCLASIPHHWYNNKTKICSEFIYGGCGGNNNNFQTEAICLVTK 103
DB 1 RPDFCQLGYSAGPCVAMFPFIFYNGASMACQTFVYGGCGNGNFFVTEKDLQTCR 56

RESULT 16
5466783-4
; Patent No. 5466783
; APPLICANT: Wun, Tze-Chain,;Kretzmer, Kuniko K.;Broze,
;George J. Jr.
; TITLE OF INVENTION: HUMAN TISSUE FACTOR INHIBITOR
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: 26
; FILING DATE: 15-JUL-1993
; PRIOR APPLICATION NUMBER: US/08/93,285
; FILING DATE: 2001-07-19
; PRIOR FILING DATE: 2000-06-06
; PRIOR APPLICATION NUMBER: GB 9913425.6
; PRIOR FILING DATE: 1999-06-09
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 8
; LENGTH: 86
; TYPE: PRT
; ORGANISM: Ixodes ricinus
; US-09-910-430-8
```

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; FILING DATE: 13-AUG-1990
; APPLICATION NUMBER: 123,753
; FILING DATE: 23-NOV-1987
; APPLICATION NUMBER: 77,366
; FILING DATE: 23-JUL-1987
; SEQ ID NO:4
; LENGTH: 77
5466783-4

Query Match 27.0%; Score 169; DB 6; Length 77;
Best Local Similarity 46.3%; Pred. No. 3.3e-10;
Matches 25; Conservative 12; Mismatches 17; Indels 0; Gaps 0;

QY 50 DICSMPOEAGPCLASIPHHWYNNKTKICSEFIYGGCGGNNNNFQTEAICLVTK 103
DB 6 DLCLPQARGPCKAALLRYFYBSTSNACEPTYGGCGGNNNFETTEMCLRICE 59

RESULT 17
5466783-4
; Patent No. 5466783
; APPLICANT: Wun, Tze-Chain,;Kretzmer, Kuniko K.;Broze,
;George J. Jr.
; TITLE OF INVENTION: HUMAN TISSUE FACTOR INHIBITOR
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/93,285
; FILING DATE: 15-JUL-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 566,280
; FILING DATE: 13-AUG-1990
; APPLICATION NUMBER: 123,753
; FILING DATE: 23-NOV-1987
; APPLICATION NUMBER: 77,366
; FILING DATE: 23-JUL-1987
; SEQ ID NO:4
; LENGTH: 77
5466783-4

Query Match 27.0%; Score 169; DB 6; Length 77;
Best Local Similarity 46.3%; Pred. No. 3.3e-10;
Matches 25; Conservative 12; Mismatches 17; Indels 0; Gaps 0;

QY 50 DICSMPOEAGPCLASIPHHWYNNKTKICSEFIYGGCGGNNNNFQTEAICLVTK 103
DB 6 DLCLPQARGPCKAALLRYFYBSTSNACEPTYGGCGGNNNFETTEMCLRICE 59

RESULT 18
US-09-910-430-8
; Sequence 8, Application US/09910430
; Patent No. 6794166
; GENERAL INFORMATION:
; APPLICANT: Godfroi, Edmond
; APPLICANT: Bollen, Alex
; APPLICANT: Lebouille, Gerard
; TITLE OF INVENTION: IDENTIFICATION AND MOLECULAR CHARACTERIZATION OF
; TITLE OF INVENTION: PROTEINS, EXPRESSED IN THE IXODES RICINUS SALIVARY
; TITLE OF INVENTION: GLANDS
; FILE REFERENCE: VANM229.001CF1
; CURRENT APPLICATION NUMBER: US/09/910,430
; CURRENT FILING DATE: 2001-07-19
; PRIOR APPLICATION NUMBER: PCT/BE00/00061
; PRIOR FILING DATE: 2000-06-06
; PRIOR APPLICATION NUMBER: GB 9913425.6
; PRIOR FILING DATE: 1999-06-09
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 8
; LENGTH: 86
; TYPE: PRT
; ORGANISM: Ixodes ricinus
; US-09-910-430-8
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QY 48 RKDICSMPQAGPCLASIPHHWYNNKTKICSEFIYGGCGGNNNFQTEAICLVTC 103
Db 1 RPDFCOLGYSAGPCVAMPFRIFYNGTSMACETFYGGCGMGNGNFFVTERKDLQTCR 56

US-07-664-989B-48
; Sequence 48, Application US/07664989B
; Patent No. 5223409
; GENERAL INFORMATION:
; APPLICANT: Ladner, Robert Charles
; APPLICANT: Guterman, Sonia Kosow
; APPLICANT: Roberts, Bruce Lindsay
; APPLICANT: Markland, William
; APPLICANT: Ley, Arthur Charles
; APPLICANT: Kent, Rachel Baribault
; TITLE OF INVENTION: Directed Evolution of No. 5223409e1
; NUMBER OF SEQUENCES: 121
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Browdy and Neimark
; STREET: 419 Seventh Street, N.W.
; CITY: Washington,
; STATE: DC
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WORDPERFECT 4.2
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/664,989B
; FILING DATE: 19910301
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US89/03731
; FILING DATE: 01-SEP-1989
; APPLICATION NUMBER: 07/487,063
; FILING DATE: 02-MAR-1990
; APPLICATION NUMBER: 07/240,160
; FILING DATE: 02-SEP-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Cooper, Iver P.
; REGISTRATION NUMBER: 28005
; REFERENCE/DOCKET NUMBER: LADNER 7
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; INFORMATION FOR SEQ ID NO: 48:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 58 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-07-664-989B-48

Query Match 26.6%; Score 166; DB 1; Length 58;
Best Local Similarity 47.3%; Pred. No. 5e-10;
Matches 26; Conservative 8; Mismatches 21; Indels 0; Gaps 0;

QY 48 RKDICSMPQAGPCLASIPHHWYNNKTKICSEFIYGGCGGNNNFQTEAICLVTC 102
Db 1 RPDFCLEPPTGCVAMPFRIFYNAGKAGLCQTFYGGCGMGNGNFKSAEDCMRTC 55

RESULT 22
US-07-664-989B-51
; Sequence 51, Application US/07664989B

; Patent No. 5223409
; GENERAL INFORMATION:
; APPLICANT: Ladner, Robert Charles
; APPLICANT: Guterman, Sonia Kosow
; APPLICANT: Roberts, Bruce Lindsay
; APPLICANT: Markland, William
; APPLICANT: Ley, Arthur Charles
; APPLICANT: Kent, Rachel Baribault
; TITLE OF INVENTION: Directed Evolution of No. 5223409e1
; NUMBER OF SEQUENCES: 121
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Browdy and Neimark
; STREET: 419 Seventh Street, N.W.
; CITY: Washington,
; STATE: DC
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WORDPERFECT 4.2
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/664,989B
; FILING DATE: 19910301
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US89/03731
; FILING DATE: 01-SEP-1989
; APPLICATION NUMBER: 07/487,063
; FILING DATE: 02-MAR-1990
; APPLICATION NUMBER: 07/240,160
; FILING DATE: 02-SEP-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Cooper, Iver P.
; REGISTRATION NUMBER: 28005
; REFERENCE/DOCKET NUMBER: LADNER 7
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; INFORMATION FOR SEQ ID NO: 51:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 58 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-07-664-989B-51

Query Match 26.6%; Score 166; DB 1; Length 58;
Best Local Similarity 47.3%; Pred. No. 5e-10;
Matches 26; Conservative 8; Mismatches 21; Indels 0; Gaps 0;

QY 48 RKDICSMPQAGPCLASIPHHWYNNKTKICSEFIYGGCGGNNNFQTEAICLVTC 102
Db 1 RPDFCLEPPTGCVAMPFRIFYNAGKAGLCQTFYGGCGMGNGNFKSAEDCMRTC 55

RESULT 23
US-08-358-160-1
; Sequence 1, Application US/08358160
; Patent No. 5663143
; GENERAL INFORMATION:
; APPLICANT: LEY, Arthur C.
; APPLICANT: LADNER, Robert C.
; APPLICANT: GUTERMAN, Sonia K.
; APPLICANT: ROBERTS, Bruce L.
; APPLICANT: MARKLAND, William
; APPLICANT: KENT, Rachel B.
; TITLE OF INVENTION: ENGINEERED HUMAN-DERIVED KUNITZ

STREET: 419 Seventh Street, N.W. Suite 300
CITY: Washington
STATE: District of Columbia
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/358,160
FILING DATE: 16-DEC-1994
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/133,031
FILING DATE: 13-OCT-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/009,319
FILING DATE: 26-JAN-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/664,989
FILING DATE: 01-MAR-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/487,063
FILING DATE: 02-MAR-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/240,160
FILING DATE: 02-SEP-1988
ATTORNEY/AGENT INFORMATION:
NAME: Cooper, Iver P.
REGISTRATION NUMBER: 28,005
REFERENCE/DOCKET NUMBER: LEY=1
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
TELEX: 248633
INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
LENGTH: 58 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-358-160-26

Query Match 26.6%; Score 166; DB 1; Length 58;
Best Local Similarity 47.3%; Pred. No. 5e-10;
Matches 26; Conservative 8; Mismatches 21; Indels 0; Gaps 0;

QY 48 RKDSCMPQEAGPCLASIPHWYKTKICSEFIYGGCGNNNFQTEAICLVTC 102
Db 1 RPDFCLEPPYTGPCIAFFRYFYNAKAGLCQTFVYGGCGNGNFKSAEDCMRTC 55

RESULT 26
US-08-358-160-27
Sequence 27, Application US/08358160
Patent No. 5663143
GENERAL INFORMATION:
APPLICANT: LEV, Arthur C.
APPLICANT: LADNER, Robert C.
APPLICANT: GUTERMAN, Sonia K.
APPLICANT: ROBERTS, Bruce L.
APPLICANT: MARKLAND, William
APPLICANT: KENT, Rachel B.
TITLE OF INVENTION: ENGINEERED HUMAN-DERIVED KUNITZ
NUMBER OF INVENTION: DOMAINS THAT INHIBIT HUMAN NEUTROPHIL ELASTASE
NUMBER OF SEQUENCES: 234
CORRESPONDENCE ADDRESS:
ADDRESSER: BROWDY AND NEIMARK
STREET: 419 Seventh Street, N.W. Suite 300
CITY: Washington

STATE: District of Columbia
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/358,160
FILING DATE: 16-DEC-1994
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/133,031
FILING DATE: 13-OCT-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/009,319
FILING DATE: 26-JAN-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/664,989
FILING DATE: 01-MAR-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/487,063
FILING DATE: 02-MAR-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/240,160
FILING DATE: 02-SEP-1988
ATTORNEY/AGENT INFORMATION:
NAME: Cooper, Iver P.
REGISTRATION NUMBER: 28,005
REFERENCE/DOCKET NUMBER: LEY=1
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
TELEX: 248633
INFORMATION FOR SEQ ID NO: 27:
SEQUENCE CHARACTERISTICS:
LENGTH: 62 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-358-160-27

Query Match 26.6%; Score 166; DB 1; Length 62;
Best Local Similarity 47.3%; Pred. No. 5.4e-10;
Matches 26; Conservative 8; Mismatches 21; Indels 0; Gaps 0;

QY 48 RKDSCMPQEAGPCLASIPHWYKTKICSEFIYGGCGNNNFQTEAICLVTC 102
Db 5 RPDFCLEPPYTGPCIAFFRYFYNAKAGLCQTFVYGGCGNGNFKSAEDCMRTC 59

RESULT 27
US-09-270-767-46540
Sequence 46540, Application US/09270767
Patent No. 6703491
GENERAL INFORMATION:
APPLICANT: Homburger et al.
TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
FILE REFERENCE: File Reference: 7326-094
CURRENT APPLICATION NUMBER: US/09/270,767
CURRENT FILING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 62517
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 46540
LENGTH: 107
TYPE: PRT
ORGANISM: Drosophila melanogaster
US-09-270-767-46540
Query Match 26.6%; Score 166; DB 4; Length 107;
Best Local Similarity 39.1%; Pred. No. 9.4e-10;

Matches	27;	Conservative	12;	Mismatches	30;	Indels	0;	Gaps	0;
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36	DB	NYNCRQPGVLK	AKAIDICEIPAEV	GCANYVTSWY	YTDQDACVQFY	GGCGGNNRPF	95
96	QY	AICLVTCCK	104				
96	DB	ESCLARCDR	104				

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RESULT 29
US-08-358-160-24
; Sequence 24, Application US/08358160
; Patent No. 5663143
; GENERAL INFORMATION:
; APPLICANT: LEY, Arthur C.
; APPLICANT: LADNER, Robert C.
; APPLICANT: GUTERMAN, Sonia K.
; APPLICANT: ROBERTS, Bruce L.
; APPLICANT: MARKLAND, William
; APPLICANT: KENT, Rachel B.
; TITLE OF INVENTION: ENGINEERED HUMAN-DERIVED KUNITZ
; TITLE OF INVENTION: DOMAINS THAT INHIBIT HUMAN NEUTROPHIL ELASTASE
; NUMBER OF SEQUENCES: 234
; CORRESPONDENCE ADDRESS:
; ADDRESS: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W. Suite 300
; CITY: Washington
; STATE: District of Columbia
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/358,160
; FILING DATE: 16-DEC-1994
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/133,031
; FILING DATE: 13-OCT-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/009,319
; FILING DATE: 26-JAN-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/664,989
; FILING DATE: 01-MAR-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/487,063
; FILING DATE: 02-MAR-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/240,160
; FILING DATE: 02-SEP-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Cooper, Iver P.
; REGISTRATION NUMBER: 28,005
; REFERENCE/DOCKET NUMBER: LEY=1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; TELEX: 248633
; INFORMATION FOR SEQ ID NO: 24:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 58 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-358-160-24

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RESULT 30
US-08-358-160-9
; Sequence 9, Application US/08358160
; Patent No. 5663143
; GENERAL INFORMATION:
; APPLICANT: LEY, Arthur C.
; APPLICANT: LADNER, Robert C.
; APPLICANT: GUTERMAN, Sonia K.
; APPLICANT: ROBERTS, Bruce L.
; APPLICANT: MARKLAND, William
; APPLICANT: KENT, Rachel B.
; TITLE OF INVENTION: ENGINEERED HUMAN-DERIVED KUNITZ
; TITLE OF INVENTION: DOMAINS THAT INHIBIT HUMAN NEUTROPHIL ELASTASE
; NUMBER OF SEQUENCES: 234
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W. Suite 300
; CITY: Washington
; STATE: District of Columbia
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/358,160
; FILING DATE: 16-DEC-1994
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/133,031
; FILING DATE: 13-OCT-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/009,319
; FILING DATE: 26-JAN-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/664,989
; FILING DATE: 01-MAR-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/487,063
; FILING DATE: 02-MAR-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/240,160
; FILING DATE: 02-SEP-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Cooper, Iver P.
; REGISTRATION NUMBER: 28,005
; REFERENCE/DOCKET NUMBER: LEY=1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; TELEX: 248633
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 58 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-358-160-9

Query Match 26.2%; Score 164; DB 1; Length 58;
Best Local Similarity 48.2%; Pred. No. 8.1e-10;
Matches 27; Conservative 8; Mismatches 21; Indels 0; Gaps 0;

Qy 48 RKDSCMPQAGCPCLASIPHHWYNNKTKICSEFIYGGCGNNNFQTEAICLVTC 103
Db 1 KEDSQLGYSAGFCVAMPFRIFYNGTSMACETFIQGGCGNGNMFVTEKDLQTCR 56

RESULT 31
US-08-829-876-211
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; Sequence 211, Application US/08829876
; Patent No. 5962366
; GENERAL INFORMATION:
; APPLICANT: White, Tyler R.
; APPLICANT: Damm, Deborah
; APPLICANT: Lesikar, David D.
; APPLICANT: McFadden, Kathleen
; APPLICANT: Garrick, Brett L.
; TITLE OF INVENTION: PROTEASE INHIBITOR PEPTIDES
; NUMBER OF SEQUENCES: 228
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/829,876
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/436,555
; FILING DATE: 08-MAY-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Pelto, Don J.
; REGISTRATION NUMBER: 33,754
; REFERENCE/DOCKET NUMBER: 56324/106/SCNO
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 211:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 61 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-829-876-211

Query Match 26.2%; Score 164; DB 2; Length 61;
Best Local Similarity 46.3%; Pred. No. 8.5e-10;
Matches 25; Conservative 9; Mismatches 20; Indels 0; Gaps 0;

Qy 49 KDICMPQAGCPCLASIPHHWYNNKTKICSEFIYGGCGNNNFQTEAICLVTC 102
Db 4 REVCSEAETGCPRAAIQHMYFDVTEGKCAFPFYGGCGNNRNFDTTEYCNVAV 57

RESULT 32
US-08-829-876-214
; Sequence 214, Application US/08829876
; Patent No. 5962266
; GENERAL INFORMATION:
; APPLICANT: White, Tyler R.
; APPLICANT: Damm, Deborah
; APPLICANT: Lesikar, David D.
; APPLICANT: McFadden, Kathleen
; APPLICANT: Garrick, Brett L.
; TITLE OF INVENTION: PROTEASE INHIBITOR PEPTIDES
; NUMBER OF SEQUENCES: 228
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
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;
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/829,876
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/436,555
; FILING DATE: 08-MAY-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Peltó, Don J.
; REGISTRATION NUMBER: 33,754
; REFERENCE/DOCKET NUMBER: 56324/106/SCNO
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 214:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 61 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-829-876-214

Query Match 26.2%; Score 164; DB 2; Length 61;
Best Local Similarity 46.3%; Pred. No. 8.5e-10;
Matches 25; Conservative 9; Mismatches 20; Indels 0; Gaps 0;

QY 49 KDICMPQAGPCLASIPHWNTKTKICSEFIYGCQGNNNFQTEAICLVTC 102
Db 4 REVCSQAETGCRALIPRWYFDVTEGKCAPFFYGCGRNNRNFDTTEYCMAVC 57

RESULT 33
US-09-234-874A-211
; Sequence 211, Application US/09234874A
; Patent No. 6376648
; GENERAL INFORMATION:
; APPLICANT: White, Tyler R.
; Lesikar, David D.
; McFadden, Kathleen
; Garrick, Brett L.
; TITLE OF INVENTION: PROTEASE INHIBITOR PEPTIDES
; NUMBER OF SEQUENCES: 228
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/234,874A
; FILING DATE: 11-Jun-2001
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/436,555
; FILING DATE: 08-MAY-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Bent, Stephen
; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 056324/0106
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 214:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 61 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; APPLICATION NUMBER: 08/436,555
; FILING DATE: 08-MAY-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Bent, Stephen
; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 056324/0106

```

```

;
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 211:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 61 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 211:
US-09-234-874A-211

Query Match 26.2%; Score 164; DB 3; Length 61;
Best Local Similarity 46.3%; Pred. No. 8.5e-10;
Matches 25; Conservative 9; Mismatches 20; Indels 0; Gaps 0;

QY 49 KDICMPQAGPCLASIPHWNTKTKICSEFIYGCQGNNNFQTEAICLVTC 102
Db 4 REVCSQAETGCRALIPRWYFDVTEGKCAPFFYGCGRNNRNFDTTEYCMAVC 57

RESULT 34
US-09-234-874A-214
; Sequence 214, Application US/09234874A
; Patent No. 6376648
; GENERAL INFORMATION:
; APPLICANT: White, Tyler R.
; Damm, Deborah
; Lesikar, David D.
; McFadden, Kathleen
; Garrick, Brett L.
; TITLE OF INVENTION: PROTEASE INHIBITOR PEPTIDES
; NUMBER OF SEQUENCES: 228
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/234,874A
; FILING DATE: 11-Jun-2001
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/436,555
; FILING DATE: 08-MAY-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Bent, Stephen
; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 056324/0106
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 214:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 61 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 214:
US-09-234-874A-214

Query Match 26.2%; Score 164; DB 3; Length 61;
Best Local Similarity 46.3%; Pred. No. 8.5e-10;

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APPLICANT: White, Tyler R.
Damm, Deborah

ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORDPERFECT 4.2
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/664,989B
FILING DATE: 19910301
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US89/03731
FILING DATE: 01-SEP-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/487,063
FILING DATE: 02-MAR-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/240,160
FILING DATE: 02-SEP-1988
ATTORNEY/AGENT INFORMATION:
NAME: Cooper, Iver P.
REGISTRATION NUMBER: 28005
REFERENCE/DOCKET NUMBER: LADNER 7
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
INFORMATION FOR SEQ ID NO: 84:
SEQUENCE CHARACTERISTICS:
LENGTH: 58 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear
MOLECULE TYPE: protein
US-07-664-989B-84

Query Match 26.1%; Score 163; DB 1; Length 58;

Best Local Similarity 47.3%; Pred. No. 1e-09;
Matches 26; Conservative 8; Mismatches 21; Indels 0; Gaps 0;

QY 48 RKDICSMPQAGPCLASIPHWYKTKICSEFIYGGCGQNNNFOTEICLVTC 102
DB 1 RPDFCLPPYTGPCVAMFPFYFNAGLQTFMYGGCGQKGNFNFKASDCMRTC 55

RESULT 38

US-08-358-160-12

; Sequence 12, Application US/08358160

; Patent No. 5663143

; GENERAL INFORMATION:

; APPLICANT: LEY, Arthur C.

; APPLICANT: LADNER, Robert C.

; APPLICANT: GUTERMAN, Sonia K.

; APPLICANT: ROBERTS, Bruce L.

; APPLICANT: MARKLAND, William

; APPLICANT: KENT, Rachel B.

; TITLE OF INVENTION: ENGINEERED HUMAN-DERIVED KUNITZ

; TITLE OF INVENTION: DOMAINS THAT INHIBIT HUMAN NEUTROPHIL ELASTASE

; NUMBER OF SEQUENCES: 234

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: BROWDY AND NEIMARK

; STREET: 419 Seventh Street, N.W. Suite 300

; CITY: Washington

; STATE: District of Columbia

; COUNTRY: USA

; ZIP: 20004

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/358,160

; FILING DATE: 16-DEC-1994

; CLASSIFICATION: 514

; PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/133,031
FILING DATE: 13-OCT-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/009,319
FILING DATE: 26-JAN-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/664,989
FILING DATE: 01-MAR-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/487,063
FILING DATE: 02-MAR-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/240,160
FILING DATE: 02-SEP-1988
ATTORNEY/AGENT INFORMATION:
NAME: Cooper, Iver P.
REGISTRATION NUMBER: 28,005
REFERENCE/DOCKET NUMBER: LEY=1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
TELEX: 248633
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 58 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-358-160-12

Query Match 26.1%; Score 163; DB 1; Length 58;

Best Local Similarity 48.2%; Pred. No. 1e-09;
Matches 27; Conservative 6; Mismatches 23; Indels 0; Gaps 0;

QY 48 RKDICSMPQAGPCLASIPHWYKTKICSEFIYGGCGQNNNFOTEICLVTC 103
DB 1 RPDFCQLGYSTGPCVAMFPFYFNAGLQTFMYGGCGMGNFNFTVKDCLQTCR 56

RESULT 39

US-08-358-160-61

; Sequence 61, Application US/08358160

; Patent No. 5663143

; GENERAL INFORMATION:

; APPLICANT: LEY, Arthur C.

; APPLICANT: LADNER, Robert C.

; APPLICANT: GUTERMAN, Sonia K.

; APPLICANT: ROBERTS, Bruce L.

; APPLICANT: MARKLAND, William

; APPLICANT: KENT, Rachel B.

; TITLE OF INVENTION: ENGINEERED HUMAN-DERIVED KUNITZ

; TITLE OF INVENTION: DOMAINS THAT INHIBIT HUMAN NEUTROPHIL ELASTASE

; NUMBER OF SEQUENCES: 234

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: BROWDY AND NEIMARK

; STREET: 419 Seventh Street, N.W. Suite 300

; CITY: Washington

; STATE: District of Columbia

; COUNTRY: USA

; ZIP: 20004

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/358,160

; FILING DATE: 16-DEC-1994

; CLASSIFICATION: 514

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/133,031

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;
; FILING DATE: 13-OCT-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/009,319
; FILING DATE: 26-JAN-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/664,989
; FILING DATE: 01-MAR-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/487,063
; FILING DATE: 02-MAR-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/240,160
; FILING DATE: 02-SEP-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Cooper, Iver P.
; REGISTRATION NUMBER: 28,005
; REFERENCE/DOCKET NUMBER: LEY=1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; TELEX: 248633
; INFORMATION FOR SEQ ID NO: 61:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 58 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-358-160-61

Query Match 26.1%; Score 163; DB 1; Length 58;
Best Local Similarity 47.3%; Pred. No. 1e-09;
Matches 26; Conservative 8; Mismatches 21; Indels 0; Gaps 0;

QY 48 RDCISMPOEAGPCLASIPHWYNNKTKICSEFIYGGCGGNNNFQTEAICLVTC 102
Db 1 RPDFCLEPPYTCVAMPFRPYNAKAGLCQTFMYGGCGKGNFKSAEDCMRTC 55

RESULT 40
US-08-463-155A-56
; Sequence 56, Application US/08463155A
; Patent No. 5780265
; GENERAL INFORMATION:
; APPLICANT: Dennis, Mark S.
; APPLICANT: Lazarus, Robert A.
; TITLE OF INVENTION: KUNITZ TYPE PLASMA KALLIKREIN INHIBITORS
; NUMBER OF SEQUENCES: 72
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/463,155A
; FILING DATE: 05-Jun-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Kubinec, Jeffrey S.
; REGISTRATION NUMBER: 36,575
; REFERENCE/DOCKET NUMBER: P0944-2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/225-8228
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 56:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 58 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
; US-08-358-160-61

Query Match 26.1%; Score 163; DB 1; Length 58;
Best Local Similarity 47.3%; Pred. No. 1e-09;
Matches 26; Conservative 8; Mismatches 21; Indels 0; Gaps 0;

QY 48 RDCISMPOEAGPCLASIPHWYNNKTKICSEFIYGGCGGNNNFQTEAICLVTC 102
Db 1 RPDFCLEPPYTCVAMPFRPYNAKAGLCQTFMYGGCGKGNFKSAEDCMRTC 55

RESULT 40
US-08-463-155A-56
; Sequence 56, Application US/08463155A
; Patent No. 5780265
; GENERAL INFORMATION:
; APPLICANT: Dennis, Mark S.
; APPLICANT: Lazarus, Robert A.
; TITLE OF INVENTION: KUNITZ TYPE PLASMA KALLIKREIN INHIBITORS
; NUMBER OF SEQUENCES: 72
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/463,155A
; FILING DATE: 05-Jun-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Kubinec, Jeffrey S.
; REGISTRATION NUMBER: 36,575
; REFERENCE/DOCKET NUMBER: P0944
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/225-8228
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 56:
; TITLE OF INVENTION: INHIBITORS OF HUMAN PLASMIN DERIVED
; FROM FROM THE KUNITZ DOMAINS
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; SEQUENCE CHARACTERISTICS:
; LENGTH: 58 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
; US-08-463-155A-56

Query Match 26.1%; Score 163; DB 1; Length 58;
Best Local Similarity 48.1%; Pred. No. 1e-09;
Matches 26; Conservative 8; Mismatches 20; Indels 0; Gaps 0;

QY 49 KDICSMPOEAGPCLASIPHWYNNKTKICSEFIYGGCGGNNNFQTEAICLVTC 102
Db 2 REVCEQAEDGFCRAAIPRWYFDVTEGKCAPFIYGGCGGNRNFDTTEYCAAVC 55

RESULT 41
US-08-463-432B-56
; Sequence 56, Application US/08463432B
; Patent No. 5786328
; GENERAL INFORMATION:
; APPLICANT: Dennis, Mark S.
; APPLICANT: Lazarus, Robert A.
; TITLE OF INVENTION: KUNITZ TYPE PLASMA KALLIKREIN INHIBITORS
; NUMBER OF SEQUENCES: 72
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/463,432B
; FILING DATE: 05-Jun-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Kubinec, Jeffrey S.
; REGISTRATION NUMBER: 36,575
; REFERENCE/DOCKET NUMBER: P0944-2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/225-8228
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 56:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 58 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
; US-08-463-432B-56

Query Match 26.1%; Score 163; DB 1; Length 58;
Best Local Similarity 48.1%; Pred. No. 1e-09;
Matches 26; Conservative 8; Mismatches 20; Indels 0; Gaps 0;

QY 49 KDICSMPOEAGPCLASIPHWYNNKTKICSEFIYGGCGGNNNFQTEAICLVTC 102
Db 2 REVCEQAEDGFCRAAIPRWYFDVTEGKCAPFIYGGCGGNRNFDTTEYCAAVC 55

RESULT 42
US-08-676-124-69
; Sequence 69, Application US/08676124
; Patent No. 6010880
; GENERAL INFORMATION:
; APPLICANT: MARKLAND, William
; APPLICANT: LADNER, Robert Charles
; TITLE OF INVENTION: INHIBITORS OF HUMAN PLASMIN DERIVED
; FROM FROM THE KUNITZ DOMAINS
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RESULT 48

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; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/234,874A
; FILING DATE: 11-Jun-2001
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/436,555
; FILING DATE: 08-MAY-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Bent, Stephen
; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 056324/0106
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 218:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 61 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 218:
US-09-234-874A-218

Query Match 26.1%; Score 163; DB 3; Length 61;
Best Local Similarity 46.3%; Pred. No. 1.1e-09;
Matches 25; Conservative 10; Mismatches 19; Indels 0; Gaps 0;

Qy 49 KDICMPQEGPCLASIPHWYNNKTKICSEFIYGGCGGNNNFQTEAICLVTC 102
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4 REVSCQAEGPCRAAIYHWYFDVTEGKCAPFFYGGCGGNRNNFDTBYCMAVC 57

RESULT 50
US-09-234-873A-180
; Sequence 180, Application US/09234873A
; Patent No. 6613890
; GENERAL INFORMATION:
; APPLICANT: White, Tyler R.
; Damm, Deborah
; Lesikar, David D.
; McFadden, Kathleen
; Garrick, Brett L.
; TITLE OF INVENTION: PROTEASE INHIBITOR PEPTIDES
; NUMBER OF SEQUENCES: 228
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/234,873A
; FILING DATE: 21-Jan-1999
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/829,876
; FILING DATE: 02-APR-1997
; APPLICATION NUMBER: 08/436,555
; FILING DATE: 08-MAY-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Bent, Stephen
; REGISTRATION NUMBER: 29,768
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;
; REFERENCE/DOCKET NUMBER: 056324/0116
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 180:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 61 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 180:
US-09-234-873A-180

Query Match 26.1%; Score 163; DB 4; Length 61;
Best Local Similarity 46.3%; Pred. No. 1.1e-09;
Matches 25; Conservative 8; Mismatches 21; Indels 0; Gaps 0;

Qy 49 KDICMPQEGPCLASIPHWYNNKTKICSEFIYGGCGGNNNFQTEAICLVTC 102
Db :::|||:|||||:|||||:|||||:|||||:|||||:|||||:|
4 REVSCQAETGCRAGIPRWYFDVTEGKCAPFFYGGCGGNRNNFDTBYCMAVC 57

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Job time : 20.3864 secs
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 21, 2005, 16:33:14 ; Search time 66.2891 Seconds
(without alignments)
650.835 Million cell updates/sec

Title: US-10-807-204-2

Perfect score: 625

Sequence: 1 EGILGKPCPKIKVECEVEEI.....GNNNNFQTEAICLVCTCKYH 106

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1826521 seqs, 407012169 residues

Total number of hits satisfying chosen parameters: 1826521

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 50 summaries

Database : Published Applications AA.*

- 1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep.*
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- 12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep.*
- 13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep.*
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- 17: /cgn2_6/ptodata/2/pubpaa/US10E_PUBCOMB.pep.*
- 18: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep.*
- 19: /cgn2_6/ptodata/2/pubpaa/US11A_PUBCOMB.pep.*
- 20: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep.*
- 21: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*
- 22: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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3	625	100.0	131	16	US-10-807-204-12
4	603	96.5	131	16	US-10-807-204-15
5	423	67.7	98	16	US-10-807-204-9
6	415	66.6	136	16	US-10-807-204-16
7	401.5	64.2	117	9	US-09-852-659A-119
8	401.5	64.2	117	15	US-10-058-993-120
9	400	64.0	102	9	US-09-852-659A-120
10	400	64.0	102	15	US-10-058-993-121
11	400	64.0	133	9	US-09-853-161-75

12	400	64.0	133	9	US-09-852-659A-75
13	400	64.0	133	9	US-09-852-797-75
14	400	64.0	133	15	US-10-058-993-75
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18	276	44.2	101	15	US-10-276-774-2606
19	258	41.3	43	16	US-10-807-204-5
20	236	37.8	58	16	US-10-361-997-5
21	236	37.8	58	17	US-10-931-153-21
22	219	35.0	51	15	US-10-058-993-118
23	197	31.5	759	17	US-10-825-692-48
24	184	29.4	64	10	US-09-896-095-160
25	184	29.4	64	14	US-10-038-722-103
26	184	29.4	64	15	US-10-115-134-17
27	182.5	29.2	571	14	US-10-369-736-3
28	182.5	29.2	571	14	US-10-369-736-49
29	182.5	29.2	571	14	US-10-369-738-3
30	182.5	29.2	571	14	US-10-369-738-49
31	182.5	29.2	571	19	US-11-028-058-3
32	182.5	29.2	571	19	US-11-028-058-49
33	180	28.8	33	16	US-10-807-204-7
34	180	28.8	33	16	US-10-807-204-10
35	177	28.3	58	14	US-10-038-722-5
36	175	28.0	67	10	US-09-896-095-147
37	175	28.0	67	14	US-10-038-722-90
38	175	28.0	67	15	US-10-115-134-4
39	173.5	27.8	503	14	US-10-007-280A-233
40	173.5	27.8	576	9	US-09-794-589-2
41	173.5	27.8	576	14	US-10-315-380-2
42	173.5	27.8	576	14	US-10-369-736-7
43	173.5	27.8	576	14	US-10-369-738-7
44	173.5	27.8	576	19	US-11-028-058-7
45	173.5	27.8	640	14	US-10-369-736-5
46	173.5	27.8	640	14	US-10-369-738-5
47	173.5	27.8	640	19	US-11-028-058-5
48	173	27.7	58	14	US-10-038-722-17
49	173	27.7	58	14	US-10-038-722-18
50	173	27.7	58	14	US-10-038-722-19

ALIGNMENTS

RESULT 1
US-10-807-204-2
; Sequence 2, Application US/10807204
; Publication No. US20040229312A1
; GENERAL INFORMATION:
; APPLICANT: Bougueleret, Lydie
; APPLICANT: Bairoch, Amos
; APPLICANT: Niknejad, Anne
; TITLE OF INVENTION: Engineered Human Kunitz-Type Protease
; TITLE OF INVENTION: Inhibitor
; FILE REFERENCE: 54720-8015.US00
; CURRENT APPLICATION NUMBER: US/10/807,204
; CURRENT FILING DATE: 2004-03-22
; PRIOR APPLICATION NUMBER: PCT/EP03/01629
; PRIOR FILING DATE: 2003-02-18
; PRIOR APPLICATION NUMBER: US 60/358,683
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 106
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (1)...(106)
; OTHER INFORMATION: mature form
; FEATURE:
; NAME/KEY: DOMAIN

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; LOCATION: (52)...(102)
; OTHER INFORMATION: Kunitz domain predicted by pfscan
; FEATURE:
; NAME/KEY: DISULFID
; LOCATION: (8)...(36)
; OTHER INFORMATION: predicted disulfide bond
; FEATURE:
; NAME/KEY: DISULFID
; LOCATION: (15)...(40)
; OTHER INFORMATION: predicted disulfide bond
; FEATURE:
; NAME/KEY: DISULFID
; LOCATION: (23)...(35)
; OTHER INFORMATION: predicted disulfide bond
; FEATURE:
; NAME/KEY: DISULFID
; LOCATION: (29)...(44)
; OTHER INFORMATION: predicted disulfide bond
; FEATURE:
; NAME/KEY: DISULFID
; LOCATION: (52)...(102)
; OTHER INFORMATION: predicted disulfide bond
; FEATURE:
; NAME/KEY: DISULFID
; LOCATION: (61)...(85)
; OTHER INFORMATION: predicted disulfide bond
; FEATURE:
; NAME/KEY: DISULFID
; LOCATION: (77)...(98)
; OTHER INFORMATION: predicted disulfide bond
US-10-807-204-2

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Query Match          100.0%; Score 625; DB 16; Length 106;
Best Local Similarity 100.0%; Pred. No. 1.4e-52;
Matches 106; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EGILGKPCPKIKVECEVEEIDQCTKPRDCPENMKCCPFCGKGLDFRDKDICSMPQEAGP 60
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
DB 1 EGILGKPCPKIKVECEVEEIDQCTKPRDCPENMKCCPFCGKGLDFRDKDICSMPQEAGP 60
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||

QY 61 CLASIPHWYNNKTKICSEFIYGGCGQNNNNNFQTEAICLVTCCKYH 106
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
DB 61 CLASIPHWYNNKTKICSEFIYGGCGQNNNNNFQTEAICLVTCCKYH 106
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||

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RESULT 2
US-10-807-204-1
; Sequence 1, Application US/10807204
; Publication No. US20040229312A1
; GENERAL INFORMATION:
; APPLICANT: Bougueleret, Lydie
; APPLICANT: Bairoch, Amos
; APPLICANT: Niknejad, Anne
; TITLE OF INVENTION: Engineered Human Kunitz-Type Protease
; TITLE OF INVENTION: Inhibitor
; FILE REFERENCE: 54720-8015.US00
; CURRENT APPLICATION NUMBER: US/10/807,204
; PRIOR FILING DATE: 2004-03-22
; PRIOR APPLICATION NUMBER: PCT/EP03/01629
; PRIOR FILING DATE: 2003-02-18
; PRIOR APPLICATION NUMBER: US 60/358,683
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 131
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (1)...(131)
; OTHER INFORMATION: eppin-like precursor
; FEATURE:

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; NAME/KEY: SIGNAL
; LOCATION: (1)...(25)
; OTHER INFORMATION: predicted by SignalP 2.0
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (26)...(131)
; OTHER INFORMATION: mature peptide
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (77)...(127)
; OTHER INFORMATION: Kunitz domain predicted by pfscan
; FEATURE:
; NAME/KEY: DISULFID
; LOCATION: (33)...(61)
; OTHER INFORMATION: predicted disulfide bond
; FEATURE:
; NAME/KEY: DISULFID
; LOCATION: (40)...(65)
; OTHER INFORMATION: predicted disulfide bond
; FEATURE:
; NAME/KEY: DISULFID
; LOCATION: (48)...(60)
; OTHER INFORMATION: predicted disulfide bond
; FEATURE:
; NAME/KEY: DISULFID
; LOCATION: (54)...(69)
; OTHER INFORMATION: predicted disulfide bond
; FEATURE:
; NAME/KEY: DISULFID
; LOCATION: (77)...(127)
; OTHER INFORMATION: predicted disulfide bond
; FEATURE:
; NAME/KEY: DISULFID
; LOCATION: (86)...(110)
; OTHER INFORMATION: predicted disulfide bond
; FEATURE:
; NAME/KEY: DISULFID
; LOCATION: (102)...(123)
; OTHER INFORMATION: predicted disulfide bond
US-10-807-204-1

Query Match          100.0%; Score 625; DB 16; Length 131;
Best Local Similarity 100.0%; Pred. No. 1.8e-52;
Matches 106; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EGILGKPCPKIKVECEVEEIDQCTKPRDCPENMKCCPFCGKGLDFRDKDICSMPQEAGP 60
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
DB 26 EGILGKPCPKIKVECEVEEIDQCTKPRDCPENMKCCPFCGKGLDFRDKDICSMPQEAGP 85
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||

QY 61 CLASIPHWYNNKTKICSEFIYGGCGQNNNNNFQTEAICLVTCCKYH 106
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
DB 86 CLASIPHWYNNKTKICSEFIYGGCGQNNNNNFQTEAICLVTCCKYH 131
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||

RESULT 3
US-10-807-204-12
; Sequence 12, Application US/10807204
; Publication No. US20040229312A1
; GENERAL INFORMATION:
; APPLICANT: Bougueleret, Lydie
; APPLICANT: Bairoch, Amos
; APPLICANT: Niknejad, Anne
; TITLE OF INVENTION: Engineered Human Kunitz-Type Protease
; TITLE OF INVENTION: Inhibitor
; FILE REFERENCE: 54720-8015.US00
; CURRENT APPLICATION NUMBER: US/10/807,204
; CURRENT FILING DATE: 2004-03-22
; PRIOR APPLICATION NUMBER: PCT/EP03/01629
; PRIOR FILING DATE: 2003-02-18
; PRIOR APPLICATION NUMBER: US 60/358,683
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: FastSeq for Windows Version 4.0

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; SEQ ID NO 12
; LENGTH: 131
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-807-204-12

Query Match      100.0%; Score 625; DB 16; Length 131;
Best Local Similarity 100.0%; Pred. No. 1.8e-52;
Matches 106; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EGILGKPCPKIKVECEVEEIDQCTKPRDCPENMKCCPFCGKKCLDFRDKDICSMPQEAGP 60
Db 26 EGILGKPCPKIKVECEVEEIDQCTKPRDCPENMKCCPFCGKKCLDFRDKDICSMPQEAGP 85

QY 61 CLASIPHHWYNNKTKICSEFIYGGCGNNNNFQTEAICLVTCCKYH 106
Db 86 CLASIPHHWYNNKTKICSEFIYGGCGNNNNFQTEAICLVTCCKYH 131

RESULT 4
US-10-807-204-15
; Sequence 15, Application US/10807204
; Publication No. US20040229312A1
; GENERAL INFORMATION:
; APPLICANT: Bougueleret, Lydie
; APPLICANT: Bairoch, Amos
; APPLICANT: Niknejad, Anne
; TITLE OF INVENTION: Engineered Human Kunitz-Type Protease
; TITLE OF INVENTION: Inhibitor
; FILE REFERENCE: 54720-8015.US00
; CURRENT APPLICATION NUMBER: US/10/807,204
; PRIOR FILING DATE: 2004-03-22
; PRIOR APPLICATION NUMBER: PCT/EP03/01629
; PRIOR FILING DATE: 2003-02-18
; PRIOR APPLICATION NUMBER: US 60/358,683
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15
; LENGTH: 131
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-807-204-15

Query Match      96.5%; Score 603; DB 16; Length 131;
Best Local Similarity 98.1%; Pred. No. 2.3e-50;
Matches 104; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 EGILGKPCPKIKVECEVEEIDQCTKPRDCPENMKCCPFCGKKCLDFRDKDICSMPQEAGP 60
Db 26 EGILGKPCPKIKVECEVEEIDQCTKPRDCPENMKCCPFCGKKCLDFRDKDICSMPQEAGP 85

QY 61 CLASIPHHWYNNKTKICSEFIYGGCGNNNNFQTEAICLVTCCKYH 106
Db 86 CLASIPHHWYNNKTKICSEFIYGGCGNNNNFQTEAICLVTCCKYH 131

RESULT 5
US-10-807-204-9
; Sequence 9, Application US/10807204
; Publication No. US20040229312A1
; GENERAL INFORMATION:
; APPLICANT: Bougueleret, Lydie
; APPLICANT: Bairoch, Amos
; APPLICANT: Niknejad, Anne
; TITLE OF INVENTION: Engineered Human Kunitz-Type Protease
; TITLE OF INVENTION: Inhibitor
; FILE REFERENCE: 54720-8015.US00
; CURRENT APPLICATION NUMBER: US/10/807,204
; PRIOR FILING DATE: 2004-03-22
; PRIOR APPLICATION NUMBER: PCT/EP03/01629
; PRIOR FILING DATE: 2003-02-18
; PRIOR APPLICATION NUMBER: US 60/358,683
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; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 98
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-807-204-9

Query Match      67.7%; Score 423; DB 16; Length 98;
Best Local Similarity 98.6%; Pred. No. 3.9e-33;
Matches 72; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 EGILGKPCPKIKVECEVEEIDQCTKPRDCPENMKCCPFCGKKCLDFRDKDICSMPQEAGP 60
Db 26 EGILGKPCPKIKVECEVEEIDQCTKPRDCPENMKCCPFCGKKCLDFRDKDICSMPQEAGP 85

QY 61 CLASIPHHWYNNK 73
Db 86 CLASIPHHWYNNK 98

RESULT 6
US-10-807-204-16
; Sequence 16, Application US/10807204
; Publication No. US20040229312A1
; GENERAL INFORMATION:
; APPLICANT: Bougueleret, Lydie
; APPLICANT: Bairoch, Amos
; APPLICANT: Niknejad, Anne
; TITLE OF INVENTION: Engineered Human Kunitz-Type Protease
; TITLE OF INVENTION: Inhibitor
; FILE REFERENCE: 54720-8015.US00
; CURRENT APPLICATION NUMBER: US/10/807,204
; CURRENT FILING DATE: 2004-03-22
; PRIOR APPLICATION NUMBER: PCT/EP03/01629
; PRIOR FILING DATE: 2003-02-18
; PRIOR APPLICATION NUMBER: US 60/358,683
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 16
; LENGTH: 136
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-807-204-16

Query Match      66.6%; Score 416; DB 16; Length 136;
Best Local Similarity 60.6%; Pred. No. 2.5e-32;
Matches 63; Conservative 20; Mismatches 21; Indels 0; Gaps 0;

QY 1 EGILGKPCPKIKVECEVEEIDQCTKPRDCPENMKCCPFCGKKCLDFRDKDICSMPQEAGP 60
Db 26 EGFFRTCTPRVVKCEVERNECTRHQCPCNKKRCCFLCFCGKKCLDFRDKDICSMPQEAGP 85

QY 61 CLASIPHHWYNNKTKICSEFIYGGCGNNNNFQTEAICLVTCCK 104
Db 86 CLAYLPRWYNNQETDLCTEFYGGCGNNNNFSEIGICTVWCCK 129

RESULT 7
US-09-852-659A-119
; Sequence 119, Application US/09852659A
; Patent No. US2002007287A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 28 Human Secreted Proteins
; FILE REFERENCE: P2003P4
; CURRENT APPLICATION NUMBER: US/09/852,659A
; CURRENT FILING DATE: 2001-05-11
; PRIOR APPLICATION NUMBER: 60/265,583
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: 09/152,060
```

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; PRIOR FILING DATE: 1998-09-11
; PRIOR APPLICATION NUMBER: PCT/US98/04858
; PRIOR FILING DATE: 1998-03-12
; PRIOR APPLICATION NUMBER: 60/040,762
; PRIOR FILING DATE: 1997-03-14
; PRIOR APPLICATION NUMBER: 60/040,710
; PRIOR FILING DATE: 1997-03-14
; PRIOR APPLICATION NUMBER: 60/050,934
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/048,100
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/048,357
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/048,189
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/057,765
; PRIOR FILING DATE: 1997-09-05
; PRIOR APPLICATION NUMBER: 60/048,970
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/068,368
; PRIOR FILING DATE: 1997-12-19
; NUMBER OF SEQ ID NOS: 121
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 119
; LENGTH: 117
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-852-659A-119

Query Match      64.2%; Score 401.5; DB 9; Length 117;
Best Local Similarity 66.0%; Pred. No. 5.4e-31;
Matches 66; Conservative 12; Mismatches 21; Indels 1; Gaps 1;

Qy  4 LGKCPKIKVCEVEEIDQCTKPRDCPENMKCCPFSCGKKCLDFRKDTCSPMPQAGPCLA 63
    ||: ||||: |||: |||: |||: ||||| ||||| ||||| ||||| ||||| |||||
Db  14 LGR-CPKIRECEFEQERDVCTKDRQCQDNKKCCVFCGKKCLDLKQDVCEMPKETGPCLA 72
    ||: ||||: |||: |||: |||: ||||| ||||| ||||| ||||| ||||| |||||
Qy  64 SIPHWYNNKTKICSEFYGGCGNNGNNNFOTEALCLVTCK 103
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db  73 YFLHWYDKKONTCSMFYGGCGNNGNNNFQSKANCLNTCK 112
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

RESULT 8
US-10-058-993-120
; Sequence 120, Application US/10058993
; Publication No. US20030225009A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 28 Human Secreted Proteins
; FILE REFERENCE: P2003P5
; CURRENT APPLICATION NUMBER: US/10/058,993
; CURRENT FILING DATE: 2002-01-30
; PRIOR APPLICATION NUMBER: 09/852,659
; PRIOR FILING DATE: 2001-05-11
; PRIOR APPLICATION NUMBER: 09/852,797
; PRIOR FILING DATE: 2001-05-11
; PRIOR APPLICATION NUMBER: 09/853,161
; PRIOR FILING DATE: 2001-05-11
; PRIOR APPLICATION NUMBER: 60/265,583
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: 09/152,060
; PRIOR FILING DATE: 1998-09-11
; PRIOR APPLICATION NUMBER: PCT/US98/04858
; PRIOR FILING DATE: 1998-03-12
; PRIOR APPLICATION NUMBER: 60/068,368
; PRIOR FILING DATE: 1997-12-19
; PRIOR APPLICATION NUMBER: 60/057,765
; PRIOR FILING DATE: 1997-09-05
; PRIOR APPLICATION NUMBER: 60/048,970
; PRIOR FILING DATE: 1997-06-05
; PRIOR APPLICATION NUMBER: 60/040,934
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/048,100
```

```
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/048,189
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/048,357
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/040,710
; PRIOR FILING DATE: 1997-03-14
; PRIOR APPLICATION NUMBER: 60/040,762
; PRIOR FILING DATE: 1997-03-14
; NUMBER OF SEQ ID NOS: 122
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 120
; LENGTH: 117
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-058-993-120

Query Match      64.2%; Score 401.5; DB 15; Length 117;
Best Local Similarity 66.0%; Pred. No. 5.4e-31;
Matches 66; Conservative 12; Mismatches 21; Indels 1; Gaps 1;

Qy  4 LGKCPKIKVCEVEEIDQCTKPRDCPENMKCCPFSCGKKCLDFRKDTCSPMPQAGPCLA 63
    ||: ||||: |||: |||: |||: ||||| ||||| ||||| ||||| ||||| |||||
Db  14 LGR-CPKIRECEFEQERDVCTKDRQCQDNKKCCVFCGKKCLDLKQDVCEMPKETGPCLA 72
    ||: ||||: |||: |||: |||: ||||| ||||| ||||| ||||| ||||| |||||
Qy  64 SIPHWYNNKTKICSEFYGGCGNNGNNNFOTEALCLVTCK 103
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db  73 YFLHWYDKKONTCSMFYGGCGNNGNNNFQSKANCLNTCK 112
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

RESULT 9
US-09-852-659A-120
; Sequence 120, Application US/09852659A
; Patent No. US20020077287A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 28 Human Secreted Proteins
; FILE REFERENCE: P2003P4
; CURRENT APPLICATION NUMBER: US/09/852,659A
; CURRENT FILING DATE: 2001-05-11
; PRIOR APPLICATION NUMBER: 60/265,583
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: 09/152,060
; PRIOR FILING DATE: 1998-09-11
; PRIOR APPLICATION NUMBER: PCT/US98/04858
; PRIOR FILING DATE: 1998-03-12
; PRIOR APPLICATION NUMBER: 60/040,762
; PRIOR FILING DATE: 1997-03-14
; PRIOR APPLICATION NUMBER: 60/040,710
; PRIOR FILING DATE: 1997-03-14
; PRIOR APPLICATION NUMBER: 60/050,934
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/048,100
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/048,357
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/048,189
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/057,765
; PRIOR FILING DATE: 1997-09-05
; PRIOR APPLICATION NUMBER: 60/048,970
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/068,368
; PRIOR FILING DATE: 1997-12-19
; NUMBER OF SEQ ID NOS: 121
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 120
; LENGTH: 102
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-852-659A-120

Query Match      64.0%; Score 400; DB 9; Length 102;
```

Best Local Similarity 66.7%; Pred. No. 6.6e-31; Mismatches 21; Indels 0; Gaps 0;
Matches 64; Conservative 11; Mismatches 21; Indels 0; Gaps 0;
QY 8 CPKIVCEVEEIDQCTKPRDCPENMKCCPFSCGKKCLDFRDKDICSMPQOAGPCLASIPH 67
Db 2 CPKIRECEFEQERDVCTKRDQCQDNKKCCVFCGKKCLDLKQDVCMPKGTGCLAYFLH 61
QY 68 WYNNKTKICSEFIYGGCGNNNNFQTEAICLVTK 103
Db 62 WYDKDNTCSMFVYGGCGNNNNFQSKANCLNTCK 97
RESULT 10
US-10-058-993-121
; Sequence 121, Application US/10058993
; Patent No. US20030225009A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 28 Human Secreted Proteins
; FILE REFERENCE: PZ003P5
; CURRENT APPLICATION NUMBER: US/10/058,993
; CURRENT FILING DATE: 2002-01-30
; PRIOR APPLICATION NUMBER: 09/852,659
; PRIOR FILING DATE: 2001-05-11
; PRIOR APPLICATION NUMBER: 09/852,797
; PRIOR FILING DATE: 2001-05-11
; PRIOR APPLICATION NUMBER: 09/853,161
; PRIOR FILING DATE: 2001-05-11
; PRIOR APPLICATION NUMBER: 60/265,583
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: 60/048,710
; PRIOR FILING DATE: 1997-03-14
; PRIOR APPLICATION NUMBER: 60/068,368
; PRIOR FILING DATE: 1997-12-19
; PRIOR APPLICATION NUMBER: PCT/US98/04858
; PRIOR FILING DATE: 1998-03-12
; PRIOR APPLICATION NUMBER: 60/057,765
; PRIOR FILING DATE: 1997-09-05
; PRIOR APPLICATION NUMBER: 60/048,970
; PRIOR FILING DATE: 1997-06-05
; PRIOR APPLICATION NUMBER: 60/050,934
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/048,100
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/048,357
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/048,189
; PRIOR FILING DATE: 1998-09-11
; PRIOR APPLICATION NUMBER: PCT/US98/04858
; PRIOR FILING DATE: 1998-03-12
; PRIOR APPLICATION NUMBER: 60/068,368
; PRIOR FILING DATE: 1997-12-19
; PRIOR APPLICATION NUMBER: 60/057,765
; PRIOR FILING DATE: 1997-09-05
; PRIOR APPLICATION NUMBER: 60/048,970
; PRIOR FILING DATE: 1997-06-05
; PRIOR APPLICATION NUMBER: 60/050,934
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/048,100
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/048,189
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/048,357
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/048,710
; PRIOR FILING DATE: 1997-03-14
; PRIOR APPLICATION NUMBER: 60/040,762
; PRIOR FILING DATE: 1997-03-14
; NUMBER OF SEQ ID NOS: 122
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 121
; LENGTH: 102
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-058-993-121
Query Match 64.0%; Score 400; DB 15; Length 102;
Best Local Similarity 66.7%; Pred. No. 6.6e-31;
Matches 64; Conservative 11; Mismatches 21; Indels 0; Gaps 0;
QY 8 CPKIVCEVEEIDQCTKPRDCPENMKCCPFSCGKKCLDFRDKDICSMPQOAGPCLASIPH 67
Db 2 CPKIRECEFEQERDVCTKRDQCQDNKKCCVFCGKKCLDLKQDVCMPKGTGCLAYFLH 61
QY 68 WYNNKTKICSEFIYGGCGNNNNFQTEAICLVTK 103
Db 62 WYDKDNTCSMFVYGGCGNNNNFQSKANCLNTCK 97

RESULT 11
US-09-853-161-75
; Sequence 75, Application US/09853161
; Patent No. US20020076756A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 28 Human Secreted Proteins
; FILE REFERENCE: PZ003P3
; CURRENT APPLICATION NUMBER: US/09/853,161
; CURRENT FILING DATE: 2001-05-11
; PRIOR APPLICATION NUMBER: 60/265,583
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: 09/152,060
; PRIOR FILING DATE: 1998-09-11
; PRIOR APPLICATION NUMBER: PCT/US98/04858
; PRIOR FILING DATE: 1998-03-12
; PRIOR APPLICATION NUMBER: 60/040,762
; PRIOR FILING DATE: 1997-03-14
; PRIOR APPLICATION NUMBER: 60/040,710
; PRIOR FILING DATE: 1997-03-14
; PRIOR APPLICATION NUMBER: 60/050,934
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/048,100
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/048,357
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/048,189
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/057,765
; PRIOR FILING DATE: 1997-09-05
; PRIOR APPLICATION NUMBER: 60/048,970
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/068,368
; PRIOR FILING DATE: 1997-12-19
; NUMBER OF SEQ ID NOS: 118
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 75
; LENGTH: 133
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-853-161-75
Query Match 64.0%; Score 400; DB 9; Length 133;
Best Local Similarity 66.7%; Pred. No. 8.5e-31;
Matches 64; Conservative 11; Mismatches 21; Indels 0; Gaps 0;
QY 8 CPKIVCEVEEIDQCTKPRDCPENMKCCPFSCGKKCLDFRDKDICSMPQOAGPCLASIPH 67
Db 33 CPKIRECEFEQERDVCTKRDQCQDNKKCCVFCGKKCLDLKQDVCMPKGTGCLAYFLH 92
QY 68 WYNNKTKICSEFIYGGCGNNNNFQTEAICLVTK 103
Db 93 WYDKDNTCSMFVYGGCGNNNNFQSKANCLNTCK 128
RESULT 12
US-09-852-659A-75
; Sequence 75, Application US/09852659A
; Patent No. US2002007287A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 28 Human Secreted Proteins
; FILE REFERENCE: PZ003P4
; CURRENT APPLICATION NUMBER: US/09/852,659A
; CURRENT FILING DATE: 2001-05-11
; PRIOR APPLICATION NUMBER: 60/265,583
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: 09/152,060
; PRIOR FILING DATE: 1998-09-11
; PRIOR APPLICATION NUMBER: PCT/US98/04858
; PRIOR FILING DATE: 1998-03-12
; PRIOR APPLICATION NUMBER: 60/040,762
; PRIOR FILING DATE: 1997-03-14

Thu Sep 22 07:16:47 2005

Db 33 CPKIRECEBFQBRDVCTKDRQCQDNKKCCVFCGKKCLDLKQDVCMPKGTGCLAYFLH 92
QY 68 WYNNKTKICSEFIYGGCGNNNNFQTEAICLVTK 103
Db 93 WYDKNDTCSEFVYGGCGNNNNFQSKANCLNTCK 128

RESULT 15
US-10-807-204-13
; Sequence 13, Application US/10807204
; Publication No. US20040229312A1
; GENERAL INFORMATION:
; APPLICANT: Bougueleret, Lydie
; APPLICANT: Bairoch, Amos
; APPLICANT: Niknejad, Anne
; TITLE OF INVENTION: Engineered Human Kunitz-Type Protease
; TITLE OF INVENTION: Inhibitor
; FILE REFERENCE: 54720-8015-US00
; CURRENT APPLICATION NUMBER: US/10/807,204
; CURRENT FILING DATE: 2004-03-22
; PRIOR APPLICATION NUMBER: PCT/EP03/01629
; PRIOR FILING DATE: 2003-02-18
; PRIOR APPLICATION NUMBER: US 60/358,683
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13
; LENGTH: 133
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-807-204-13

Query Match 64.0%; Score 400; DB 16; Length 133;
Best Local Similarity 66.7%; Pred. No. 8.5e-31;
Matches 64; Conservative 11; Mismatches 21; Indels 0; Gaps 0;

QY 8 CPKIKVECEVEIDQCTKPRDCPENMKCCPFCGKKCLDLFRKDICSMPQAGPCLASIPH 67
Db 33 CPKIRECEBFQBRDVCTKDRQCQDNKKCCVFCGKKCLDLKQDVCMPKGTGCLAYFLH 92
QY 68 WYNNKTKICSEFIYGGCGNNNNFQTEAICLVTK 103
Db 93 WYDKNDTCSEFVYGGCGNNNNFQSKANCLNTCK 128

RESULT 16
US-10-807-204-14
; Sequence 14, Application US/10807204
; Publication No. US20040229312A1
; GENERAL INFORMATION:
; APPLICANT: Bougueleret, Lydie
; APPLICANT: Bairoch, Amos
; APPLICANT: Niknejad, Anne
; TITLE OF INVENTION: Engineered Human Kunitz-Type Protease
; TITLE OF INVENTION: Inhibitor
; FILE REFERENCE: 54720-8015-US00
; CURRENT APPLICATION NUMBER: US/10/807,204
; CURRENT FILING DATE: 2004-03-22
; PRIOR APPLICATION NUMBER: PCT/EP03/01629
; PRIOR FILING DATE: 2003-02-18
; PRIOR APPLICATION NUMBER: US 60/358,683
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14
; LENGTH: 134
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-807-204-14

Query Match 56.3%; Score 352; DB 16; Length 134;
Best Local Similarity 55.7%; Pred. No. 3.6e-26;
Matches 54; Conservative 20; Mismatches 23; Indels 0; Gaps 0;

QY 8 CPKIKVECEVEIDQCTKPRDCPENMKCCPFCGKKCLDLFRKDICSMPQAGPCLASIPH 67
Db 33 CPKIRECEBFQBRDVCTKDRQCQDNKKCCVFCGKKCLDLKQDVCMPKGTGCLAYFLH 92
QY 68 WYNNKTKICSEFIYGGCGNNNNFQTEAICLVTK 104
Db 93 WYDKNDTCSEFVYGGCGNNNNFQSKANCLNTCK 129

RESULT 17
US-10-807-204-21
; Sequence 21, Application US/10480988
; Publication No. US20050069877A1
; GENERAL INFORMATION:
; APPLICANT: GANDHI, Ameena R.; KABLE, Amy E.;
; APPLICANT: SWARNAKAR, Anita; HAFALIA, April J.A.;
; APPLICANT: TRAN, Bao; DUGGAN, Brendan M.;
; APPLICANT: WARREN, Bridget A.; ISON, Craig H.;
; APPLICANT: HONCHELLU, Cynthia D.; NGUYEN, Dannel B.;
; APPLICANT: LU, Dyung Aina M.; LEE, Ernestine A.;
; APPLICANT: YUE, Henry; FORSYTHE, Ian J.;
; APPLICANT: BARROSO, Ines; RAMKUMAR, Javalaxmi;
; APPLICANT: GRIFFIN, Jennifer A.; LI, Joana X.;
; APPLICANT: YANG, Junming; THANGAVELU, Kavitha;
; APPLICANT: GIETZEN, Kimberly J.; DING, Li;
; APPLICANT: BAUGHN, Mariah R.; BOROWSKY, Mark L.;
; APPLICANT: YAO, Monique G.; CHAWLA, Narinder K.;
; APPLICANT: MASON, Patricia M.; GURURAJAN, Rajagopal;
; APPLICANT: LEE, Sally; BECHA, Shanya D.;
; APPLICANT: LEE, Soo Yeun; TRAN, Uyen K.;
; APPLICANT: ELLIOTT, Vicki S.; LUO, Wen;
; APPLICANT: SPRAGUE, William W.; TANG, Y. Tom;
; APPLICANT: LU, Yan; ZEBARJADIAN, Yeganeh
; TITLE OF INVENTION: PROTEIN MODIFICATION AND MAINTENANCE MOLECULES
; FILE REFERENCE: PP-1040 USN
; CURRENT APPLICATION NUMBER: US/10/480,988
; CURRENT FILING DATE: 2003-12-16
; PRIOR APPLICATION NUMBER: PCT/US02/19360
; PRIOR FILING DATE: 2002-06-18
; PRIOR APPLICATION NUMBER: US 60/300,508
; PRIOR FILING DATE: 2001-06-22
; PRIOR APPLICATION NUMBER: US 60/303,445
; PRIOR FILING DATE: 2001-07-06
; PRIOR APPLICATION NUMBER: US 60/305,405
; PRIOR FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: US 60/311,442
; PRIOR FILING DATE: 2001-08-09
; PRIOR APPLICATION NUMBER: US 60/314,821
; PRIOR FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: US 60/315,992
; PRIOR FILING DATE: 2001-08-29
; PRIOR APPLICATION NUMBER: US 60/378,205
; PRIOR FILING DATE: 2002-05-03
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: PERL Program
; SEQ ID NO 21
; LENGTH: 86
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No: 7675588CD1
US-10-480-988-21

Query Match 44.2%; Score 276; DB 17; Length 86;
Best Local Similarity 98.0%; Pred. No. 5e-19;
Matches 48; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 EGIIGKPCPKIKVECEVEIDQCTKPRDCPENMKCCPFCGKKCLDLFRK 49
Db 26 EGIIGKPCPKIKVECEVEIDQCTKPRDCPENMKCCPFCGKKCLDLFRK 74

RESULT 18
US-10-276-774-2606
; Sequence 2606, Application US/10276774
; Publication No. US20040053245A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; APPLICANT: Tang, Y, Tom et al
; TITLE OF INVENTION: No. US20040053245A1el Nucleic Acids and Polypeptides
; FILE REFERENCE: 21272-030
; CURRENT APPLICATION NUMBER: US/10/276,774
; CURRENT FILING DATE: 2002-11-18
; PRIOR APPLICATION NUMBER: 09/560,875
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: 09/496,914
; PRIOR FILING DATE: 2000-02-03
; NUMBER OF SEQ ID NOS: 2700
; SOFTWARE: Custom
; SEQ ID NO 2606
; LENGTH: 101
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-276-774-2606

Query Match 44.2%; Score 276; DB 15; Length 101;
Best Local Similarity 98.0%; Pred. No. 5.8e-19;
Matches 48; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1 EGILGKPCPKIKVECEVEIDQCTKPRDCPENMKCCPFSCGKKCLDFRK 49
Db 41 EGILGKPCPKIKVECEVEIDQCTKPRDCPENMKCCPFSCGKKCLDFRK 89

RESULT 19
US-10-807-204-5
; Sequence 5, Application US/10807204
; Publication No. US20040229312A1
; GENERAL INFORMATION:
; APPLICANT: Bougueleret, Lydie
; APPLICANT: Bairoch, Amos
; APPLICANT: Niknejad, Anne
; TITLE OF INVENTION: Engineered Human Kunitz-Type Protease
; TITLE OF INVENTION: Inhibitor
; FILE REFERENCE: 54720-8015.US00
; CURRENT APPLICATION NUMBER: US/10/807,204
; CURRENT FILING DATE: 2004-03-22
; PRIOR APPLICATION NUMBER: PCT/EP03/01629
; PRIOR FILING DATE: 2003-02-18
; PRIOR APPLICATION NUMBER: US 60/358,683
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 43
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-807-204-5

Query Match 41.3%; Score 258; DB 16; Length 43;
Best Local Similarity 100.0%; Pred. No. 1.4e-17;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 7 PCPKIKVECEVEIDQCTKPRDCPENMKCCPFSCGKKCLDFRK 49
Db 1 PCPKIKVECEVEIDQCTKPRDCPENMKCCPFSCGKKCLDFRK 43

RESULT 20
US-10-361-997-5
; Sequence 5, Application US/10361997
; Publication No. US2004017194A1
; GENERAL INFORMATION:
; APPLICANT: Ladner, Robert Charles

; APPLICANT: Ley, Arthur C.
; TITLE OF INVENTION: KUNITZ DOMAIN PEPTIDES
; FILE REFERENCE: 3421.1015-000
; CURRENT APPLICATION NUMBER: US/10/361,997
; CURRENT FILING DATE: 2003-02-07
; PRIOR APPLICATION NUMBER: US 60/355,547
; PRIOR FILING DATE: 2002-02-07
; NUMBER OF SEQ ID NOS: 84
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 58
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-361-997-5

Query Match 37.8%; Score 236; DB 16; Length 58;
Best Local Similarity 66.1%; Pred. No. 2.4e-15;
Matches 37; Conservative 8; Mismatches 11; Indels 0; Gaps 0;
Qy 48 RKDICSMPQEAGPCLASIPHWYNNKTKICSEFYGGCGQNNNNFQTEAICLVTK 103
Db 1 KQDVCEMPKETGPCLAYFLHWYDKKONTCSMFYGGCGQNNNNFQSKANCLNTCK 56

RESULT 21
US-10-931-153-21
; Sequence 21, Application US/10931153
; Publication No. US20050089515A1
; GENERAL INFORMATION:
; APPLICANT: Ley, Arthur C.
; APPLICANT: Sato, Aaron K.
; APPLICANT: Ladner, Robert C.
; APPLICANT: Stochl, Mark
; TITLE OF INVENTION: POLY-PGYLATED PROTEASE INHIBITORS
; FILE REFERENCE: 10280-119001
; CURRENT APPLICATION NUMBER: US/10/931,153
; CURRENT FILING DATE: 2004-08-30
; PRIOR APPLICATION NUMBER: US 60/498,845
; PRIOR FILING DATE: 2003-08-29
; PRIOR APPLICATION NUMBER: US 60/598,967
; PRIOR FILING DATE: 2004-08-04
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 21
; LENGTH: 58
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-931-153-21

Query Match 37.8%; Score 236; DB 17; Length 58;
Best Local Similarity 66.1%; Pred. No. 2.4e-15;
Matches 37; Conservative 8; Mismatches 11; Indels 0; Gaps 0;
Qy 48 RKDICSMPQEAGPCLASIPHWYNNKTKICSEFYGGCGQNNNNFQTEAICLVTK 103
Db 1 KQDVCEMPKETGPCLAYFLHWYDKKONTCSMFYGGCGQNNNNFQSKANCLNTCK 56

RESULT 22
US-10-058-993-118
; Sequence 118, Application US/10058993
; Publication No. US20030225009A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 28 Human Secreted Proteins
; FILE REFERENCE: PZ003P5
; CURRENT APPLICATION NUMBER: US/10/058,993
; CURRENT FILING DATE: 2002-01-30
; PRIOR APPLICATION NUMBER: 09/852,659
; PRIOR FILING DATE: 2001-05-11
; PRIOR APPLICATION NUMBER: 09/852,797
; PRIOR FILING DATE: 2001-05-11
; PRIOR APPLICATION NUMBER: 09/853,161


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; PRIORITY FILING DATE: 2001-05-11
; PRIOR APPLICATION NUMBER: 60/265,583
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: 09/152,060
; PRIOR FILING DATE: 1998-09-11
; PRIOR APPLICATION NUMBER: PCT/US98/04858
; PRIOR FILING DATE: 1998-03-12
; PRIOR APPLICATION NUMBER: 60/048,970
; PRIOR FILING DATE: 1997-06-05
; PRIOR APPLICATION NUMBER: 60/050,934
; PRIOR FILING DATE: 1997-12-19
; PRIOR APPLICATION NUMBER: 60/057,765
; PRIOR FILING DATE: 1997-09-05
; PRIOR APPLICATION NUMBER: 60/048,368
; PRIOR FILING DATE: 1997-03-14
; PRIOR APPLICATION NUMBER: 60/040,710
; PRIOR FILING DATE: 1997-03-14
; PRIOR APPLICATION NUMBER: 60/040,762
; PRIOR FILING DATE: 1997-03-14
; NUMBER OF SEQ ID NOS: 122
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 118
; LENGTH: 51
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-058-993-118

Query Match      35.0%; Score 219; DB 15; Length 51;
Best Local Similarity 68.6%; Pred. No. 9.3e-14;
Matches 35; Conservative 5; Mismatches 11; Indels 0; Gaps 0;

QY 52 CSMPOBAGPCLASIPHHWYKTKICSEFIYGGCGNNNNFQTEAICLVTC 102
Db 1 CEMPKEGTCLAYFLHWDYDKDNTCSMFYGGCGNNNNFQSKANCLNTC 51

RESULT 23
US-10-825-692-48
; Sequence 48, Application US/10825692
; Publication No. US20050042232A1
; GENERAL INFORMATION:
; APPLICANT: Hotez, Peter
; APPLICANT: Ashcom, James
; APPLICANT: Bdamchian, Mahnaz
; APPLICANT: Zhan, Bin
; APPLICANT: Wang, Yan
; APPLICANT: Hawdon, John
; APPLICANT: Loukas, Alexander
; APPLICANT: Williamson, Angela
; APPLICANT: Jones, Brian
; APPLICANT: Bethony, Jeffrey
; APPLICANT: Goud, Gaddam
; APPLICANT: Botazzi, Maria E.
; APPLICANT: Mendez, Susana
; TITLE OF INVENTION: Hookworm Vaccine
; FILE REFERENCE: 03740007aa
; CURRENT APPLICATION NUMBER: US/10/825,692
; CURRENT FILING DATE: 2004-04-16
; PRIOR APPLICATION NUMBER: US 60/329,533
; PRIOR FILING DATE: 2001-10-17
; PRIOR APPLICATION NUMBER: US 60/332,007
; PRIOR FILING DATE: 2001-11-23
; PRIOR APPLICATION NUMBER: US 60/375,404
; PRIOR FILING DATE: 2002-04-26
; PRIOR APPLICATION NUMBER: PCT US02/33106
; PRIOR FILING DATE: 2002-10-17
; NUMBER OF SEQ ID NOS: 114

; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 48
; LENGTH: 759
; TYPE: PRT
; ORGANISM: Ancylostoma caninum
; US-10-825-692-48

Query Match      31.5%; Score 197; DB 17; Length 759;
Best Local Similarity 46.1%; Pred. No. 1.6e-10;
Matches 35; Conservative 13; Mismatches 26; Indels 2; Gaps 1;

QY 31 ENMKCCPESCCKKCL--DFRKDICSMPQOAGPCLASIPHHWYKTKICSEFIYGGCGN 88
Db 560 ETMEDCTFTCEORLAKPELEKDVCSQPITAGPCRASIPRYGVDKSKKCKVKFTYGGCKGN 619

QY 89 NNNFQTEAICLVTKK 104
Db 620 GNRFFTKNECEKTKR 635

RESULT 24
US-09-896-095-160
; Sequence 160, Application US/09896095
; Publication No. US20030219886A1
; GENERAL INFORMATION:
; APPLICANT: LADNER, Charles C.
; APPLICANT: GUTERMAN, Sonia K.
; APPLICANT: ROBERTS, Bruce L.
; APPLICANT: MARKLAND, William
; APPLICANT: LEY, Arthur C.
; APPLICANT: KENT, Rachel B.
; TITLE OF INVENTION: DIRECTED EVOLUTION OF NOVEL BINDING PROTEINS
; FILE REFERENCE: LADNER=7L
; CURRENT APPLICATION NUMBER: US/09/896,095
; CURRENT FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: 08/415,922
; PRIOR FILING DATE: 1995-03-04
; PRIOR APPLICATION NUMBER: 08/009,319
; PRIOR FILING DATE: 1993-01-26
; PRIOR APPLICATION NUMBER: 07/664,989
; PRIOR FILING DATE: 1991-03-01
; PRIOR APPLICATION NUMBER: 08/993,776
; PRIOR FILING DATE: 1997-12-18
; NUMBER OF SEQ ID NOS: 274
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 160
; LENGTH: 64
; TYPE: PRT
; ORGANISM: Caretta sp.
; US-09-896-095-160

Query Match      29.4%; Score 184; DB 10; Length 64;
Best Local Similarity 48.2%; Pred. No. 2.7e-10;
Matches 27; Conservative 14; Mismatches 15; Indels 0; Gaps 0;

QY 48 RKDICSMPQOAGPCLASIPHHWYKTKICSEFIYGGCGNNNNFQTEAICLVTC 103
Db 4 KRDIKRLPPEQFCCKGRLPRFYFNPSRMCESFIYGGCKGNKKNFKTKAECVRACR 59

RESULT 25
US-10-038-722-103
; Sequence 103, Application US/10038722
; Publication No. US20030175919A1
; GENERAL INFORMATION:
; APPLICANT: LEY, Arthur C.
; APPLICANT: GUTERMAN, Sonia K.
; APPLICANT: MARKLAND, William
; APPLICANT: KENT, Rachel B.
; APPLICANT: ROBERTS, Bruce L.
; APPLICANT: LADNER, Robert C.
; TITLE OF INVENTION: ITI-DI KUNITZ DOMAIN MUTANTS AS RHE INHIBITORS
; FILE REFERENCE: LEY=1B
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5


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; PRIOR APPLICATION NUMBER: PCT/EP03/01629
; PRIOR FILING DATE: 2003-02-18
; PRIOR APPLICATION NUMBER: US 60/358,683
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 33
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-807-204-7

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Query Match	28.8%	Score 180;	DB 16;	Length 33;
Best Local Similarity	97.0%;	Pred. No. 3.5e-10;		
Matches 32;	Conservative 0;	Mismatches 1;	Indels 0;	Gaps 0;
Qy	74	TKICSEFIYGGCGGNNNNNFQTEAICLVTCCKYH	106	
Db	1	TKICSEFIYGGCGGNNNNNFQTEAICLVTCCKYH	33	

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RESULT 34
US-10-807-204-10
; Sequence 10, Application US/10807204
; Publication No. US20040229312A1
; GENERAL INFORMATION:
; APPLICANT: Bougueleret, Lydie
; APPLICANT: Bairoch, Amos
; APPLICANT: Niknejad, Anne
; TITLE OF INVENTION: Engineered Human Kunitz-Type Protease
; TITLE OF INVENTION: Inhibitor
; FILE REFERENCE: 54720-8015 US00
; CURRENT APPLICATION NUMBER: US/10/807,204
; CURRENT FILING DATE: 2004-03-22
; PRIOR APPLICATION NUMBER: PCT/EP03/01629
; PRIOR FILING DATE: 2003-02-18
; PRIOR APPLICATION NUMBER: US 60/358,683
; PRIOR FILING DATE: 2003-02-21
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 33
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-807-204-10

```

	Query Match	28.8%	Score 180;	DB 16;	Length 33;
	Best Local Similarity	97.0%	Prod. No. 3.5e-10;		
	Matches 32;	Conservative 0;	Mismatches 1;	Indels 0;	Gaps 0;
Qy	74	TKICSEFIYGGCGGNNNNFQTEAICLVTCCKYH	106		
Db	1	TKICSEFIYGGCGGNNNNFQTEAICLVTCCKYH	33		

```

RESULT 35
US-10-038-722-5
; Sequence 5, Application US/10038722
; Publication No. US20030175919A1
; GENERAL INFORMATION:
; APPLICANT: LEY, Arthur C.
; APPLICANT: GUTERMAN, Sonia K.
; APPLICANT: MARKLAND, William
; APPLICANT: KENT, Rachel B.
; APPLICANT: ROBERTS, Bruce L.
; APPLICANT: LADNER, Robert C.
; TITLE OF INVENTION: ITI-DI KUNITZ DOMAIN MUTANTS AS THE INHIBITORS
; FILE REFERENCE: LEY-1B
; CURRENT APPLICATION NUMBER: US/10/038,722
; CURRENT FILING DATE: 2002-01-08
; PRIOR APPLICATION NUMBER: US 08/849,406
; PRIOR FILING DATE: 1999-07-21
; PRIOR APPLICATION NUMBER: PCT/US95/16349

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; PRIOR FILING DATE: 1998-12-15
; PRIOR APPLICATION NUMBER: US 08/358,160
; PRIOR FILING DATE: 1994-12-16
; NUMBER OF SEQ ID NOS: 129
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; LENGTH: 58
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Consensus Kunitz domain
US-10-038-722-5

```

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Query Match      28.3%; Score 177; DB 14; Length 58;
Best Local Similarity 56.4%; Pred. No. 1.2e-09;
Matches 31; Conservative 5; Mismatches 19; Indels 0; Gaps 0;

QY 48 RKDICSMPQBPAGCLASIPHWYNNKTKIGSEFTYGGCGQNNNNFQEAICLVTC 102
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1 RNPFCILPATGTGRCRAMT PRFYNAKSGKCEPFTYGGCGGANNFKTEEECRRT 55
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

```

```

RESULT 36
US-09-896-095-147
; Sequence 147, Application US/09896095
; Publication No. US20030219886A1
; GENERAL INFORMATION:
; APPLICANT: LADNER, Charles C.
; APPLICANT: GUTERMAN, Sonia K.
; APPLICANT: ROBERTS, Bruce L.
; APPLICANT: MARKLAND, William
; APPLICANT: LEV, Arthur C.
; APPLICANT: KENT, Rachel B.
; TITLE OF INVENTION: DIRECTED EVOLUTION OF NOVEL BINDING PROTEINS
; FILE REFERENCE: LADNER-7L
; CURRENT APPLICATION NUMBER: US/09/896.095
; CURRENT FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: 08/415,922
; PRIOR FILING DATE: 1995-03-04
; PRIOR APPLICATION NUMBER: 08/009,319
; PRIOR FILING DATE: 1993-01-26
; PRIOR APPLICATION NUMBER: 07/664,989
; PRIOR FILING DATE: 1991-03-01
; PRIOR APPLICATION NUMBER: 08/993,776
; PRIOR FILING DATE: 1997-12-18
; NUMBER OF SEQ ID NOS: 274
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 147
; LENGTH: 67
; TYPE: PRT
; ORGANISM: Bos taurus
US-09-896-095-147

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Query Match	28.0%	Score 175;	DB 10;	Length 67;
Best Local Similarity	50.0%;	Pred.No. 2.le-09;		
Matches 27;	Conservative 10;	Mismatches 17;	Indels 0;	Gaps 0
Qv	50	DICMPGEAGFCCLASIPHHWYNNKTKTCSFIFYGCGCGNMMNFOTEALCVLTCVK	103	
db	6	DLCOLPAARGFCCKAALLRFYNSTNSACEPFTYGCCGGNMMNPFTEMLCIAE	59	

RESULT 37
US-10-038-722-90
; Sequence 90, Application US/10038722
; Publication No. US2003017591A1
; GENERAL INFORMATION:
; APPLICANT: LEY, Arthur C.
; APPLICANT: GUTERMAN, Sonia K.
; APPLICANT: KENTLAND, William
; APPLICANT: KENT, Rachel B.
; APPLICANT: ROBERTS, Bruce L.
; APPLICANT: LADNER, Robert C.

```

; TITLE OF INVENTION: ITI-D1 KUNITZ DOMAIN MUTANTS AS THE INHIBITORS
; FILE REFERENCE: LEY=1B
; CURRENT APPLICATION NUMBER: US/10/038,722
; PRIOR FILING DATE: 2002-01-08
; NUMBER OF SEQ ID NOS: 406
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 233
; LENGTH: 503
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-007-280A-233

Query Match      27.8%; Score 173.5; DB 14; Length 503;
Best Local Similarity 31.8%; Pred. No. 2e-08;
Matches 35; Conservative 10; Mismatches 36; Indels 29; Gaps 3;

QY 22 QCTKP---RDCPENM-----KCCPF-----SCGKKCLDFRKDIC 52
DB 258 ECLKPPDSEDGCEQTRWHFDAQANNCLTFTFGCHRNLNHFETYEACMLACMSGGLAAC 317

QY 53 SMPQAGPCLASIPHWYNNKTKICSEFIYGGCGGNNNNFQTEAICLVTC 102
DB 318 SLPALQGPCKAYAPRWAYNSQTGCQSFYGGCEGNGNNFESREACEESC 367

RESULT 40
US-09-794-589-2
; Sequence 2, Application US/09794589
; Patent No. US20020004224A1
; GENERAL INFORMATION:
; APPLICANT: Sheppard, Paul O.
; TITLE OF INVENTION: KUNITZ DOMAIN POLYPEPTIDE ZKUN8
; FILE REFERENCE: 00-01
; CURRENT APPLICATION NUMBER: US/09/794,589
; PRIOR FILING DATE: 2001-02-27
; PRIOR APPLICATION NUMBER: US 60/186,069
; PRIOR FILING DATE: 2000-02-29
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 576
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-794-589-2

Query Match      27.8%; Score 173.5; DB 9; Length 576;
Best Local Similarity 31.8%; Pred. No. 2.3e-08;
Matches 35; Conservative 10; Mismatches 36; Indels 29; Gaps 3;

QY 22 QCTKP---RDCPENM-----KCCPF-----SCGKKCLDFRKDIC 52
DB 327 ECLKPPDSEDGCEQTRWHFDAQANNCLTFTFGCHRNLNHFETYEACMLACMSGGLAAC 386

QY 53 SMPQAGPCLASIPHWYNNKTKICSEFIYGGCGGNNNNFQTEAICLVTC 102
DB 387 SLPALQGPCKAYAPRWAYNSQTGCQSFYGGCEGNGNNFESREACEESC 436

RESULT 41
US-10-315-380-2
; Sequence 2, Application US/10315380
; Publication No. US20030129577A1
; GENERAL INFORMATION:
; APPLICANT: Sheppard, Paul O.
; TITLE OF INVENTION: KUNITZ DOMAIN POLYPEPTIDE ZKUN8
; FILE REFERENCE: 00-01
; CURRENT APPLICATION NUMBER: US/10/315,380
; CURRENT FILING DATE: 2002-12-09
; PRIOR APPLICATION NUMBER: US/09/794,589
; PRIOR FILING DATE: 2001-02-27
; PRIOR APPLICATION NUMBER: US 60/186,069
; PRIOR FILING DATE: 2000-02-29
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: FastSeq for Windows Version 3.0

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; TITLE OF INVENTION: ITI-D1 KUNITZ DOMAIN MUTANTS AS THE INHIBITORS
; FILE REFERENCE: LEY=1B
; CURRENT APPLICATION NUMBER: US/10/038,722
; PRIOR FILING DATE: 2002-01-08
; NUMBER OF SEQ ID NOS: 406
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 90
; LENGTH: 67
; TYPE: PRT
; ORGANISM: Bos taurus
US-10-038-722-90

Query Match      28.0%; Score 175; DB 14; Length 67;
Best Local Similarity 50.0%; Pred. No. 2.1e-09;
Matches 27; Conservative 10; Mismatches 17; Indels 0; Gaps 0;

QY 50 DICSMPOEAGPCLASIPHWYNNKTKICSEFIYGGCGGNNNNFQTEAICLVTC 103
DB 6 DLCLPQARGPCKAALLRYFNSTSNACBPFTYGGCGGNNNNFETTEMCLRICE 59

RESULT 38
US-10-115-134-4
; Sequence 4, Application US/10115134
; Publication No. US20030223977A1
; GENERAL INFORMATION:
; APPLICANT: LEY, Arthur Charles
; APPLICANT: GUTERMAN, Sonia Kosow
; APPLICANT: MARKLAND, William
; APPLICANT: KENT, Rachel Baribault
; APPLICANT: ROBERTS, Bruce Lindsay
; APPLICANT: LADNER, Robert Charles
; TITLE OF INVENTION: DOMAIN MUTANTS AS CATHEPSIN G INHIBITORS
; FILE REFERENCE: LEY=1C
; CURRENT APPLICATION NUMBER: US/10/115,134
; CURRENT FILING DATE: 2002-04-04
; PRIOR APPLICATION NUMBER: 08/849,406
; PRIOR FILING DATE: 2001-07-21
; NUMBER OF SEQ ID NOS: 92
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 4
; LENGTH: 67
; TYPE: PRT
; ORGANISM: Bos taurus
US-10-115-134-4

Query Match      28.0%; Score 175; DB 15; Length 67;
Best Local Similarity 50.0%; Pred. No. 2.1e-09;
Matches 27; Conservative 10; Mismatches 17; Indels 0; Gaps 0;

QY 50 DICSMPOEAGPCLASIPHWYNNKTKICSEFIYGGCGGNNNNFQTEAICLVTC 103
DB 6 DLCLPQARGPCKAALLRYFNSTSNACBPFTYGGCGGNNNNFETTEMCLRICE 59

RESULT 39
US-10-007-280A-233
; Sequence 233, Application US/10007280A
; Publication No. US20030059784A1
; GENERAL INFORMATION:
; APPLICANT: Sun, Yongming
; APPLICANT: Recipon, Herve
; APPLICANT: Salceda, Susana
; APPLICANT: Chenghua, Liu
; TITLE OF INVENTION: Compositions and Methods Relating to Ovary Specific Genes and Pro
; FILE REFERENCE: DEX-0257
; CURRENT APPLICATION NUMBER: US/10/007,280A

```



```
; SEQ ID NO 5
; LENGTH: 640
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-369-736-5

Query Match      27.8%; Score 173.5; DB 14; Length 640;
Best Local Similarity 31.8%; Pred. No. 2.6e-08;
Matches 35; Conservative 10; Mismatches 36; Indels 29; Gaps 3;

QY 22 QCTKP---RDCPENM-----KCCPF-----SCGKKCLDFRKDTC 52
DB 391 ECLKPPDSEDCGEQTRWHFDAQANNCLTFTFGHCHRNLNHPETYEACMLACMGPPLAAC 450
QY 53 SMPQEAGPCLASIPHWYNNKTKICSEFIYGGCGGNNNNFQTEAICLVTC 102
DB 451 SLPALQGPCKAYAPRWAYNSQTGCQSFVYGGCGEGNGNPFESREACEESC 500

RESULT 46
US-10-369-738-5
; Sequence 5, Application US/10369738
; Publication No. US20030180306A1
; GENERAL INFORMATION:
; APPLICANT: HILL, JENNIFER J.
; APPLICANT: WOLFMAN, NEIL M.
; TITLE OF INVENTION: FOLLISTATIN DOMAIN CONTAINING PROTEINS
; FILE REFERENCE: 08702.0014-00
; CURRENT APPLICATION NUMBER: US/10/369,738
; CURRENT FILING DATE: 2003-02-21
; PRIOR APPLICATION NUMBER: 60/357,846
; PRIOR FILING DATE: 2002-02-21
; PRIOR APPLICATION NUMBER: 60/434,645
; PRIOR FILING DATE: 2002-12-20
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 640
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-369-738-5

Query Match      27.8%; Score 173.5; DB 14; Length 640;
Best Local Similarity 31.8%; Pred. No. 2.6e-08;
Matches 35; Conservative 10; Mismatches 36; Indels 29; Gaps 3;

QY 22 QCTKP---RDCPENM-----KCCPF-----SCGKKCLDFRKDTC 52
DB 391 ECLKPPDSEDCGEQTRWHFDAQANNCLTFTFGHCHRNLNHPETYEACMLACMGPPLAAC 450
QY 53 SMPQEAGPCLASIPHWYNNKTKICSEFIYGGCGGNNNNFQTEAICLVTC 102
DB 451 SLPALQGPCKAYAPRWAYNSQTGCQSFVYGGCGEGNGNPFESREACEESC 500

RESULT 47
US-11-028-058-5
; Sequence 5, Application US/11028058
; Publication No. US20050106154A1
; GENERAL INFORMATION:
; APPLICANT: HILL, JENNIFER J.
; APPLICANT: WOLFMAN, NEIL M.
; TITLE OF INVENTION: FOLLISTATIN DOMAIN CONTAINING PROTEINS
; FILE REFERENCE: 08702.0015-00
; CURRENT APPLICATION NUMBER: US/11/028,058
; CURRENT FILING DATE: 2005-01-04
; PRIOR APPLICATION NUMBER: US/10/369,736
; PRIOR FILING DATE: 2003-02-21
; PRIOR APPLICATION NUMBER: 60/357,846
; PRIOR FILING DATE: 2002-02-21
; PRIOR APPLICATION NUMBER: 60/434,645
; PRIOR FILING DATE: 2002-12-20
; NUMBER OF SEQ ID NOS: 53

; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 640
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-028-058-5

Query Match      27.7%; Score 173; DB 14; Length 58;
Best Local Similarity 50.0%; Pred. No. 2.9e-09;
Matches 28; Conservative 7; Mismatches 21; Indels 0; Gaps 0;

QY 48 RKDICSMPQEAGPCLASIPHWYNNKTKICSEFIYGGCGGNNNNFQTEAICLVTC 103
DB 1 RPDFCQLGYSAGPCVAMPFRFYNGTSMACQTFVYGGCMGNGNPFVTEKDLQTCR 56

RESULT 49
US-10-038-722-18
; Sequence 18, Application US/10038722
; Publication No. US20030175919A1
; GENERAL INFORMATION:
; APPLICANT: LEY, Arthur C.
; APPLICANT: GUTERMAN, Sonia K.
; APPLICANT: MARKLAND, William
; APPLICANT: KENT, Rachel B.
; APPLICANT: ROBERTS, Bruce L.
; APPLICANT: LADNER, Robert C.
; TITLE OF INVENTION: ITI-D1 KUNITZ DOMAIN MUTANTS AS THE INHIBITORS
; FILE REFERENCE: LEY-1B
; CURRENT APPLICATION NUMBER: US/10/038,722
; CURRENT FILING DATE: 2002-01-08
; PRIOR APPLICATION NUMBER: US 08/849,406
; PRIOR FILING DATE: 1999-07-21
; PRIOR APPLICATION NUMBER: PCT/US95/16349
; PRIOR FILING DATE: 1995-12-15
; PRIOR APPLICATION NUMBER: US 08/358,160
; PRIOR FILING DATE: 1994-12-16
; NUMBER OF SEQ ID NOS: 129
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 17
; LENGTH: 58
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: BITI-E7-141
US-10-038-722-17

; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 640
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-028-058-5

Query Match      27.8%; Score 173.5; DB 19; Length 640;
Best Local Similarity 31.8%; Pred. No. 2.6e-08;
Matches 35; Conservative 10; Mismatches 36; Indels 29; Gaps 3;

QY 22 QCTKP---RDCPENM-----KCCPF-----SCGKKCLDFRKDTC 52
DB 391 ECLKPPDSEDCGEQTRWHFDAQANNCLTFTFGHCHRNLNHPETYEACMLACMGPPLAAC 450
QY 53 SMPQEAGPCLASIPHWYNNKTKICSEFIYGGCGGNNNNFQTEAICLVTC 102
DB 451 SLPALQGPCKAYAPRWAYNSQTGCQSFVYGGCGEGNGNPFESREACEESC 500

RESULT 48
US-10-038-722-17
; Sequence 17, Application US/10038722
; Publication No. US20030175919A1
; GENERAL INFORMATION:
; APPLICANT: LEY, Arthur C.
; APPLICANT: GUTERMAN, Sonia K.
; APPLICANT: MARKLAND, William
; APPLICANT: KENT, Rachel B.
; APPLICANT: ROBERTS, Bruce L.
; APPLICANT: LADNER, Robert C.
; TITLE OF INVENTION: ITI-D1 KUNITZ DOMAIN MUTANTS AS THE INHIBITORS
; FILE REFERENCE: LEY-1B
; CURRENT APPLICATION NUMBER: US/10/038,722
; CURRENT FILING DATE: 2002-01-08
; PRIOR APPLICATION NUMBER: US 08/849,406
; PRIOR FILING DATE: 1999-07-21
; PRIOR APPLICATION NUMBER: PCT/US95/16349
; PRIOR FILING DATE: 1995-12-15
; PRIOR APPLICATION NUMBER: US 08/358,160
; PRIOR FILING DATE: 1994-12-16
; NUMBER OF SEQ ID NOS: 129
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 17
; LENGTH: 58
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: BITI-E7-141
US-10-038-722-17

; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 640
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-028-058-5

Query Match      27.8%; Score 173.5; DB 19; Length 640;
Best Local Similarity 31.8%; Pred. No. 2.6e-08;
Matches 35; Conservative 10; Mismatches 36; Indels 29; Gaps 3;

QY 22 QCTKP---RDCPENM-----KCCPF-----SCGKKCLDFRKDTC 52
DB 391 ECLKPPDSEDCGEQTRWHFDAQANNCLTFTFGHCHRNLNHPETYEACMLACMGPPLAAC 450
QY 53 SMPQEAGPCLASIPHWYNNKTKICSEFIYGGCGGNNNNFQTEAICLVTC 102
DB 451 SLPALQGPCKAYAPRWAYNSQTGCQSFVYGGCGEGNGNPFESREACEESC 500

RESULT 49
US-10-038-722-18
; Sequence 18, Application US/10038722
; Publication No. US20030175919A1
; GENERAL INFORMATION:
; APPLICANT: LEY, Arthur C.
; APPLICANT: GUTERMAN, Sonia K.
; APPLICANT: MARKLAND, William
; APPLICANT: KENT, Rachel B.
; APPLICANT: ROBERTS, Bruce L.
; APPLICANT: LADNER, Robert C.
; TITLE OF INVENTION: ITI-D1 KUNITZ DOMAIN MUTANTS AS THE INHIBITORS
; FILE REFERENCE: LEY-1B
```

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; CURRENT APPLICATION NUMBER: US/10/038,722
; CURRENT FILING DATE: 2002-01-08
; PRIOR APPLICATION NUMBER: US 08/849,406
; PRIOR FILING DATE: 1999-07-21
; PRIOR APPLICATION NUMBER: PCT/US95/16349
; PRIOR FILING DATE: 1995-12-15
; PRIOR APPLICATION NUMBER: US 08/358,160
; PRIOR FILING DATE: 1994-12-16
; NUMBER OF SEQ ID NOS: 129
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 18
; LENGTH: 58
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: MUTT26A
US-10-038-722-18

Query Match      27.7%; Score 173; DB 14; Length 58;
Best Local Similarity 50.0%; Pred. No. 2.9e-09;
Matches 28; Conservative 7; Mismatches 21; Indels 0; Gaps 0;

QY 48 RKDSCMPQEGAPCLASIPHWYNNKTKICSEFIYGGCGNNNFQTEAICLVTK 103
DB 1 RPDFCQLGYSAGPCVAMPFRYPYNGASMACQTFVYGGCGNGNFFVTEKDCIQTCR 56

RESULT 50
US-10-038-722-19
; Sequence 19, Application US/10038722
; Publication No. US20030175919A1
; GENERAL INFORMATION:
; APPLICANT: LEY, Arthur C.
; APPLICANT: GUTERMAN, Sonia K.
; APPLICANT: MARKLAND, William
; APPLICANT: KENT, Rachel B.
; APPLICANT: ROBERTS, Bruce L.
; APPLICANT: LADNER, Robert C.
; TITLE OF INVENTION: ITI-DI KUNITZ DOMAIN MUTANTS AS mHE INHIBITORS
; FILE REFERENCE: LEY=1B
; CURRENT APPLICATION NUMBER: US/10/038,722
; CURRENT FILING DATE: 2002-01-08
; PRIOR APPLICATION NUMBER: US 08/849,406
; PRIOR FILING DATE: 1999-07-21
; PRIOR APPLICATION NUMBER: PCT/US95/16349
; PRIOR FILING DATE: 1995-12-15
; PRIOR APPLICATION NUMBER: US 08/358,160
; PRIOR FILING DATE: 1994-12-16
; NUMBER OF SEQ ID NOS: 129
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 19
; LENGTH: 58
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: MUTQE
US-10-038-722-19

Query Match      27.7%; Score 173; DB 14; Length 58;
Best Local Similarity 50.0%; Pred. No. 2.9e-09;
Matches 28; Conservative 7; Mismatches 21; Indels 0; Gaps 0;

QY 48 RKDSCMPQEGAPCLASIPHWYNNKTKICSEFIYGGCGNNNFQTEAICLVTK 103
DB 1 RPDFCQLGYSAGPCVAMPFRYPYNGTSMACETFVYGGCGNGNFFVTEKDCIQTCR 56
```


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OM protein - protein search, using sw model

Run on: September 21, 2005, 16:21:48 ; Search time 15.3215 Seconds
(without alignments)
665.663 Million cell updates/sec

Title: US-10-807-204-2

Perfect score: 625

Sequence: 1 EGILGKPCPKIKVEVEBEI.....GNNNNQTEAICLVTKKYH 106

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 50 summaries

Database :

PIR79:*

1: PIR1:*

2: PIR2:*

3: PIR3:*

4: PIR4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	186	29.8	110	1 TITTOR	basic proteinase inhibitor
2	184.5	29.5	1522	2 H8380	protein T22F7.3 [i
3	172.5	27.6	1599	2 T16210	hypothetical prote
4	172	27.5	67	1 TIBOC	trypsin inhibitor,
5	171	27.4	1416	2 E88550	protein ZC84.1 [im
6	171	27.4	2844	2 S28291	hypothetical prote
7	168	26.9	922	2 T23573	hypothetical prote
8	165	26.4	1474	2 D88550	protein ZC84.6 [im
9	161	25.8	62	2 A44180	taicatoxin serine
10	161	25.8	747	2 JH0773	Alzheimer's diseas
11	160	25.6	57	2 A59204	basic proteinase i
12	160	25.6	252	2 JG0185	hepatocyte growth
13	160	25.6	1743	2 T26859	hypothetical prote
14	157	25.1	58	1 TTHABK	isoalbinhibitor K (BP
15	157	25.1	111	2 S41082	amyloid precursor
16	157	25.1	337	1 T1PGBI	alpha-1-microglobu
17	157	25.1	751	2 A49974	beta-amyloid precu
18	157	25.1	763	2 A49321	amyloid beta (A4)
19	157	25.1	765	2 S42880	amyloid precursor-
20	155.5	24.9	2150	2 T32497	hypothetical prote
21	154	24.6	484	4 A32761	hypothetical Alzhe
22	154	24.6	770	1 QRHUA4	Alzheimer's diseas
23	153	24.5	62	2 S19327	venom basic protei
24	152	24.3	62	2 S07451	proteinase inhibit
25	152	24.3	76	2 S06678	Alzheimer's diseas
26	152	24.3	76	2 S03607	Alzheimer's diseas
27	152	24.3	352	1 HCHU	alpha-1-microglobu
28	152	24.3	352	1 T1BOBI	alpha-1-microglobu
29	151	24.2	65	1 TIVIVC	venom basic protei

30	151	24.2	100	2 A32282	Alzheimer's diseas
31	149.5	23.9	62	2 S01802	chymotrypsin inhib
32	149.5	23.9	249	2 T32060	hypothetical prote
33	149	23.8	57	1 T1FHPB	proteinase inhibit
34	149	23.8	76	2 S04855	Alzheimer's diseas
35	149	23.8	123	2 A29652	inter-alpha-trypsi
36	148.5	23.8	62	2 S01803	chymotrypsin inhib
37	147.5	23.6	372	2 JC2556	alpha-1-microglobu
38	147	23.5	125	1 T1HOBI	basic proteinase i
39	146	23.4	100	1 T1BO	lipoprotein-associ
40	146	23.4	300	2 S12143	hypothetical prote
41	146	23.4	805	2 T34212	protein C37C3.6a [
42	146	23.4	1558	2 C89114	hypothetical prote
43	146	23.4	2167	2 T34395	uterine plasmin/tr
44	145	23.2	122	1 A55115	tissue factor path
45	145	23.2	299	2 I46937	short epsilon-dend
46	144	23.0	57	2 B59399	venom basic protei
47	144	23.0	59	1 T1EPED	isoaprotinin Gl -
48	144	23.0	59	2 S00371	Long epsilon-dendr
49	144	23.0	59	2 A59399	serum basic protei
50	144	23.0	60	1 T1BOR	

ALIGNMENTS

RESULT 1

TITTOR

basic proteinase inhibitor - loggerhead

C:Species: Caretta caretta (loggerhead)

C>Date: 31-May-1979 #sequence_revision 23-Oct-1981 #text_change 09-Jul-2004

C:Accession: A01224

R:Kato, I.; Tominaga, N.

Ref. Proc. 38, 832, 1979

A:Title: Trypsin-subtilisin inhibitor from red sea turtle eggwhite consists of two tan

A:Reference number: A01224

A:Accession: A01224

A:Molecule type: protein

A:Residues: 1-110 <KAT>

A:Cross-references: UNIPROT:P00993

C:Comment: This inhibitor, isolated from egg white, consists of two nonhomologous domain

C:Superfamily: loggerhead basic proteinase inhibitor; animal Kunitz-type proteinase inh

C:Keywords: pyroglutamic acid; serine proteinase inhibitor

F:8-58/Domain: animal Kunitz-type proteinase inhibitor homology <BPI>

F:63-105/Domain: antileukoproteinase repeat homology <ALP>

F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

F:8-58,17-41,33-54,67-93,76-97,80-92,86-101/Diulfide bonds: #status predicted

F:18/Inhibitory site: Lys (trypsin) #status predicted

Query Match 29.8%; Score 186; DB 1; Length 110;

Best Local Similarity 50.0%; Pred. No. 8.7e-10;

Matches 28; Conservative 13; Mismatches 15; Indels 0; Gaps 0;

QY 48 RKDICSMPQEAQPCLASIPHWYNNKTKICSEFIYGGCGGNNNNFQTEAICLVTK 103

Db 4 KRDICRLPPEQGPCRGRIPIRYFNPASRMCESEFIYGGCKGNKFNFKTAEVCRA 59

RESULT 2

H8380

protein T22F7.3 [imported] - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C>Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 10-May-2001

C:Accession: H8380

R:anonymous, The C. elegans Sequencing Consortium.

Science 282, 2012-2018, 1998

A:Title: Genome sequence of the nematode C. elegans: a platform for investigating biolo

A:Reference number: A75000; MUID:99069613; PMID:9851916

A:Note: see websites genome.wustl.edu/gsc/C.elegans/ and www.sanger.ac.uk/Projects/c_el

A:Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; an

A:Accession: H8380

A>Status: preliminary

A:Molecule type: DNA

A;Residues: 1-1522 <STO>
A;Cross-references: GB:chr_III; PIDN:AAA20672.1; PID:9529714; GSPDB:GN00021; CESP:T22F7.
A;Note: highly similar to ZC84.1
C;Genetics:
A;Gene: T22F7.3
A;Map position: 3

Query Match 29.5%; Score 184.5; DB 2; Length 1522;
Best Local Similarity 34.3%; Pred. No. 9.4e-09;
Matches 35; Conservative 14; Mismatches 44; Indels 9; Gaps 2;

Qy 12 KVECEV-----VEIDQCTKPRDCPENMKCCPFSGKKCLDFRDXICSMPOEAGPCLAS 64
Db 488 KLVCENGHLRGESWQRCETNADCPSSHSC--QSHKVCCTPQASLCTQPKLGDCTSA 545

Qy 65 IPHWYNNKTKICSEFFIYGGCGGNNNNFQTEAICLVTKYH 106
Db 546 VRRYVYNAATRSCEMFQVTCGCGNDNNFNTLMACQCKRGIH 587

RESULT 3
T16210
hypothetical protein F30H5.3 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
C;Accession: T16210
R;Pauley, A.; Stelliyes, L.
A;Submitted to the EMBL Data Library, June 1995
A;Description: The sequence of C. elegans cosmid F30H5.
A;Reference number: Z18478
A;Accession: T16210
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-1599 <PAU>
A;Cross-references: UNIPROT:Q09983; EMBL:U29096; NID:g861390; PID:g861393; PIDN:AAA68408
A;Experimental source: strain Bristol N2
C;Genetics:
A;Gene: CESP:F30H5.3
A;Introns: 12/1; 59/2; 85/3; 124/3; 217/2; 534/3; 560/1; 1549/1

Query Match 27.6%; Score 172.5; DB 2; Length 1599;
Best Local Similarity 35.4%; Pred. No. 1.1e-07;
Matches 35; Conservative 13; Mismatches 42; Indels 9; Gaps 2;

Qy 12 KVECEV-----EBIDQCTKPRDCPENMKCCPFSGKKCLDFRDXICSMPOEAGPCLAS 64
Db 518 KLQCKYGTPLKTGSSNQRCASADCFSTHEC--QSDHNVCPRPQAICSQPLRLGDCKQS 575

Qy 65 IPHWYNNKTKICSEFFIYGGCGGNNNNFQTEAICLVTK 103
Db 576 VRRYVYNAVTRACEIFDYTCGCGNDNNFETLLECQNTCE 614

RESULT 4
T160C
trypsin inhibitor, colostrum (BPI type) - bovine
C;Species: Bos primigenius taurus (cattle)
C;Date: 24-Apr-1984 #sequence_revision 31-Dec-1993 #text_change 09-Jul-2004
C;Accession: A01207
R;Cechova, D.; Jonakova, V.; Sorm, F.
Collect. Czech. Chem. Commun. 36, 3342-3357, 1971
A;Title: Primary structure of trypsin inhibitor from cow colostrum (component B2).
A;Reference number: A90928
A;Accession: A01207
A;Molecule type: protein
A;Residues: 1-26,'B',28-67 <CEC>
A;Cross-references: UNIPROT:P00976
A;Note: the residue identified as Asx is bound to carbohydrate; therefore, we have shown
R;Cechova, D.; Ber, E.
Collect. Czech. Chem. Commun. 39, 680-688, 1974
A;Title: Disulfide bonds of trypsin inhibitor from cow colostrum.
A;Reference number: A90929
A;Contents: annotation; disulfide bonds

R;Cechova, D.; Muszynska, G.
FEBS Lett. 8, 84-86, 1970
A;Title: Role of lysine 18 in active center of cow colostrum trypsin inhibitor.
A;Reference number: A91440
A;Contents: annotation
A;Note: the inhibitory site was determined
C;Superfamily: basic proteinase inhibitor; animal Kunitz-type proteinase inhibitor homol
C;Keywords: colostrum; glycoprotein; serine proteinase inhibitor
F;8-58/Domain: animal Kunitz-type proteinase inhibitor homology <BPI>
F;8-58,17-41,33-54/Disulfide bonds: #status experimental
F;18/inhibitory site: Lys (trypsin) #status experimental
F;27/Binding site: carbohydrate (Asn) (covalent) #status experimental

Query Match 27.5%; Score 172; DB 1; Length 67;
Best Local Similarity 48.1%; Pred. No. 1e-08;
Matches 26; Conservative 11; Mismatches 17; Indels 0; Gaps 0;

Qy 50 DICSMPOEAGPCLASIPHWYNNKTKICSEFFIYGGCGGNNNNFQTEAICLVTK 103
Db 6 DLCQLPQARGPCKAALLRYFYNSTNACEPTYGGCGGNBNFETTEMCLRICE 59

RESULT 5
E88550
protein ZC84.1 [imported] - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
C;Accession: E88550
R;Anonymous, The C. elegans Sequencing Consortium.
Science 282, 2012-2018, 1998
A;Title: Genome sequence of the nematode C. elegans: a platform for investigating biolog
A;Reference number: A75000; MUID:99069613; PMID:9851916
A;Note: see websites genome.wustl.edu/gsc/C_elegans/ and www.sanger.ac.uk/projects/C_ele
A;Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; and
A;Accession: E88550
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-1416 <STO>
A;Cross-references: UNIPROT:Q03610; GB:chr_III; PIDN:CAA79569.1; PID:g3881446; GSPDB:GN0
A;Note: similar to Serine protease inhibitor, Kunitz type
C;Genetics:
A;Gene: ZC84.1
A;Map position: 3

Query Match 27.4%; Score 171; DB 2; Length 1416;
Best Local Similarity 30.4%; Pred. No. 1.4e-07;
Matches 35; Conservative 14; Mismatches 34; Indels 32; Gaps 3;

Qy 12 KVECEV-----EBIDQCTKPRDCPENMK-----CCPFSGKKCLDFR 48
Db 380 KHECEMYCARLQCEGSPRLRGEEAQRQNNNAQCPSHSHECKADQGVCCP-----RK 430

Qy 49 KDICSMPOEAGPCLASIPHWYNNKTKICSEFFIYGGCGGNNNNFQTEAICLVTK 103
Db 431 QTICAPLRLIGDCTENKRYWYNARTQCFEYTCGCGNDNNFDSIMDCQNFCK 485

RESULT 6
S28291
hypothetical protein ZC84.1 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004
C;Accession: S28291
R;Thomas, K.
submitted to the EMBL Data Library, December 1992
A;Reference number: S28285
A;Accession: S28291
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-2844 <THO>
A;Cross-references: UNIPROT:Q03610; EMBL:Z19157
C;Genetics:
A;Introns: 14/1; 32/3; 57/1; 192/3; 277/1; 398/1; 439/1; 474/1; 497/1; 813/1; 1135/1; 12/

[illegible]

Db 307 KAVCSQEAATGFCRAVMPRWYFDLSKGKCVRIYGGCGGNRNPFSEDYCMVACK 361

RESULT 19

S42880

amyloloid precursor-like protein - rat

C:Species: Rattus norvegicus (Norway rat)

C>Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 09-Jul-2004

C:Accession: S42880; S47528

R:Sandbrink, R.; Masters, C.L.; Beyreuther, K.

A:Submitted to the EMBL Data Library, March 1994

A:Description: Complete nucleotide ad deduced amino acid sequence of rat amyloloid precure

A:Reference number: S42880

A:Accession: S42880

A:Molecule type: mRNA

A:Residues: 1-765 <SAN>

A:Cross-references: UNIPROT:P15943; EMBL:X77934

R:Sandbrink, R.; Masters, C.L.; Beyreuther, K.

Biochim. Biophys. Acta 1219, 167-170, 1994

A:Title: Complete nucleotide and deduced amino acid sequence of rat amyloloid protein prec

A:Reference number: S47528; MUID:94368849; PMID:8086458

A:Accession: S47528

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-765 <SA2>

A:Cross-references: EMBL:X77934

C:Superfamily: Alzheimer's disease amyloloid beta protein; animal Kunitz-type proteinase i

C:Keywords: alternative splicing

F:312-362/Domain: animal Kunitz-type proteinase inhibitor homology <BPI>

Query Match 25.1%; Score 157; DB 2; Length 765;

Best Local Similarity 45.5%; Pred. No. 1.5e-06;

Matches 25; Conservative 8; Mismatches 22; Indels 0; Gaps 0;

QY 49 KDICSMQEAAGPCLASIPHHWYNNKTKICSEFIYGGCGGNNNFQTEAICLVTC 103

Db 309 KAVCSQEAATGFCRAVMPRWYFDLSKGKCVRIYGGCGGNRNPFSEDYCMVACK 363

RESULT 20

T32497

hypothetical protein C08G9.2 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C>Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 09-Jul-2004

C:Accession: T32497

R:Geisel, C.; Stelliyes, L.

A:Submitted to the EMBL Data Library, December 1997

A:Description: The sequence of C. elegans cosmid C08G9.

A:Reference number: Z21179

A:Accession: T32497

A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-2150 <GBI>

A:Cross-references: UNIPROT:O44131; EMBL:AF036687; PIDN:AAB88311.1; GSPDB:GN00022; CBSP:

A:Experimental source: strain Bristol N2; clone C08G9

C:Genetics:

A:Gene: CESP:C08G9.2

A:Map position: 4

A:Introns: 242/1; 306/1; 340/3; 485/1; 545/1; 736/2; 791/1; 829/1; 886/3; 942/1; 1079/2;

Query Match 24.9%; Score 155.5; DB 2; Length 2150;

Best Local Similarity 25.2%; Pred. No. 4.6e-06;

Matches 38; Conservative 18; Mismatches 34; Indels 61; Gaps 5;

QY 13 VCEVEEIDQCCKPRDCP-----ENMK--CC----- 36

Db 1773 IETRTQQYSCSTQSTVCPGVYCTAFDDNMHGVCCPGANSIKSIGEHNGLTCPHGDPFSS 1832

QY 37 -----PFSC-----GKK-----CLDFRKDICKMPOEAGPCLASIPHHWYN 71

Db 1833 LADGTPFSCVLTNGCPATHYGSTMPGQKKGICCVSKRYVCNQLORDAGPCTATVTRFFYS 1892

QY 72 KTKICSEFIYGGCGGNNNFQTEAICLVTC 102

Db 1893 SLTHSCTPFYDYGCGGGLNNFNFAFTRDCNNFC 1923

RESULT 21

A32761

hypothetical Alzheimer's disease amyloloid beta protein, Alu-containing clone - human (fra

C:Species: Homo sapiens (man)

C>Date: 29-Jan-1990 #sequence_revision 10-Apr-1996 #text_change 10-Apr-1996

C:Accession: A32761

R:de Sauvage, F.; Octave, J.N.

Science 245, 651-653, 1989

A:Title: A novel mRNA of the A4 amyloloid precursor gene coding for a possibly secreted pr

A:Reference number: A32761; MUID:89346754; PMID:2589763

A:Accession: A32761

A:Molecule type: mRNA

A:Residues: 1-484 <DES>

A:Cross-references: GB:M28373

A>Note: the authors translated the codon ATG for residue 433 as Leu

C:Comment: This is the hypothetical translation of a sequence believed to contain clonin

C:Keywords: cloning artifact

Query Match 24.6%; Score 154; DB 4; Length 484;

Best Local Similarity 44.4%; Pred. No. 1.9e-06;

Matches 24; Conservative 8; Mismatches 22; Indels 0; Gaps 0;

QY 49 KDICSMQEAAGPCLASIPHHWYNNKTKICSEFIYGGCGGNNNFQTEAICLVTC 102

Db 209 REVCSQEAETGFCRAMISRMYFDVTEGKCAPFFYGGCGGNRNPFDEYCMVAVC 262

RESULT 22

QRHUA4

Alzheimer's disease amyloloid beta protein precursor [validated] - human

N:Alternate names: Alzheimer's disease amyloloid A4 protein; coagulation factor X1a inhibi

N:Contains: amyloloid beta protein long, plaque form; amyloloid beta protein short, vascular

protein precursor splice form APP(770)

C:Species: Homo sapiens (man)

C>Date: 30-Jun-1987 #sequence_revision 28-Jul-1995 #text_change 15-Sep-2000

C:Accession: S02260; S05194; A32277; A33486; I39451; I39452; I39453; I59562; A44

4668; A28583; A29302; A60805; JLO038; S06121; A60355; A59011; A38384; S29076; S3

N:Le Maire, H.G.; Salbaum, J.M.; Multhaup, G.; Kang, J.; Bayney, R.M.; Unterbeck, A.; Bey

Nucleic Acids Res. 17, 517-522, 1989

A:Title: The PreA4(685) precursor protein of Alzheimer's disease A4 amyloid is encoded b

A:Reference number: S02260; MUID:89128427; PMID:2783775

A:Accession: S02260

A:Molecule type: DNA

A:Residues: 1-288,'V',365-770 <LEM1>

A:Cross-references: EMBL:X13466

A>Note: alternative splice form APP(695)

R:Le Maire, H.G.

submitted to the EMBL Data Library, November 1988

A:Reference number: S05194

A:Accession: S05194

A:Molecule type: DNA

A:Residues: 1-14,'VW',17-288,'V',365-770 <LEM2>

A:Cross-references: EMBL:X13466; NID:G35598; PIDN:CAA31830.1; PID:G871360

A>Note: alternative splice form APP(695)

R:La Fauci, G.; Lahiri, D.K.; Salton, S.R.J.; Robakis, N.K.

Biochem. Biophys. Res. Commun. 159, 297-304, 1989

A:Title: Characterization of the 5'-end region and the first two exons of the beta-prote

A:Reference number: A32277; MUID:89165870; PMID:2538123

A:Accession: A32277

A:Molecule type: DNA

A:Residues: 1-75 <LAF>

A:Cross-references: GB:M24546; GB:M24547; NID:G341202; PIDN:AAC13654.1; PID:G516074

R:Johnstone, E.M.; Chaney, M.O.; Moore, R.E.; Ward, K.E.; Norris, F.H.; Little, S.P.

Biochem. Biophys. Res. Commun. 163, 1248-1255, 1989

A:Title: Alzheimer's disease amyloloid peptide is encoded by two exons and shows similarit

A:Reference number: A33260; MUID:89392030; PMID:2675837

A:Accession: A33260

A:Molecule type: DNA

A;Residues: 656-737 <JOH>
 A;Cross-references: GB:M29270; NID:G178863; PIDN:AAAS1768.1; PID:G178865
 R;Prelli, F.; Levy, E.; van Duinen, S.G.; Bots, G.T.A.M.; Luyendijk, W.; Frangione, B.
 Biochem. Biophys. Res. Commun. 170, 301-307, 1990
 A;Title: Expression of a normal and variant Alzheimer's beta-protein gene in amyloid of
 A;Reference number: A35486; MUID:90321244; PMID:2196878
 A;Accession: A35486
 A;Molecule type: DNA
 A;Residues: 672-710 <PRE1>
 A;Note: 693-Gln was found in DNA isolated from HCHWA-D patients
 R;Yoshikai, S.I.; Sakaki, H.; Doh-ura, K.; Furuya, H.; Sakaki, Y.
 Gene 87, 257-263, 1990
 A;Title: Genomic organization of the human amyloid beta-protein precursor gene.
 A;Reference number: I39451; MUID:90236318; PMID:2110105
 A;Accession: I39452
 A;Status: nucleic acid sequence not shown; translation not shown; translated from GB/EMBL
 A;Molecule type: DNA
 A;Residues: 1-770 <YOS1>
 A;Cross-references: GB:M33112; NID:G178613; PIDN:AAB59502.1; PID:G178616
 A;Accession: I39451
 A;Status: nucleic acid sequence not shown; translation not shown; translated from GB/EMBL
 A;Molecule type: DNA
 A;Residues: 1-530, 'QWLMPVTPAFWEAKVGR' <YOS2>
 A;Cross-references: GB:M34875; NID:G178608; PIDN:AAB59501.1; PID:G178615
 R;Yoshikai, S.I.; Sakaki, H.; Doh-ura, K.; Furuya, H.; Sakaki, Y.
 Gene 102, 291-292, 1991
 A;Reference number: A59020; MUID:91340168; PMID:1908403
 A;Contents: annotation; erratum
 A;Note: revised physical map for reference I39451
 R;Levy, E.; Carman, M.D.; Fernandez-Madrid, I.O.; Power, M.D.; Lieberburg, I.; van Duine
 Science 248, 1124-1126, 1990
 A;Title: Mutation of the Alzheimer's disease amyloid gene in hereditary cerebral hemorrh
 A;Reference number: I39453; MUID:90260663; PMID:2111584
 A;Accession: I39453
 A;Status: translated from GB/EMBL/DDBJ
 A;Molecule type: DNA
 A;Residues: 656-737 <LEV>
 A;Cross-references: GB:M7896; NID:G178618; PIDN:AAAS1727.1; PID:G178620
 A;Note: a mutation with 693-Gln is presented
 R;Murrell, J.; Farlow, M.; Ghetti, B.; Benson, M.D.
 Science 254, 97-99, 1991
 A;Title: A mutation in the amyloid precursor protein associated with hereditary Alzheimer
 A;Reference number: I59562; MUID:92022553; PMID:1925564
 A;Accession: I59562
 A;Status: translated from GB/EMBL/DDBJ
 A;Molecule type: DNA
 A;Residues: 689-716, 'F', 718-737 <MUR>
 A;Cross-references: GB:S57865; NID:G236720; PIDN:AAB19991.1; PID:G236721
 R;Kamino, K.; Orr, H.T.; Payami, H.; Wijeman, E.M.; Alonso, M.E.; Pulet, S.M.; Anderson,
 arakis, S.E.; Korenberg, J.R.; Sharma, V.; Kukull, W.; Larson, E.; Heston, L.L.; Martin,
 Am. J. Hum. Genet. 51, 998-1014, 1992
 A;Title: Linkage and mutational analysis of familial Alzheimer disease kindreds for the
 A;Reference number: A44017; MUID:93035397; PMID:1415269
 A;Accession: A44017
 A;Molecule type: DNA
 A;Residues: 687-692, 'G', 694-718 <KAM1>
 A;Cross-references: GB:S45135; NID:G257377; PIDN:AAB23645.1; PID:G257378
 A;Experimental source: familial Alzheimer disease family SB
 A;Note: sequence extracted from NCBI backbone (NCBIP:115374)
 A;Note: sequence extracted from NCBI backbone (NCBIP:115374)
 A;Accession: B44017
 A;Molecule type: DNA
 A;Residues: 687-718 <KAM2>
 A;Cross-references: GB:S45136; NID:G257379; PIDN:AAB23646.1; PID:G257380
 A;Experimental source: familial Alzheimer disease family LIT
 A;Note: sequence extracted from NCBI backbone (NCBIP:115376)
 A;Note: this sequence has a silent mutation
 R;Kang, J.; Lemaire, H.G.; Unterbeck, A.; Salbaum, J.M.; Masters, C.L.; Grzeschik, K.H.;
 Nature 325, 733-736, 1987
 A;Title: The precursor of Alzheimer's disease amyloid A4 protein resembles a cell-surf
 A;Reference number: A03134; MUID:87144572; PMID:2881207
 A;Accession: A03134
 A;Molecule type: mRNA
 A;Residues: 1-288, 'V', 365-770 <KAN>

A;Cross-references: GB:Y00264; NID:G28525; PIDN:CAA68374.1; PID:G28526
 A;Note: alternative splice form APP(695)
 R;Rabakis, N.K.; Ramakrishna, N.; Wolfe, G.; Wisniewski, H.M.
 Proc. Natl. Acad. Sci. U.S.A. 84, 4190-4194, 1987
 A;Title: Molecular cloning and characterization of a cDNA encoding the cerebrovascular a
 A;Reference number: A29030; MUID:87231571; PMID:3035574
 A;Accession: A29030
 A;Molecule type: mRNA
 A;Residues: 284-288, 'V', 365-646, 'E', 648-770 <ROB>
 A;Cross-references: GB:M16765; NID:G178539; PIDN:AAAS1722.1; PID:G178540
 A;Note: the authors translated the codon GAG for residue 647 as Asp
 R;Goldgaber, D.; Lerman, M.I.; McBride, O.W.; Saffiotti, U.; Gajdusek, D.C.
 Science 235, 877-880, 1987
 A;Title: Characterization and chromosomal localization of a cDNA encoding brain amyloid
 A;Reference number: A47584; MUID:87120328; PMID:3810169
 A;Accession: A47584
 A;Molecule type: mRNA
 A;Residues: 674-756, 'S', 758-770 <GOL>
 A;Cross-references: GB:M15533; NID:G178706; PIDN:AAA35540.1; PID:G178707
 A;Experimental source: brain
 R;Tanzi, R.E.; Gusella, J.F.; Watkins, P.C.; Bruns, G.A.P.; St George-Hyslop, P.; Van Ke
 Science 235, 880-884, 1987
 A;Title: Amyloid beta protein gene: cDNA, mRNA distribution, and genetic linkage near th
 A;Reference number: A47585; MUID:87120329; PMID:2949367
 A;Accession: A47585
 A;Molecule type: mRNA
 A;Residues: 674-703 <TAN1>
 A;Cross-references: GB:M15532; NID:G177957; PIDN:AAA51564.1; PID:G177958
 R;Dyrks, T.; Weidemann, A.; Multhaup, G.; Salbaum, J.M.; Lemaire, H.G.; Kang, J.; Mueller
 EMBO J. 7, 949-957, 1988
 A;Title: Identification, transmembrane orientation and biogenesis of the amyloid A4 pre
 A;Reference number: S02638; MUID:88296437; PMID:2900137
 A;Accession: S02638
 A;Molecule type: mRNA
 A;Residues: 672-678 <DVR>
 R;Tanzi, R.E.; McClatchey, A.I.; Lamperti, E.D.; Villa-Komaroff, L.; Gusella, J.F.; Neve
 Nature 331, 528-530, 1988
 A;Title: Protease inhibitor domain encoded by an amyloid protein precursor mRNA associ
 A;Reference number: S00707; MUID:88122640; PMID:2893290
 A;Accession: S00707
 A;Molecule type: mRNA
 A;Residues: 286-344, 'I', 365-366 <TAN2>
 A;Cross-references: EMBL:X06982; NID:G28817; PIDN:CAA30042.1; PID:G929612
 A;Experimental source: promyelocytic leukemia cell line HL60
 A;Note: alternative splice form APP(751)
 R;Ponte, P.; Gonzalez-DeHitt, P.; Schilling, J.; Miller, J.; Hsu, D.; Greenberg, B.; D
 Nature 331, 525-527, 1988
 A;Title: A new A4 amyloid mRNA contains a domain homologous to serine proteinase inhibi
 A;Reference number: S00925; MUID:88122639; PMID:2893289
 A;Accession: S00925
 A;Molecule type: mRNA
 A;Residues: 1-344, 'I', 365-770 <PO2>
 A;Cross-references: GB:X06989; EMBL:Y00297; NID:G28720; PIDN:CAA30050.1; PID:G28721
 A;Note: alternative splice form APP(751)
 R;Kitaguchi, N.; Takahashi, Y.; Tokushima, Y.; Shiojiri, S.; Ito, H.
 Nature 331, 530-532, 1988
 A;Title: Novel precursor of Alzheimer's disease amyloid protein shows protease inhibi
 A;Reference number: A38949; MUID:88122641; PMID:2893291
 A;Accession: A38949
 A;Molecule type: mRNA
 A;Residues: 287-367 <KIT>
 A;Cross-references: GB:X06981; NID:G28816; PIDN:CAA30041.1; PID:G929611
 A;Experimental source: glioblastoma cell line
 A;Note: alternative splice form APP(770)
 R;Vitek, M.P.; Rasool, C.G.; de Sauvage, F.; Vitek, S.M.; Bartus, R.T.; Beer, B.; Ashton
 Brain Res. Mol. Brain Res. 4, 121-131, 1988
 A;Title: Absence of mutation in the beta-amyloid cDNAs cloned from the brains of three
 A;Reference number: A30320
 A;Accession: A30320
 A;Status: not compared with conceptual translation
 A;Molecule type: mRNA
 A;Residues: 284-288, 'V', 365-770 <VIT1>
 A;Accession: B30320

[illegible]

RESULT 27

HCHU

alpha-1-microglobulin/inter-alpha-trypsin inhibitor precursor [validated] - human
 N;Alternate names: bikunin; complex-forming glycoprotein heterogeneous in charge (HC) pr
 rich protein
 N;Contains: alpha-1-microglobulin (protein HC); inter-alpha-trypsin inhibitor
 C;Species: Homo sapiens (man)
 C;Date: 15-Oct-1982 #sequence revision 30-Jun-1987 #text change 09-Jul-2004
 C;Accession: S13433; S10778; A93642; A90074; A90225; A90686; P90450; B39079; A61580; B25
 3217
 R;Vetr, H.; Gebhard, W.
 Biol. Chem. Hoppe-Seyler 371, 1185-1196, 1990
 A;Title: Structure of the human alpha(1)-microglobulin-bikunin gene.
 A;Reference number: S13433; MUID:91214554; PMID:1708673
 A;Accession: S13433
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-352 <VET1>
 A;Cross-references: UNIPROT:P02760; EMBL:X54816; NID:G24475; PIDN:CAA38595.1; PID:982561
 R;Diarra-Mehrpour, M.; Bourguignon, J.; Seabouee, R.; Salier, J.P.; Leveillard, T.; Marb
 Eur. J. Biochem. 191, 131-139, 1990
 A;Title: Structural analysis of the human inter-alpha-trypsin inhibitor light-chain gene
 A;Reference number: S10778; MUID:90336621; PMID:1696200
 A;Accession: S10778
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-202 <DIA>
 R;Kaumeyer, J.F.; Polazzi, J.O.; Kotick, M.P.
 Nucleic Acids Res. 14, 7839-7850, 1986
 A;Title: The mRNA for a proteinase inhibitor related to the HI-30 domain of inter-alpha-
 A;Reference number: A93642; MUID:87040757; PMID:2430261
 A;Accession: A93642
 A;Molecule type: mRNA
 A;Residues: 1-352 <XAU>
 A;Cross-references: GB:X04494; NID:G24478; PIDN:CAA28182.1; PID:G24479
 R;Lopez Otin, C.; Grubb, A.O.; Mendez, E.
 Arch. Biochem. Biophys. 228, 544-554, 1984
 A;Title: The complete amino acid sequence of human complex-forming glycoprotein heteroge
 A;Reference number: A90074; MUID:84126849; PMID:6198962
 A;Accession: A90074
 A;Molecule type: protein
 A;Residues: 20-56,58-202 <LOP>
 A;Experimental source: individual with tubular proteinuria
 A;Note: no evidence of sequence heterogeneity could be found, in spite of persistent het
 R;Takagi, T.; Takagi, K.; Kawai, T.
 Biochem. Biophys. Res. Commun. 98, 957-1001, 1981
 A;Title: Complete amino acid sequence of human alpha-1-microglobulin.
 A;Reference number: A90225; MUID:81184038; PMID:6164372
 A;Accession: A90225
 A;Molecule type: protein
 A;Residues: 20-47;58-136,138-141,'T',143-144,146-198 <TAK>
 A;Experimental source: pooled urine of patients with tubular proteinuria
 R;Reisinger, P.; Hochstrasser, K.; Albrecht, G.J.; Lempart, K.; Salier, J.P.
 Biol. Chem. Hoppe-Seyler 366, 479-483, 1985
 A;Title: Human inter-alpha-trypsin inhibitor: localization of the kunitz-type domains in
 A;Reference number: A90686; MUID:85225968; PMID:2408638
 A;Accession: A90686
 A;Molecule type: protein
 A;Residues: 206-290,'VI',293-342,'E',344-350 <REI>
 R;Atmani, F.; Lacour, B.; Strecker, G.; Parvy, P.; Drueke, T.; Daudon, M.
 Biochem. Biophys. Res. Commun. 191, 1158-1165, 1993
 A;Title: Molecular characteristics of uronic-acid-rich protein, a strong inhibitor of ca
 A;Reference number: P90450; MUID:93221481; PMID:8466493
 A;Accession: P90450
 A;Molecule type: protein
 A;Residues: 206-214,'X' <ATM1>
 R;Englild, J.J.; Salvesen, G.; Hefta, S.A.; Thøgersen, I.B.; Rutherford, S.; Pizzo, S.V.
 J. Biol. Chem. 266, 747-751, 1991
 A;Title: Chondroitin 4-sulfate covalently cross-links the chains of the human blood pro
 A;Reference number: A39079; MUID:91093267; PMID:1898736
 A;Accession: B39079
 A;Molecule type: protein
 A;Residues: 206-225 <ENG1>

R;Chirat, F.; Balduyck, M.; Mizon, C.; Laroui, S.; Sautiere, P.; Mizon, J.
 Int. J. Biochem. 23, 1201-1203, 1991
 A;Title: A chondroitin-sulfate chain is located on serine-10 of the urinary trypsin inh
 A;Reference number: A61580; MUID:92175157; PMID:1794445
 A;Accession: A61580
 A;Molecule type: protein
 A;Residues: 214,'X',216-222,'X' <CHI>
 R;McKeehan, W.L.; Sakagami, Y.; Hoshi, H.; McKeehan, K.A.
 J. Biol. Chem. 261, 5378-5383, 1986
 A;Title: Two apparent human endothelial cell growth factors from human hepatoma cells ar
 A;Reference number: A92583; MUID:86168278; PMID:3007499
 A;Accession: B25604
 A;Molecule type: protein
 A;Residues: 206-214,'X',216-230,'X',232-239,'X',241-248,'XX',251-252,'X',254 <MCK>
 R;Englild, J.J.; Thøgersen, I.B.; Pizzo, S.V.; Salvesen, G.
 J. Biol. Chem. 264, 15975-15981, 1989
 A;Title: Analysis of inter-alpha-trypsin inhibitor and a novel trypsin inhibitor, pre-al
 A;Reference number: A92736; MUID:89380192; PMID:2476436
 A;Accession: C34245
 A;Molecule type: protein
 A;Residues: 206-225 <ENG2>
 R;Traboni, C.; Cortese, R.
 Nucleic Acids Res. 14, 6340, 1986
 A;Title: Sequence of a full length cDNA coding for human protein HC (alpha-1-microglobul
 A;Reference number: A25303; MUID:86312901; PMID:2428011
 A;Accession: A25303
 A;Molecule type: mRNA
 A;Residues: 1-218,'HW' <TRA>
 A;Note: this mRNA sequence appears to contain errors after residue 218
 R;Calero, M.; Escribano, J.; Grubb, A.; Mendez, E.
 J. Biol. Chem. 269, 384-389, 1994
 A;Title: Location of a novel type of interpolypeptide chain linkage in the human protei
 A;Reference number: A53110; MUID:94103241; PMID:7506257
 A;Accession: A53110
 A;Molecule type: protein
 A;Residues: 45-57 <CAL1>
 R;Vetr, H.; Koesler, M.; Gebhard, W.
 FEBS Lett. 245, 137-140, 1989
 A;Title: The domain structure of the inhibitor subunit of human inter-alpha-trypsin inh
 A;Reference number: S03552; MUID:89171290; PMID:2466696
 A;Accession: S03552
 A;Status: nucleic acid sequence not shown
 A;Molecule type: DNA
 A;Residues: 206-352 <VET2>
 R;Malik, N.; Balduyck, M.; Maes, P.; Capon, C.; Mizon, C.; Han, K.K.; Tartar, A.; Four
 Biol. Chem. Hoppe-Seyler 373, 1009-1018, 1992
 A;Title: The heavy chains of human plasma inter-alpha-trypsin inhibitor: their isolatio
 A;Reference number: S28928; MUID:93039735; PMID:1384548
 A;Accession: S28930
 A;Status: preliminary
 A;Molecule type: protein
 A;Residues: 206-215 <MAL>
 R;Moralle, W.; Capon, C.; Balduyck, M.; Sautiere, P.; Kouach, M.; Michaleki, C.; Fourne
 Eur. J. Biochem. 221, 881-888, 1994
 A;Title: Chondroitin sulphate covalently cross-links the three polypeptide chains of in
 A;Reference number: S43466; MUID:94229087; PMID:7513643
 A;Accession: S43466
 A;Status: preliminary
 A;Molecule type: protein
 A;Residues: 206-221 <MOR>
 R;Wisniewski, H.G.; Burgess, W.H.; Oppenheim, J.D.; Vilcek, J.
 Biochemistry 33, 7423-7429, 1994
 A;Title: TSG-6, an arthritis-associated hyaluronan binding protein, forms a stable comp
 A;Reference number: A53642; MUID:94271799; PMID:7516184
 A;Accession: A53642
 A;Status: preliminary
 A;Molecule type: protein
 A;Residues: 206-217 <WIS>
 R;Calero, M.; Mendez, E.; Garcia, E.
 Biochim. Biophys. Acta 1249, 91-99, 1995
 A;Title: Expression of the human complex-forming glycoprotein HC (alpha-1-microglobulin
 A;Reference number: S55688; MUID:95284116; PMID:7539295
 A;Accession: S55688

A:Reference number: A01223
A:Accession: A01223
A:Molecule type: protein
A:Residues: 1-65 <RT>
A:Cross-references: UNIPROT:P00992
C:Superfamily: basic proteinase inhibitor; animal Kunitz-type proteinase inhibitor homolog
C:Keywords: serine proteinase inhibitor; venom
F;7-57/Domain: animal Kunitz-type proteinase inhibitor homology <BPI>
F;7-57,16-40,32-53/Disulfide bonds: #status predicted
F;17/inhibitory site: Leu (chymotrypsin) #status predicted

Query Match 24.2%; Score 151; DB 1; Length 65;
Best Local Similarity 47.3%; Pred. No. 7.2e-07;
Matches 26; Conservative 9; Mismatches 20; Indels 0; Gaps 0;

QY 48 RNDICSMPOBAGPCLASIPHWYNNKTKICSEFYGGCGQNNNFQTEAICLVTC 102
Db 3 RPKFCYLPADPGRCCLAYMPFRFYNPASNCKEKFYGGCGGNANNFKTWDECRHTC 57

RESULT 30
A32282
Alzheimer's disease amyloid beta protein precursor - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 17-Aug-1989 #sequence_revision 17-Aug-1989 #text_change 09-Jul-2004
C:Accession: A32282
R;Yamada, T.; Sasaki, H.; Dohura, K.; Goto, I.; Sakaki, Y.
Biochem. Biophys. Res. Commun. 158, 906-912, 1989
A:Title: Structure and expression of the alternatively-spliced forms of mRNA for the mouse
A:Reference number: A32282; MUID:89149813; PMID:2493250
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-100 <YAM>
A:Cross-references: UNIPROT:P12023; GB:M24397; NID:G200350; PID:AAA39929.1; PID:G200350
C:Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase inhibitor
C:Keywords: alternative splicing
F;11-61/Domain: animal Kunitz-type proteinase inhibitor homology <BPI>

Query Match 24.2%; Score 151; DB 2; Length 100;
Best Local Similarity 44.4%; Pred. No. 1e-06;
Matches 24; Conservative 7; Mismatches 23; Indels 0; Gaps 0;

QY 49 KDICSMPOBAGPCLASIPHWYNNKTKICSEFYGGCGQNNNFQTEAICLVTC 102
Db 8 REVCSQATGTPCRAMISRWYFDVTEGKVPFFYGGCGGNRNNFDTEECMAVC 61

RESULT 31
S01802
Chymotrypsin inhibitor I - silkworm
C:Species: Bombyx mori (silkworm)
C:Date: 30-Sep-1989 #sequence_revision 30-Sep-1989 #text_change 09-Jul-2004
C:Accession: S01802
R;Sasaki, T.
Biol. Chem. Hoppe-Seyler 369, 1235-1241, 1988
A:Title: Amino-acid sequences of two basic chymotrypsin inhibitors from silkworm larval
A:Reference number: S01802; MUID:89228538; PMID:3072972
A:Accession: S01802
A:Molecule type: protein
A:Residues: 1-62 <SAS>
A:Cross-references: UNIPROT:P10831
C:Superfamily: basic proteinase inhibitor; animal Kunitz-type proteinase inhibitor homolog
C:Keywords: serine proteinase inhibitor
F;9-60/Domain: animal Kunitz-type proteinase inhibitor homology <BPI>

Query Match 23.9%; Score 149.5; DB 2; Length 62;
Best Local Similarity 54.4%; Pred. No. 9.4e-07;
Matches 31; Conservative 4; Mismatches 21; Indels 1; Gaps 1;

QY 49 KDICSMPOBAGPCLASIPHWYNNKTKICSEFYGGCGQNNNFQTEAICLVTC 104
Db 6 KPICEQAFGNSGPCFAIVKLYSYNQTKCKEEFYGGCGGNRNNRFTLAECEQCKIK 62

RESULT 32
T32060
hypothetical protein R12A1.3 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 09-Jul-2004
C:Accession: T32060
R;Pauley, A.; Andrews, S.
submitted to the EMBL Data Library, July 1997
A:Description: The sequence of C. elegans cosmid R12A1.
A:Reference number: Z21118
A:Accession: T32060
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-249 <PAU>
A:Cross-references: UNIPROT:O16701; EMBL:AF016680; PIDN:AA866164.1; GSPDB:GN00023; CESP
A:Experimental source: strain Bristol N2; clone R12A1
C:Genetics:
A:Gene: CESP:R12A1.3
A:Map position: 5
A:Introns: 75/1; 139/1

Query Match 23.9%; Score 149.5; DB 2; Length 249;
Best Local Similarity 31.1%; Pred. No. 2.8e-06;
Matches 33; Conservative 16; Mismatches 46; Indels 11; Gaps 3;

QY 8 CPK-IKVECEVEEIDQCTKPRDCPENMKCC-----PFSCGKKCLD----PRKDICSMPQ 56
Db 88 CRRPLGISVFDNTTIGCWMDSNCPGQKCCVEPNVTNSATRICRDPVGIASISICSLPL 147

QY 57 EAGPCLASIPHWYNNKTKICSEFYGGCGQNNNFQTEAICLVTC 102
Db 148 AVGSCTAPAVRFYYDASSGRCNQFMYSGGGNANNFQSLSSCGTC 193

RESULT 33
TIFHBP
proteinase inhibitor - flesh fly (Sarcophaga bullata)
C:Species: Sarcophaga bullata
C:Date: 07-Feb-1992 #sequence_revision 22-Jul-1994 #text_change 09-Jul-2004
C:Accession: A37294
R;Papayannopoulos, I.A.; Biemann, K.
Protein Sci. 1, 278-288, 1992
A:Title: Amino acid sequence of a protease inhibitor isolated from Sarcophaga bullata
A:Reference number: A37294; MUID:93284121; PMID:1304909
A:Accession: A37294
A:Molecule type: protein
A:Residues: 1-57 <PAP>
A:Cross-references: UNIPROT:P26228
A:Experimental source: hemolymph
C:Superfamily: basic proteinase inhibitor
C:Keywords: serine proteinase inhibitor
F;8-56/Domain: animal Kunitz-type proteinase inhibitor homology <BPI>
F;6-56,15-39,31-52/Disulfide bonds: #status predicted
F;16/inhibitory site: Arg (chymotrypsin) #status predicted

Query Match 23.8%; Score 149; DB 1; Length 57;
Best Local Similarity 48.1%; Pred. No. 9.8e-07;
Matches 26; Conservative 7; Mismatches 21; Indels 0; Gaps 0;

QY 49 KDICSMPOBAGPCLASIPHWYNNKTKICSEFYGGCGQNNNFQTEAICLVTC 102
Db 3 KSACLPQKVGPCRKSDFFVFFYNADTKACEEFLYGCGGNRNNRFTKKECEKIC 56

RESULT 34
S04855
Alzheimer's disease amyloid A4 protein - mouse (fragment)
C:Species: Mus musculus domesticus (western European house mouse)
C:Date: 28-Feb-1990 #sequence_revision 28-Feb-1990 #text_change 09-Jul-2004
C:Accession: S04855
R;Fukuchi, K.I.; Martin, G.M.; Deeb, S.S.

C:Superfamily: alpha-1-microglobulin and inter-alpha-trypsin inhibitor light chain precursor
C:Keywords: duplication; glycoprotein; plasma; serine proteinase inhibitor
F:7-57/Domain: animal Kunitz-type proteinase inhibitor homology <BPI>
F:63-113/Domain: animal Kunitz-type proteinase inhibitor homology <BP2>
F:7-57,16-40,32-53,63-113,72-96,88-109/Disulfide bonds: #status predicted
F:17/inhibitory site: Leu (chymotrypsin, elastase) #status predicted
F:26/Binding site: carboxylate (Asn) (covalent) #status experimental
F:73/inhibitory site: Arg (trypsin) #status predicted

Query Match 23.5%; Score 147; DB 1; Length 125;
Best Local Similarity 42.9%; Pred. No. 2.7e-06;
Matches 24; Conservative 9; Mismatches 23; Indels 0; Gaps 0;

QY 48 RKDSCMPQEAQPCPLASIPHWYNNKTKICSFYIYGGCGNNNNFQTEAICLVTC 103
DB 3 KEDSCQLDHAQPCGLMISRYFYNGTSMACETFYGGCLNGNFPASQKCLQTCR 58

RESULT 39

TIBO

basic proteinase inhibitor precursor - bovine
N:Alternate names: aprotinin; basic pancreatic trypsin inhibitor; BPTI; cationic kallikrein
C:Species: Bos primigenius taurus (cattle)
C:Date: 24-Apr-1984 #sequence revision 22-Jul-1994 #text change 09-Jul-2004
C:Accession: S00277; A30333; S10546; S02486; S28197; A90162; A90736; A90927; A34
R:Creighton, T.E.; Charles, I.G.
J. Mol. Biol. 194, 11-22, 1987

A:Title: Sequences of the genes and polypeptide precursors for two bovine protease inhib
A:Reference number: S00274; MUID:87283904; PMID:2441071

A:Accession: S00277

A:Molecule type: DNA; mRNA

A:Residues: 1-100 <CR2>

A:Cross-references: UNIPROT:P00974; GB:M20934; GB:X05274; NID:g162767; PIDN:AAD13685.1;
R:Creighton, T.E.; Charles, I.G.
Cold Spring Harb. Symp. Quant. Biol. 52, 511-519, 1987

A:Title: Biosynthesis, processing, and evolution of bovine pancreatic trypsin inhibitor.
A:Reference number: A90926; MUID:88295740; PMID:2456884

A:Accession: A30333

A:Molecule type: DNA

A:Residues: 1-100 <CRE>

A:Cross-references: GB:M20934; GB:X05274; NID:g162767; PIDN:AAD13685.1; PID:g162769
R:Kingston, I.B.; Anderson, S.
Biochem. J. 233, 443-450, 1986

A:Title: Sequences encoding two trypsin inhibitors occur in strikingly similar genomic e
A:Reference number: S10546; MUID:86158754; PMID:2420326

A:Accession: S10546

A:Molecule type: DNA

A:Residues: 34-97 <KIN>

R:Fioretti, E.; Angeletti, M.; Fiorucci, L.; Barra, D.; Bossa, F.; Ascoli, F.
Biol. Chem. Hoppe-Seyler 369(Suppl.), 37-42, 1988

A:Title: Aprotinin-like isoforms in bovine organs.
A:Reference number: S02485; MUID:89076531; PMID:2462435

A:Accession: S02486

A:Molecule type: protein

A:Residues: 36-93 <PIO>

R:Ikemita, M.; Jones, C.S.; Kamo, M.; Tsugita, A.; Kizuki, K.; Moriya, H.
Protein Seq. Data Anal. 5, 7-11, 1992

A:Title: Purification and characterization of the major cationic kallikrein inhibitor in
A:Reference number: S28197; MUID:93150003; PMID:1283464

A:Accession: S28197

A:Molecule type: protein

A:Residues: 36-93 <IKE>

R:Kassell, B.; Laskowski, M.
Biochem. Biophys. Res. Commun. 20, 463-468, 1965

A:Title: The basic trypsin inhibitor of bovine pancreas. V. The disulfide linkages.
A:Reference number: A90162; MUID:66083012; PMID:5860161

A:Contents: annotation; disulfide bonds

A:Accession: A90162

A:Molecule type: protein

A:Residues: 36-93 <RAS>

R:Anders, F.A.; Hornle, S.
J. Biol. Chem. 241, 1569-1572, 1966

A:Title: The disulfide linkages in kallikrein inactivator of bovine lung.

A:Reference number: A92023; MUID:66171231; PMID:5296424

A:Contents: annotation; disulfide bonds

A:Accession: A92023

A:Molecule type: protein

A:Residues: 36-93 <AN2>

R:Chauvet, J.; Acher, R.
Bull. Soc. Chim. Biol. 49, 985-1000, 1967

A:Title: La structure covalente d'un inhibiteur polypeptidique de la trypsine (inhibiteu
A:Reference number: A90736; MUID:68012003; PMID:6053284

A:Contents: annotation; disulfide bonds

A:Accession: A90736

A:Molecule type: protein

A:Residues: 36-93 <CH>

R:Diouha, V.; Pospisilova, D.; Meloun, B.; Sorm, F.
Collect. Czech. Chem. Commun. 33, 1363-1365, 1968

A:Title: Sequence of residues 18-20 in pancreatic trypsin inhibitor.
A:Reference number: A90927

A:Accession: A90927

A:Molecule type: protein

A:Residues: 36-93 <DLO>

R:Huber, R.; Kukla, D.; Ruhlmann, A.; Epp, O.; Formanek, H.
Naturwissenschaften 57, 389-392, 1970

A:Title: The basic trypsin inhibitor of bovine pancreas. I. Structure analysis and conf
A:Reference number: A3410; MUID:70255230; PMID:5447861

A:Contents: annotation; X-ray crystallography of basic protease inhibitor, 2.5 angstroms
R:Lewis, R.V.; Ray, P.; Cogull, R.; Kruggel, W.
Biochem. Biophys. Res. Commun. 167, 543-547, 1990

A:Title: Presence of pancreatic trypsin inhibitor in adrenal medullary chromaffin cells
A:Reference number: A34658; MUID:90211226; PMID:2322242

A:Accession: A34658

A:Molecule type: protein

A:Residues: 36-53,55-81 <LEW>

R:Anderson, S.; Kingston, I.B.
Proc. Natl. Acad. Sci. U.S.A. 80, 6838-6842, 1983

A:Title: Isolation of a genomic clone for bovine pancreatic trypsin inhibitor by using a
A:Reference number: A93977; MUID:84070725; PMID:6580617

A:Accession: A93977

A:Molecule type: DNA

A:Residues: 'PSLFNDRPPIPA',34-97,'GKTGRAGEGKG' <AND>

A:Cross-references: GB:X03365; GB:K00966; NID:g142; PIDN:CAA27062.1; PID:g1364183
R:Siekman, J.; Wenzel, H.R.; Schroeder, W.; Tschesche, H.
Biol. Chem. Hoppe-Seyler 369, 157-163, 1988

A:Title: Characterization and sequence determination of six aprotinin homologues from bo
A:Reference number: S00371; MUID:88221840; PMID:2453200

A:Accession: S10062

A:Molecule type: protein

A:Residues: 36-66,'p',68-82,'s',84-93 <SIE>

A:Experimental source: lung

A:Note: the authors designated this protein as isoprotinin 2

C:Comment: basic proteinase inhibitor is an intracellular polypeptide found in many tis
C:Genetics:

A:Introns: 34/1; 98/1

A:Superfamily: basic proteinase inhibitor; animal Kunitz-type proteinase inhibitor homol
C:Keywords: serine proteinase inhibitor

F:1-20/Domain: signal sequence #status predicted <SIG>

F:21-35/Domain: signal sequence #status predicted <PRO>

F:36-100/Product: basic proteinase inhibitor #status experimental <MAT>

F:40-90/Domain: animal Kunitz-type proteinase inhibitor homology <BPI>

F:40-90,49-73,65-86/Disulfide bonds: #status experimental

F:50/inhibitory site: Lys (trypsin, chymotrypsin, kallikrein, plasmin) #status experime

Query Match 23.4%; Score 146; DB 1; Length 100;
Best Local Similarity 43.6%; Pred. No. 2.8e-06;
Matches 24; Conservative 8; Mismatches 23; Indels 0; Gaps 0;

QY 48 RKDSCMPQEAQPCPLASIPHWYNNKTKICSFYIYGGCGNNNNFQTEAICLVTC 102
DB 36 RPDFCLPEPYTGPKARIIRYFNAGKLCQTFYVGGCRKNFPAEDCMRTC 90

RESULT 40
S12143
lipoprotein-associated coagulation inhibitor precursor - rabbit

A:Reference number: A55115; MUID:95014140; PMID:7929061

A:Accession: A55115

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-122 <STA>

A:Cross-references: UNIPROT:Q29100; GB:U14282; NID:G682652; PIDN:AAA62425.1; PID:G682653

A>Note: authors translated the codon GGC for residue 36 as Ala, AGC for residue 48 as Arg

C:Superfamily: basic proteinase inhibitor; animal Kunitz-type proteinase inhibitor homolog

C:Keywords: serine proteinase inhibitor

F:38-88/Domain: animal Kunitz-type proteinase inhibitor homolog <BPI>

Query Match 23.2%; Score 145; DB 1; Length 122;

Best Local Similarity 47.1%; Pred. No. 4e-06;

Matches 24; Conservative 5; Mismatches 22; Indels 0; Gaps 0;

QY 52 CSMPOEAGPCLASIPHHWYNNKTKICSEFYGGCCGQNNNNFOTEALCLVTC 102

DB 38 CREPPYTGCSAHFVYFNATYTGTCQSFYGGCRKQNNFWDKECLHTC 88

RESULT 45

I46937

tissue factor pathway inhibitor - rabbit

C:Species: Oryctolagus cuniculus (domestic rabbit)

C>Date: 04-Sep-1997 #sequence_revision 04-Sep-1997 #text_change 09-Jul-2004

C:Accession: I46937

R:Belaouaj, A.; Kuppusewamy, M.N.; Birktoft, J.J.; Bajaj, S.P.

Thromb. Res. 69, 547-553, 1993

A:Title: Revised cDNA sequence of rabbit tissue factor pathway inhibitor.

A:Reference number: I46937; MUID:93276427; PMID:8503123

A:Accession: I46937

A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-299 <BEL>

A:Cross-references: UNIPROT:P19761; GB:S61902; NID:G386015; PIDN:AAB26836.1; PID:G386016

C:Superfamily: tissue factor pathway inhibitor; animal Kunitz-type proteinase inhibitor

F:49-99/Domain: animal Kunitz-type proteinase inhibitor homolog <BPII>

F:120-170/Domain: animal Kunitz-type proteinase inhibitor homolog <BPI>

F:212-262/Domain: animal Kunitz-type proteinase inhibitor homolog <BPI2>

Query Match 23.2%; Score 145; DB 2; Length 299;

Best Local Similarity 33.7%; Pred. No. 8.2e-06;

Matches 31; Conservative 15; Mismatches 38; Indels 8; Gaps 2;

QY 14 ECEVEIEDQCTK--PRDCPNMKCCPFCGKCLDFRDKDICSMPQAGPCLASIPHHWYN 71

DB 86 ENRFESLECKEKARDYPKMTTKLTFQKGK-----PDFCFLEDPGICRGVITRYFN 139

QY 72 KTKICSEFYGGCCGQNNNNFOTEALCLVTC 103

DB 140 NQSKQCFRKYGGLGNLNNFESLECKNTCE 171

RESULT 46

B59399

short epsilon-dendrotoxin His55, subunit - Dendroaspis angusticeps

C:Species: Dendroaspis angusticeps

C>Date: 31-Dec-2001 #sequence_revision 31-Dec-2001 #text_change 09-Jul-2004

C:Accession: B59399

R:Sigle, R.; Hackett, M.; Aird, S.D.

Toxicon 40, 297-308, 2002

A:Title: Primary structure of four dendrotoxin E homologs from the venom of Dendroaspis

A:Reference number: A59399

A:Accession: B59399

A>Status: preliminary

A:Molecule type: protein

A:Residues: 1-57 <AIR>

A:Cross-references: UNIPROT:Q7LZE3

A>Note: trypsin inhibitor; K+ channel antagonist

C:Superfamily: basic proteinase inhibitor; animal Kunitz-type proteinase inhibitor homolog

F:5-55/Disulfide bonds: #status experimental

F:14-38/Disulfide bonds: #status experimental

F:30-51/Disulfide bonds: #status experimental

Query Match 23.0%; Score 144; DB 2; Length 57;
Best Local Similarity 48.1%; Pred. No. 2.7e-06;
Matches 26; Conservative 5; Mismatches 23; Indels 0; Gaps 0;

QY 49 KDICSMPOEAGPCLASIPHHWYNNKTKICSEFYGGCCGQNNNNFOTEALCLVTC 102

DB 2 RTFCLELPAPGPGCKASIPAFYNNWAAKKQLPHYGGCKGNANRFSTIEKCRHAC 55

RESULT 47

TIEPED

venom basic proteinase inhibitor E - black mamba

C:Species: Dendroaspis polylepsis polylepsis (black mamba)

C>Date: 30-Nov-1980 #sequence_revision 30-Nov-1980 #text_change 09-Jul-2004

C:Accession: A01215

R:Joubert, F.J.; Strydom, D.J.

Eur. J. Biochem. 87, 191-198, 1978

A:Title: Snake venoms. The amino-acid sequence of trypsin inhibitor E of Dendroaspis poly

A:Reference number: A01215; MUID:78214615; PMID:668688

A:Accession: A01215

A:Molecule type: protein

A:Residues: 1-59 <JOU>

A:Cross-references: UNIPROT:P00984

A>Note: this protein inhibits trypsin and binds transition metal ions such as copper an

C:Superfamily: basic proteinase inhibitor; animal Kunitz-type proteinase inhibitor homolog

C:Keywords: serine proteinase inhibitor; venom

F:7-57/Domain: animal Kunitz-type proteinase inhibitor homolog <BPI>

F:7-57,16-40,32-53/Disulfide bonds: #status predicted

Query Match 23.0%; Score 144; DB 1; Length 59;

Best Local Similarity 48.1%; Pred. No. 2.8e-06;

Matches 26; Conservative 5; Mismatches 23; Indels 0; Gaps 0;

QY 49 KDICSMPOEAGPCLASIPHHWYNNKTKICSEFYGGCCGQNNNNFOTEALCLVTC 102

DB 4 RTFCLELPAPGPGCKASIPAFYNNWAAKKQLPHYGGCKGNANRFSTIEKCRHAC 57

RESULT 48

S00371

isoaprotinin G1 - bovine hybrid

C:Species: Bos primigenius indicus x Bos primigenius taurus (cattle)

C>Date: 31-Dec-1990 #sequence_revision 31-Dec-1990 #text_change 09-Jul-2004

C:Accession: S00371

R:Siekmann, J.; Wenzel, H.R.; Schroeder, W.; Tschesche, H.

Biol. Chem. Hoppe-Seyler 369, 157-163, 1988

A:Title: Characterization and sequence determination of six aprotinin homologues from b

A:Reference number: S00371; MUID:88221840; PMID:2453200

A:Accession: S00371

A:Molecule type: protein

A:Residues: 1-59 <SIE>

A:Cross-references: UNIPROT:Q7M311

C:Superfamily: basic proteinase inhibitor; animal Kunitz-type proteinase inhibitor homolog

C:Keywords: pyroglutamic acid; serine proteinase inhibitor

F:6-56/Domain: animal Kunitz-type proteinase inhibitor homolog <BPI>

F:7/Modified site: pyrrolidone carboxylic acid (Gln) #status predicted

F:16/Inhibitory site: Lys (trypsin) #status predicted

Query Match 23.0%; Score 144; DB 2; Length 59;

Best Local Similarity 41.8%; Pred. No. 2.8e-06;

Matches 23; Conservative 10; Mismatches 22; Indels 0; Gaps 0;

QY 48 RKDICSMPQEAGPCLASIPHHWYNNKTKICSEFYGGCCGQNNNNFOTEALCLVTC 102

DB 2 RPDFCLEPPYTGPGCKARMIRYFNKAGLCQPFVYGGCRKSNFNFKSADCDMRTC 56

RESULT 49

A59399

Long epsilon-dendrotoxin Arg55, subunit - Dendroaspis angusticeps

C:Species: Dendroaspis angusticeps

C>Date: 31-Dec-2001 #sequence_revision 31-Dec-2001 #text_change 09-Jul-2004

Search completed: September 21, 2005, 16:41:13
Job time : 16.3215 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 21, 2005, 15:41:33 ; Search time 58.472 Seconds
(without alignments)
928.315 Million cell updates/sec

Title: US-10-807-204-2

Perfect score: 625

Sequence: 1 EGILGKPCPKIKVECEVEEI.....GNNNNFQTEAICLVTCCKYH 106

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 50 summaries

Database : UniProt 03: *
1: uniprot_sprot: *
2: uniprot_trembl: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	449	71.8	137	2 Q9BDL0	Q9bd01 oryctolagus
2	446	71.4	131	1 WFD6 HUMAN	Q9bqv6 homo sapien
3	408	65.3	182	2 Q6I5I9	Q6ie19 rattus norv
4	400	64.0	133	1 EPPI HUMAN	Q95925 homo sapien
5	400	64.0	143	2 Q86TF9	Q86tp9 homo sapien
6	393	62.9	133	2 Q8H245	Q8hz45 papio papio
7	388	62.1	133	1 EPPI MACMU	Q9bd11 macaca mula
8	352	56.3	134	1 EPPI MOUSE	Q9da01 mus musculus
9	216	34.6	241	1 WFD8 HUMAN	Q8iua0 homo sapien
10	197	31.5	759	2 Q8IT91	Q8it91 ancylostoma
11	187	29.9	2772	2 Q9VAV4	Q9vav4 drosophila
12	187	29.9	2776	2 Q869A0	Q869a0 drosophila
13	187	29.9	2894	2 Q7KEX2	Q7krx2 drosophila
14	187	29.9	2898	2 Q868Z9	Q868z9 drosophila
15	186	29.8	110	1 IBP CARCR	P00993 caretta car
16	184.5	29.5	988	2 Q2Z585	Q22585 caenorhabdi
17	182.5	29.2	571	2 Q7TQN3	Q7tqn3 mus musculus
18	182	29.1	2419	2 Q7PXZ1	Q7pxz1 anopheles g
19	173.5	27.8	576	2 Q8TU88	Q8teu8 homo sapien
20	173.5	27.8	576	2 Q6UXZ9	Q6uxz9 homo sapien
21	173.5	27.8	3198	2 Q9UG88	Q9ug88 manduca sex
22	173	27.7	587	2 Q6AX20	Q6ax20 xenopus lae
23	173	27.7	751	2 Q708Z0	Q708z0 xenopus lae
24	172.5	27.6	1599	2 Q09983	Q09983 caenorhabdi
25	172	27.5	67	1 IBPC BOVIN	P00976 bos taurus
26	172	27.5	750	2 Q6DJB6	Q6djbe xenopus tro
27	171	27.4	1416	1 YN81 CAEEL	Q03610 caenorhabdi
28	170.5	27.3	122	1 BT1A_BOOMI	P83609 boophilus m
29	170	27.2	83	2 Q6ITB9	Q6itb9 pseudechis
30	169	27.0	83	2 Q6ITB5	Q6itb5 oxyuranus m
31	169	27.0	169	2 Q9N0X7	Q9n0x7 bos taurus

32	169	27.0	516	2 Q7T363	Q7t363 brachydanio
33	168	26.9	86	2 Q9GP15	Q9gp15 ixodes ricci
34	168	26.9	922	2 Q21418	Q21418 caenorhabdi
35	167.5	26.8	1297	2 Q9N343	Q9n343 caenorhabdi
36	167	26.7	80	2 Q8T3S7	Q8t3s7 araneus ven
37	167	26.7	83	2 Q6ITB4	Q6itb4 oxyuranus m
38	167	26.7	83	2 Q6ITB6	Q6itb6 oxyuranus g
39	167	26.7	90	2 Q8T6S5	Q8t6s5 bitis gabon
40	166.5	26.6	515	2 Q6DRJ1	Q6drj1 brachydanio
41	166	26.6	83	2 Q90WAI	Q90wal pseudonaja
42	166	26.6	507	2 Q6I750	Q6i750 rattus norv
43	165.5	26.5	2174	2 Q9GQ00	Q9gqro drosophila
44	165	26.4	234	2 Q7YRQ8	Q7yrq8 bos taurus
45	165	26.4	283	2 Q6ZNI4	Q6zni4 homo sapien
46	165	26.4	342	2 Q7SZ46	Q7sz46 xenopus lae
47	165	26.4	507	1 SPT1 MOUSE	Q9r097 mus musculus
48	165	26.4	1474	2 Q6Z504	Q6z504 caenorhabdi
49	163.5	26.2	69	1 CRPT_BOOMI	P81162 boophilus m
50	163.5	26.2	750	2 Q708Y9	Q708y9 xenopus lae

ALIGNMENTS

RESULT 1

Q9BDL0 PRELIMINARY; PRT; 137 AA.
AC Q9BDL0;
DT 01-JUN-2001 (TREMELrel. 17, Created)
DT 01-JUN-2001 (TREMELrel. 17, Last sequence update)
DT 01-MAR-2004 (TREMELrel. 26, Last annotation update)
DE Eppin.
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
ON NCBI_TaxID=9986;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Testis;
RX MEDLINE=22791380; PubMed=12909348; DOI=10.1016/S0378-1119(03)00608-5;
RA Sivashanmugam P., Hall S.H., Hamil K.G., French F.S., O'Rand M.G.,
RA Richardson R.T.;
RT "Characterization of mouse Eppin and a gene cluster of similar
RT protease inhibitors on mouse chromosome 2.";
RL Gene 312:125-134(2003).
CC -1- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.
DR EMBL; AF345415; AAK31337.1; -.
DR HSP; Q16039; IAP.
DR GO; GO:0004867; F:serine-type endopeptidase inhibitor activity; IEA.
DR InterPro; IPR002223; Prot_Inh_Kunz-m.
DR InterPro; IPR008197; WAP.
DR Pfam; PF00014; Kunitz_BPTI; 1.
DR Pfam; PF00095; WAP; 1.
DR PRINTS; PRO0003; 4DISULPHCORE.
DR PRINTS; PRO0759; BASICPTASE.
DR ProDom; PD000222; Prot_Inh_Kunz-m; 1.
DR SMART; SM00131; KU; 1.
DR SMART; SM00217; WAP; 1.
DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
DR PROSITE; PS00279; BPTI_KUNITZ_2; 1.
SQ SEQUENCE 137 AA; 15773 MW; F397AF4E065D626B CRC64;

Query Match 71.8%; Score 449; DB 2; Length 137;

Best Local Similarity 70.9%; Pred. No. 7.3e-36;

Matches 73; Conservative 13; Mismatches 17; Indels 0; Gaps 0;

QY 1 EGILGKPCPKIKVECEVEIDQCTKPRDCPENKCCPFSCGKKCLDFRDKICSMPOEAGP 60

Db 26 EGGFIKTCPIKVKVEVESECTRRHRCPDKNKCLFNCGKKCLDLRDKVCSMPKETGP 85

QY 61 CLASIPHWYWKTKICSEFIYGGCGGNNNNFQTEAICLVTC 103

Db 86 CLAFIPRWYDKEREICTEFYGGCGGNNNNFQTEAICLVICQ 128

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RESULT 2
WFD6 HUMAN
ID WFD6 HUMAN STANDARD; PRT; 131 AA.
AC Q9BQY6; Q9NFV6;
DT 10-OCT-2003 (Rel. 42, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE WAP four-disulfide core domain protein 6 precursor (Putative protease
DE inhibitor WAP6).
GN Name=WFD6; Synonyms=C20orf171, WAP6;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM 2).
RX MEDLINE=22304654; PubMed=12206714; DOI=10.1042/BJ20020869;
RA Clauss A., Lilja H., Lundwall A.;
RT "A locus on human chromosome 20 contains several genes expressing
RT protease inhibitor domains with homology to whey acidic protein.";
RL Biochem. J. 368:233-242(2002).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RX MEDLINE=21638749; PubMed=11780052; DOI=10.1038/414865a;
RA Deloukas P., Matthews L.H., Ashurst J.L., Burton J., Gilbert J.G.R.,
RA Jones M., Stavrides G., Almeida J.P., Babbage A.K., Bagguley C.B.,
RA Bailey J., Barlow K.F., Bates K.N., Beard L.M., Beare D.M.,
RA Beasley O.P., Bird C.P., Blakey S.E., Bridgeman A.M., Brown A.J.,
RA Buck D., Burrill W.D., Butler A.P., Carder C., Carter N.P.,
RA Chapman J.C., Clamp M., Clark A.P., Clark L.N., Clark S.Y., Clee C.M.,
RA Clegg S., Cobley V.E., Collier R.E., Connor R.E., Corby N.R.,
RA Coulson A., Coville G.J., Deadman R., Dhani P.D., Dunn M.,
RA Ellington A.G., Frankland J.A., Fraser A., French L., Garner P.,
RA Gramham D.V., Griffiths C., Griffiths M.N.D., Gwilliam R., Hall R.E.,
RA Hammond S., Harley J.L., Heath P.D., Ho S., Holden J.L., Howden P.J.,
RA Huckle B., Hunt A.R., Hunt S.E., Jekosch K., Johnson C.M., Johnson D.,
RA Kay M.P., Kimberley A.M., King A., Knights A., Laird G.K., Lawlor S.,
RA Levaesliao M.H., Leversha M.A., Lloyd C., Lloyd D.M., Lovell J.D.,
RA Marsh V.L., Martin S.L., McConachie L.J., McIlroy K., McMurray A.A.,
RA Milne S.A., Mistry D., Moore M.J.F., Mullikin J.C., Nickerson T.,
RA Oliver K., Parker A., Patel R., Pearce T.A.V., Peck A.I.,
RA Phillimore B.J.C.T., Prathalingam S.R., Plumb R.W., Ramsay H.,
RA Rice C.M., Ross M.T., Scott C.E., Sehra H.K., Showkeen R., Sims S.,
RA Skuce C.D., Smith M.L., Soderlund C., Steward C.A., Sulston J.E.,
RA Swann R.D., Sycamore N., Taylor R., Tee L., Thomas D.W., Thorpe A.,
RA Tracey A., Tromans A.C., Vaudin M., Wall M., Wallis J.M.,
RA Whitehead S.L., Whittaker P., Willey D.L., Williams L., Williams S.A.,
RA Wilming L., Wray P.W., Hubbard T., Durbin R.M., Bentley D.R., Beck S.,
RA Rogers J.;
RT "The DNA sequence and comparative analysis of human chromosome 20.";
RL Nature 414:865-871(2001).
CC -!- SUBCELLULAR LOCATION: Secreted (Potential).
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=1;
CC IsoId=Q9BQY6-1; Sequences=Displayed;
CC Name=2;
CC IsoId=Q9BQY6-2; Sequences=VSP_007550, VSP_007551;
CC -!- TISSUE SPECIFICITY: Ubiquitously expressed, but the highest levels
CC are found in epididymis, testis and trachea.
CC -!- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.
CC -!- SIMILARITY: Contains 1 WAP-type domain.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC -----
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DR EMBL; AF411861; AAN03684.1; -.
DR EMBL; AL031663; CAC36264.1; -.
DR HSSP; P02760; 1B1K.
DR Genew; HGNC:16164; WFD6.
DR InterPro; IPR002223; Prot_inh_Kunz-m.
DR InterPro; IPR008197; WAP.
DR Pfam; PF00014; Kunitz_BPTI; 1.
DR Pfam; PF00095; WAP; 1.
DR PRINTS; PR00759; BASICPTASE.
DR PRODOM; PD000222; Prot_inh_Kunz-m; 1.
DR SMART; SMO0131; KU; 1.
DR SMART; SMO0217; WAP; 1.
DR PROSITE; PS00317; 4_DISULFIDE_CORE; FALSE_NEG.
DR PROSITE; PS00280; BPTI_KUNITZ_1; FALSE_NEG.
DR PROSITE; PS02079; BPTI_KUNITZ_2; 1.
KW Alternative splicing; Serine protease inhibitor; Signal.
FT SIGNAL 1 25 Potential.
FT CHAIN 26 131 WAP four-disulfide core domain protein 6.
FT DOMAIN 31 69 WAP.
FT DOMAIN 70 128 BPTI/Kunitz inhibitor.
FT DISULFID 33 61 By similarity.
FT DISULFID 48 60 By similarity.
FT DISULFID 54 69 By similarity.
FT VARSPLIC 75 86 IYAVCHRRLLAPA -> VSLTLYHKEELE (in isoform
FT 2).
FT VARSPLIC 87 131 /FTId=VSP_007550.
FT VARSPLIC 87 131 Missing (in isoform 2).
SQ SEQUENCE 131 AA; 14626 MW; 2F6D06EF43EB7564 CRC64;
Query Match 71.4%; Score 446; DB 1; Length 131;
Best Local Similarity 78.3%; Pred. No. 1.4e-35;
Matches 83; Conservative 1; Mismatches 22; Indels 0; Gaps 0;
QY 1 EGILGKCPKIKVCEVEEIDQCTKPRDCPENMKCCPFSCGKCLDFRKYAVCHRRLLAP 60
Db 26 EGILGKCPKIKVCEVEEIDQCTKPRDCPENMKCCPFSCGKCLDFRKYAVCHRRLLAP 85
QY 61 CLASIPHWYNNKTKICSEFIYGGCGQNNNNNFQEAICLVTCCKYH 106
Db 86 AWPPYHTGGTITKTKICSEFIYGGCGQNNNNNFQEAICLVTCCKYH 131
RESULT 3
Q9IE19
ID Q9IE19 PRELIMINARY; PRT; 182 AA.
AC Q6IE19;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE WAP four-disulfide core 6-like 1.
GN Name=wfd6l1;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Sprague-Dawley;
RX PubMed=15060002; DOI=10.1101/gr.1946304;
RT Puentes X.S., Lopez-Otin C.;
RT "A genomic analysis of rat proteases and protease inhibitors.";
RL Genome Res. 14:609-622(2004).
CC -!- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.
CC -!- MISCELLANEOUS: The sequence shown here is derived from an
CC EMBL/GenBank/DDJB third party annotation (TPA) entry.
DR EMBL; BN00374; CAES1900.1; -.
DR HSSP; P00974; 1K6U.
DR GO; GO:0004867; F:serine-type endopeptidase inhibitor activity; IEA.
DR InterPro; IPR002223; Prot_inh_Kunz-m.
DR InterPro; IPR008197; WAP.
DR Pfam; PF00014; Kunitz_BPTI; 1.
DR Pfam; PF00095; WAP; 1.
```

DR PRINTS; PRO0003; 4DISULPHCORE.
DR PRINTS; PRO0759; BASICPTASE.
DR ProDom; PD000222; Prot_Inh_Kunz-m; 1.
DR SMART; SM00131; KU; 1.
DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
DR PROSITE; PS00279; BPTI_KUNITZ_2; 1.
SQ SEQUENCE 182 AA; 21018 MW; EB12D7BF7F76707E CRC64;

Query Match 65.3%; Score 408; DB 2; Length 182;
Best Local Similarity 58.5%; Pred. No. 8.9e-32;
Matches 62; Conservative 19; Mismatches 25; Indels 0; Gaps 0;

QY 1 EGILGKPCPKIKVECEVBSIDQTKRDCPENKCKPSCGKKCLDFKDKICSMPEQACG 60
DB 26 EGLFFTKCPKIKDFERSQGRKQCPKQRCMPACGKCLDLNEDICSLPQDAGP 85

QY 61 CLASTPHWYKTKICSEFIYGGCGNNNFQTEAICLVTKCKYH 106
DB 86 CLAYLPRWYKTKNLCTQFIYGGCGNTNFLSKDICTSICTRKH 131

RESULT 4
EPTI_HUMAN
ID EPTI_HUMAN STANDARD; PRT; 133 AA.
AC O95925; Q96SD7; Q9HD30;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Eppin precursor (Epididymal protease inhibitor) (Serine protease
inhibitor-like with Kunitz and WAP domains 1) (WAP four-disulfide core
domain protein 7) (Protease inhibitor WAP7).
GN Name=SPINLW1; Synonyms=WAP7, WFDC7;
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
RC TISSUE=Epididymis, and Testis;
RX MEDLINE=21297183; PubMed=11404006; DOI=10.1016/S0378-1119(01)00462-0;
RA Richardson R.T., Sivashanmugam P., Hall S.H., Hamil K.G., Moore P.A.,
RA Ruben S.M., French P.S., O'Rand M.G.;
RT "Cloning and sequencing of human Eppin: a novel family of protease
inhibitors expressed in the epididymis and testis.";
RL Gene 270:93-102(2001).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RA Stavrides G.S., Huckle E.J., Deloukas P.;
RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=21638749; PubMed=11780052; DOI=10.1038/414865a;
RA Deloukas P., Matthews L.H., Ashurst J.L., Burton J., Gilbert J.G.R.,
RA Jones M., Stavrides G., Almeida J.P., Babbage A.K., Baggeley C.L.,
RA Bailey J., Barlow K.F., Bates K.N., Beard L.M., Beare D.M.,
RA Beasley O.P., Bird C.P., Blakey S.E., Bridgeman A.M., Brown A.J.,
RA Buck D., Burrill W.D., Butler A.P., Carder C., Carter N.P.,
RA Chapman J.C., Clamp M., Clark G., Clark L.N., Clark S.V., Clee C.M.,
RA Clegg S., Copley V.E., Collier R.E., Connor R.E., Corby N.R.,
RA Coulson A., Coville G.J., Deadman R., Dhani P.D., Dunn M.,
RA Ellington A.G., Frankland J.A., Fraser A., French L., Garner P.,
RA Grafham D.V., Griffiths C., Griffiths M.N.D., Gwilliam R., Hall R.E.,
RA Hammond S., Harley J.L., Heath P.D., Ho S., Holden J.L., Howden P.J.,
RA Huckle E., Hunt A.R., Hunt S.E., Jekosch K., Johnson C.M., Johnson D.,
RA Kay M.P., Kimberley A.M., King A., Knights A., Laird G.K., Lawlor S.,
RA Leharvestaiho M.H., Leverhwa M.A., Lloyd C., Lloyd D.M., Lovell J.D.,
RA Marsh V.L., Martin S.L., McConachie L.J., McKay K., McMurray A.A.,
RA Milne S.A., Mistry D., Moore M.J.F., Mullikin J.C., Nickerson T.,
RA Oliver K., Parker A., Patel R., Pearce T.A.V., Peck A.I.,
RA Phillimore B.J.C.T., Prathalingam S.R., Plumb R.W., Ramsay H.,
RA Rice C.M., Ross M.T., Scott C.E., Sehra H.K., Showkeen R., Sims S.,
RA Skuce C.D., Smith M.L., Soderlund C., Steward C.A., Sulston J.E.,
RA Swann R.M., Sycamore N., Taylor R., Tee L., Thomas D.W., Thorpe A.,

RA Tracey A., Tromans A.C., Vaudin M., Wall M., Wallis J.M.,
RA Whitehead S.L., Whitaker P., Willey D.L., Williams L., Williams S.A.,
RA Wilming L., Wray P.W., Hubbard T., Durbin R.M., Bentley D.R., Beck S.,
RT Rogers J.;
RL "The DNA sequence and comparative analysis of human chromosome 20.";
RN Nature 414:865-871(2001).
RP [4]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RX TISSUE=Brain;
RC MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.P., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Datchenko K.L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raba S.S., Lequellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalios D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC -!- SUBCELLULAR LOCATION: Secreted (Potential).
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=1;
CC IsoId=O95925-1; Sequence=Displayed;
CC Name=2;
CC IsoId=O95925-2; Sequence=VSP_006755;
CC -!- TISSUE SPECIFICITY: Expressed in epididymis and testis.
CC -!- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.
CC -!- SIMILARITY: Contains 1 WAP-type domain.
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EMBL; AF286370; AAG00548.1; -
EMBL; AF286369; AAG00547.1; -
EMBL; AF286368; AAG00546.1; -
EMBL; AL118493; CAB56343.1; -
EMBL; AL031663; CAB37635.1; -
EMBL; AL031663; CAB37635.1; -
EMBL; BC053363; CAC3265.1; -
EMBL; BC053363; AHA53369.1; -
HSSP; P00974; 1BPTI.
Genew; HGNC:15932; SPINLW1.
InterPro; IPR002223; Prot_Inh_Kunz-m.
InterPro; IPR008197; WAP.
Pfam; PF00014; Kunitz_BPTI; 1.
Pfam; PF00095; WAP; 1.
PRINTS; PRO0003; 4DISULPHCORE.
PRINTS; PRO0759; BASICPTASE.
ProDom; PD000222; Prot_Inh_Kunz-m; 1.
SMART; SM00131; KU; 1.
SMART; SM00217; WAP; 1.
PROSITE; PS00317; 4 DISULFIDE_CORE; 1.
PROSITE; PS00280; BPTI_KUNITZ_1; 1.
PROSITE; PS00279; BPTI_KUNITZ_2; 1.
Alternative splicing; Serine protease inhibitor; Signal.
SIGNAL 1 21 Potential.
CHAIN 22 133 Eppin.
FT

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FT DOMAIN 29 73 WAP.
FT BPTI 77 127 BPTI/Kunitz inhibitor.
FT DISULFID 33 61 By similarity.
FT DISULFID 40 65 By similarity.
FT DISULFID 48 60 By similarity.
FT DISULFID 54 69 By similarity.
FT DISULFID 77 127 By similarity.
FT DISULFID 86 110 By similarity.
FT DISULFID 102 123 By similarity.
FT VARSPIC 1 31 MGSLSLSLVFLVLANVQGLTDWLFPR -> MLSKAH
FT GCKTALSUG (in isoform 2).
SQ SEQUENCE 133 AA; 15284 MW; 7831B20336D9DC CRC64;

Query Match 64.0%; Score 400; DB 1; Length 133;
Best Local Similarity 66.7%; Pred. No. 3.9e-31;
Matches 64; Conservative 11; Mismatches 21; Indels 0; Gaps 0;

Qy 8 CPKIKVEVEEIDQCTKPRDCPENMKCCPFCGKCKLDPRKIDICSMFQEQAGPCLASIPH 67
Db 33 CPKIRECEFEQERDVCTKDRQCDNKKCCVFCGKCKLDLKQDVCMPKETGPGCLAYFLH 92

Qy 68 WYNNKTKICSEFYGGCGNNNNFQTEAICLVTC 103
Db 93 WYDCKDNTCSMFVYGGCGNNNNFQSKANCLNTCK 128

RESULT 5
Q86TP9 ID Q86TP9 PRELIMINARY; PRT; 143 AA.
AC Q86TP9;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE SPINLWI protein (fragment).
GN Name=SPINLWI;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Collins E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shemen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Griewood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smalish D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RX TISSUE=Brain;
RA Strausberg R.;
RC TISSUE=Brain;
RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.
DR EMBL; BC044829; AAH4829.1; -.
DR HSSP; P00974; 1UUA.
DR GO; GO:0004867; F:serine-type endopeptidase inhibitor activity; IEA.

DR InterPro; IPR002223; Prot_Inh_Kunz-m.
DR InterPro; IPR008197; WAP.
DR Pfam; PF00014; Kunitz_BPTI; 1.
DR Pfam; PF00095; WAP; 1.
DR PRINTS; PR00003; 4DISULPHCORE.
DR PRINTS; PR00759; BASICPTASE.
DR ProDom; PD000222; Prot_Inh_Kunz-m; 1.
DR SMART; SM00131; KU; 1.
DR SMART; SM00217; WAP; 1.
DR PROSITE; PS00317; 4_DISULFIDE_CORE; 1.
DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
DR PROSITE; PS02079; BPTI_KUNITZ_2; 1.
FT NON TER 1
SQ SEQUENCE 143 AA; 16506 MW; 92BF56C2B7977508 CRC64;

Query Match 64.0%; Score 400; DB 2; Length 143;
Best Local Similarity 66.7%; Pred. No. 4.2e-31;
Matches 64; Conservative 11; Mismatches 21; Indels 0; Gaps 0;

Qy 8 CPKIKVEVEEIDQCTKPRDCPENMKCCPFCGKCKLDPRKIDICSMFQEQAGPCLASIPH 67
Db 43 CPKIRECEFEQERDVCTKDRQCDNKKCCVFCGKCKLDLKQDVCMPKETGPGCLAYFLH 102

Qy 68 WYNNKTKICSEFYGGCGNNNNFQTEAICLVTC 103
Db 103 WYDCKDNTCSMFVYGGCGNNNNFQSKANCLNTCK 138

RESULT 6
Q8HZ45 ID Q8HZ45 PRELIMINARY; PRT; 133 AA.
AC Q8HZ45;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Epididymal protease inhibitor 1.
GN Name=Eppin;
OS Papio papio (Guinea baboon).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheidae;
OC Cercopitheinae; Papio.
OX NCBI_TaxID=100937;
RN [1]
RP SEQUENCE FROM N.A.
RX TISSUE=Testis;
RA Sivashanmugam P., O'Rand M.G., Richardson R.T.;
RL Submitted (AUG-2002) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.
DR EMBL; AY141973; AA080507.1; -.
DR HSSP; P00974; 1UUA.
DR GO; GO:0008233; F:peptidase activity; IEA.
DR GO; GO:0004867; F:serine-type endopeptidase inhibitor activity; IEA.
DR InterPro; IPR002223; Prot_Inh_Kunz-m.
DR InterPro; IPR008197; WAP.
DR Pfam; PF00014; Kunitz_BPTI; 1.
DR Pfam; PF00095; WAP; 1.
DR PRINTS; PR00759; BASICPTASE.
DR ProDom; PD000222; Prot_Inh_Kunz-m; 1.
DR SMART; SM00131; KU; 1.
DR SMART; SM00217; WAP; 1.
DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
DR PROSITE; PS02079; BPTI_KUNITZ_2; 1.
KW Protease.
SQ SEQUENCE 133 AA; 15277 MW; B33AE57ECBEBE84 CRC64;

Query Match 62.9%; Score 393; DB 2; Length 133;
Best Local Similarity 65.6%; Pred. No. 1.9e-30;
Matches 63; Conservative 9; Mismatches 24; Indels 0; Gaps 0;

Qy 8 CPKIKVEVEEIDQCTKPRDCPENMKCCPFCGKCKLDPRKIDICSMFQEQAGPCLASIPH 67
Db 33 CPKIRECEFEQERDVCTKDRQCDNKKCCVFCGKCKLDLKQDVCMPNETGPGCLAFFIR 92
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RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Boesak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny K.C., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC -!- SUBCELLULAR LOCATION: Secreted (Potential).
CC -!- TISSUE SPECIFICITY: Expressed in epididymis and testis.
CC -!- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.
CC -!- SIMILARITY: Contains 1 WAP-type domain.
CC -----
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CC or send an email to license@isb-sib.ch)
CC -----
CC EMBL; AF346413; AAK31335.1; -
CC EMBL; AK006296; BAB24514.1; -
CC EMBL; BC048637; AAH48637.1; -
CC HSSP; P31713; 1SHP.
CC MGD; MGI:1922776; Spinlwl.
CC GO; GO:0001669; C.acrosome; IDA.
CC GO; GO:0005737; C.cyttoplasm; IDA.
CC GO; GO:0005737; C.cyttoplasm; IDA.
CC InterPro; IPR002223; Prot_Inh_Kunz-m.
CC InterPro; IPR008197; WAP.
CC Pfam; PF00014; Kunitz_BPTI; 1.
CC Pfam; PF00095; WAP; 1.
CC PRINTS; PR00003; 4DISULPHCORE.
CC PRINTS; PR00759; BASICPTASE.
CC ProDom; PD000222; Prot_Inh_Kunz-m; 1.
CC PROSITE; PS00317; 4 DISULFIDE CORE; 1.
CC PROSITE; PS00280; BPTI_KUNITZ_1; 1.
CC PROSITE; PS0279; BPTI_KUNITZ_2; 1.
KW Serine protease inhibitor; Signal.
FT SIGNAL 1 21 Potential.
FT CHAIN 22 134 Eppin.
FT DOMAIN 29 73 WAP.
FT DOMAIN 77 127 BPTI/Kunitz inhibitor.
FT DISULFID 33 61 By similarity.
FT DISULFID 40 65 By similarity.
FT DISULFID 48 60 By similarity.
FT DISULFID 54 69 By similarity.
FT DISULFID 77 127 By similarity.
FT DISULFID 86 110 By similarity.
FT DISULFID 102 123 By similarity.
SQ SEQUENCE 134 AA; 15470 MW; DFEB63D4D4C427F CRC64;

Query Match 56.3%; Score 352; DB 1; Length 134;
Best Local Similarity 55.7%; Pred. No. 1.8e-26;
Matches 54; Conservative 20; Mismatches 23; Indels 0; Gaps 0;

QY 8 CPKIVKEVEIDCTKPRDCPENMKCCPFSCGKKCLDFRDKICSMPOEAGPCIASIPH 67
Db |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
33 CPFRFEECHQBRDLCTDRDCPKKCCVFCNGKKCLNPPQDICSPLPKSCVWYFR 92
QY 68 WYNNKTKICSFYIGGCGNNGNNNFQTEAICLVTCCK 104
Db |||:|||||:|||||:|||||:|||||:|||||:|||||:
93 WNFENKNSCTQVFIYGGCGNNGNNNFQSQSICQNACEK 129

RESULT 9
WFD8_HUMAN STANDARD; PRT; 241 AA.
ID WFD8_HUMAN
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AC Q8IUAO; Q96A34;
DT 10-OCT-2003 (Rel. 42, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE WAP four-disulfide core domain protein 8 precursor (Putative protease
DE inhibitor WAP8).
GN Name=WFD8; Synonyms=C20orf170, WAP8;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RN SEQUENCE FROM N.A.
RX MEDLINE=22304654; PubMed=12206714; DOI=10.1042/BJ20020869;
RT "A locus on human chromosome 20 contains several genes expressing
RT protease inhibitor domains with homology to whey acidic protein.";
RL Biochem. J. 368:233-242(2002).
RN [2]
RN SEQUENCE FROM N.A.
RX MEDLINE=21638749; PubMed=11780052; DOI=10.1038/414865a;
RA Deloukas P., Matthews L.H., Ashurst J.L., Burton J., Gilbert J.G.R.,
RA Jones M., Stavrides G., Almeida J.P., Babbage A.K., Bagguley C.L.,
RA Bailey J., Barlow K.F., Bates K.N., Beare D.M., Beare D.M.,
RA Beasley O.P., Bird C.P., Blakey S.E., Bridgeman A.M., Brown A.J.,
RA Buck D., Burrill W.D., Butler A.P., Carder C., Carter N.P.,
RA Chapman J.C., Clamp M., Clark G., Clark L.N., Clark S.Y., Clee C.M.,
RA Clegg S., Cobley V.E., Collier R.E., Connor R.E., Corby N.R.,
RA Coulson A., Coville G.J., Deadman R., Dhani P.D., Dunn M.,
RA Ellington A.G., Frankland J.A., Fraser A., French L., Garner P.,
RA Grafham D.V., Griffiths C., Griffiths M.N.D., Gwilliam R., Hall R.E.,
RA Hammond S., Harley J.L., Heath P.D., Ho S., Holden J.L., Howden P.J.,
RA Huckle E., Hunt A.R., Hunt S.E., Jekosch K., Johnson C.M., Johnson D.,
RA Kay M.P., Kimberley A.M., King A., Knights A., Laird G.K., Lawlor S.,
RA Lehaeslaio M.H., Leversha M.A., Lloyd C., Lloyd D.M., Lovell J.D.,
RA Marsh V.L., Martin S.L., McConachie L.J., McLeay K., McMurray A.A.,
RA Milne S.A., Mistry D., Moore M.J.F., Mullikin J.C., Nickerson T.,
RA Oliver K., Parker A., Patel R., Pearce T.A.V., Peck A.I.,
RA Phillimore B.J.C.T., Prathalingam S.R., Plumb R.W., Ramsay H.,
RA Rice C.M., Ross M.T., Scott C.E., Senra H.K., Shownkeen R., Sims S.,
RA Skuce C.D., Smith M.L., Soderlund C., Steward C.A., Sulston J.E.,
RA Swann R.M., Sycamore N., Taylor R., Tee L., Thomas D.W., Thorpe A.,
RA Tracey A., Tromans A.C., Vaudin M., Wall M., Wallis J.M.,
RA Whitehead S.L., Whittaker P., Willey D.L., Williams L., Williams S.A.,
RA Wilming L., Wray P.W., Hubbard T., Durbin R.M., Bentley D.R., Beck S.,
RA Rogers J.;
RT "The DNA sequence and comparative analysis of human chromosome 20.";
RL Nature 414:865-871(2001).
CC -!- SUBCELLULAR LOCATION: Secreted (Potential).
CC -!- TISSUE SPECIFICITY: Expressed ubiquitously, the highest levels are
CC found in the epididymis followed by testis and trachea.
CC -!- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.
CC -!- SIMILARITY: Contains 3 WAP-type domains.
CC -----
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CC -----
CC EMBL; AF492015; AAN70997.1; -
CC EMBL; AF492016; AAN70998.1; -
CC EMBL; AL031663; CAB37634.2; -
CC EMBL; AL591715; CAB39449.1; -
CC HSSP; P31713; 1SHP.
CC Genew; HGNC:16163; WFD8.
CC InterPro; IPR002223; Prot_Inh_Kunz-m.
CC InterPro; IPR008197; WAP.
CC Pfam; PF00014; Kunitz_BPTI; 1.
CC Pfam; PF00095; WAP; 3.
CC PRINTS; PR00003; 4DISULPHCORE.
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DR PRINTS; PR00759; BASICTPTASE.
DR ProDom; PD000222; Prot_Inh_Kunzt-m; 1.
DR SMART; SM00131; KU; 1.
DR SMART; SM00217; WAP; 3.
DR PROSITE; PS00317; 4 DISULFIDE CORE; 3.
DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
DR PROSITE; PS00279; BPTI_KUNITZ_2; 1.
KW Repeat; Serine protease inhibitor; Signal.
FT SIGNAL 1 38 Potential.
FT CHAIN 39 241 WAP four-disulfide core domain protein 8.
FT DOMAIN 47 90 WAP 1.
FT DOMAIN 95 145 BPTI/Kunitz inhibitor.
FT DOMAIN 150 193 WAP 2.
FT DOMAIN 197 239 WAP 3.
FT DISULFID 51 79 By similarity.
FT DISULFID 58 83 By similarity.
FT DISULFID 66 78 By similarity.
FT DISULFID 95 145 By similarity.
FT DISULFID 104 128 By similarity.
FT DISULFID 120 141 By similarity.
FT DISULFID 72 87 By similarity.
FT DISULFID 154 182 By similarity.
FT DISULFID 165 186 By similarity.
FT DISULFID 169 181 By similarity.
FT DISULFID 175 190 By similarity.
FT DISULFID 201 229 By similarity.
FT DISULFID 208 232 By similarity.
FT DISULFID 216 228 By similarity.
FT DISULFID 222 236 By similarity.
SQ SEQUENCE 241 AA; 27797 MW; 2566B54AF4BDC57B CRC64;

Query Match 34.6%; Score 216; DB 1; Length 241;
Best Local Similarity 40.4%; Pred. No. 4.6e-13;
Matches 40; Conservative 12; Mismatches 45; Indels 2; Gaps 1;

QY 6 KP-CPKIKVEVEIDQCTKPRDCPENKCKPSCGKGLDFRKIDICSMPOEAGPCLIA 63
DB 47 KPGCLCPKRLTCTTELPDSCNTDFDCKEYKQCFACQKCKMDPFPQPCWLPVRHGCNHN 106
QY 64 SIPHWYNNKTKICSEFYGGCGNNNNQTEAICLVTC 102
DB 107 EAQRWHDFKNVRCYTPFKYRGCEGNANFLSEDACTAC 145

RESULT 10
Q8IT91 PRELIMINARY; PRT; 759 AA.
AC Q8IT91;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Kunitz-like protease inhibitor precursor.
OS Ancylostoma caninum (Dog hookworm).
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Strongylida;
OC Ancylostomatidae; Ancylostomatinae; Ancylostominae; Ancylostoma.
OX NCBI_TaxID=29170;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Baltimore;
RX MEDLINE=22645137; PubMed=12760667;
RA Hawdon J.M., Datu B., Crowell M.;
RT "Molecular cloning of a novel multidomain Kunitz-type proteinase
inhibitor from the hookworm Ancylostoma caninum.";
RL J. Parasitol. 89:402-407(2003).
CC -1- SIMILARITY: Contains 12 BPTI/Kunitz inhibitor domains.
DR ENBL; AFS33590; AAN10061.1; -.
DR HSSP; P31713; 1SHP.
DR GO; GO:0008213; F:peptidase activity; IEA.
DR GO; GO:0004867; F:serine-type endopeptidase inhibitor activity; IEA.
DR InterPro; IPR002223; Prot_inh_Kunzt-m.
DR Pfam; PF00014; Kunitz BPTI; 12.
DR PRINTS; PR00759; BASICTPTASE.
DR SMART; SM00131; KU; 12.

DR PROSITE; PS00280; BPTI_KUNITZ_1; 10.
DR PROSITE; PS00279; BPTI_KUNITZ_2; 12.
KW Protease; Signal.
FT SIGNAL 1 16 Potential.
SQ SEQUENCE 759 AA; 84886 MW; C431A3C3F418F40A CRC64;

Query Match 31.5%; Score 197; DB 2; Length 759;
Best Local Similarity 46.1%; Pred. No. 9.3e-11;
Matches 35; Conservative 13; Mismatches 26; Indels 2; Gaps 1;

QY 31 ENMKCCPFCGKCKCL--DPRKIDICSMPOEAGPCLASIPHWYNNKTKICSEFYGGCGGN 88
DB 560 ETMEDCTFTCFQRLAKPFLKDVCSQPIAGFCRASIPRYGVDSKKRCKVFTYGSCKGN 619
QY 89 NNNFQTEAICLVTCCK 104
DB 620 GNRFPCKNECEKTKCR 635

RESULT 11
Q9VAV4 PRELIMINARY; PRT; 2772 AA.
AC Q9VAV4; Q9VAV3;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE CG33103-PB.
GN Name=Ppt; ORFNames=CG33103;
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=10731132; PubMed=10731132; DOI=10.1126/science.287.5461.2185;
RA Adams M.D., Ceiniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scher S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.H., Blazek R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Gabor G.L.,
RA Abail J.F., Agbayani A., An H.J., Andrews-Pfannkuch C., Baldwin D.,
RA Balow R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brotter P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Deicher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Flesler C., Gabrielian A.E., Gaig N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.H., Ibegwam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Laeko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupek M.P., Smith T.,
RA Spier E., Spradling A.C., Stapieton M., Strong R., Sun E.,
RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.Y., Wassarman D.A., Weinstein G.M., Weissbach J.,
RA Williams S.M., Woodgett, Worley K.C., Wu D., Yang S., Yao Q.A., Ye J.,
RA Yeh R.F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong P.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster."
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DR PROSITE; PSS00092; TSP1; 5.
KW Matrix protein.
SQ SEQUENCE 2776 AA; 299741 MW; 92D38A17360D2D42 CRC64;

Query Match          29.9%; Score 187; DB 2; Length 2776;
Best Local Similarity 33.3%; Pred. No. 2.9e-09;
Matches 38; Conservative 13; Mismatches 33; Indels 30; Gaps 5;

QY 21 DOCTKPR---DCPENN-----KCCPF---SCG-----KKCLD-----FRKD 50
DB 1788 DRCALPKQTGDCSEKLAHWFSESEKRCVPFYSGGKNNFPTLESCDCRPRQVAKD 1847

QY 51 ICSMPQEAQCLASPHWYNNKTKICSEFYVGGCGGNNNNFTQTAICLVTKK 104
DB 1848 ICEIPAEEGECANYTSTWYTDQACRQFYVGGCGGNNENRFTTEESCLARCDR 1901

RESULT 13
Q7KRX2 PRELIMINARY; PRT; 2894 AA.
AC Q7KRX2;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE CG33103-PA.
GN Name=Ppn; ORFNames=CG33103;
OS Drosophila melanogaster (fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxId=7227;
[1]
SEQUENCE FROM N.A.
RX MEDLINE=2019606; PubMed=10731132; DOI=10.1126/science.287.5461.2185;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.H., Blazee R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Gabor G.L.,
RA Abril J.F., Agbayani A., An H.J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Folsler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.H., Ibegwam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Matrei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E.C., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirskaas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.Y., Wassarman D.A., Weinstock G.M., Weissbach J.,
RA Williams S.M., Woodagel, Worley K.C., Wu D., Yang S., Yao Q.A., Ye J.,
RA Yeh R.F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster."
RN Science 287:2185-2195(2000).
[2]

SEQUENCE FROM N.A.
RX MEDLINE=22426065; PubMed=12537568;
RA Celniker S.E., Wheeler D.A., Krommiller B., Carlson J.W., Halpern A.,
RA Patel S., Adams M., Champe M., Dugan S.P., Friese E., Hodgson A.,
RA George R.A., Hoskins R.A., Lavery T., Muzny D.M., Nelson C.R.,
RA Pacleb J.M., Park S., Pfeiffer B.D., Richards S., Sodergren E.J.,
RA Svirskaas R., Tabor P.E., Wan K., Stapleton M., Sutton G.G., Venter C.,
RA Weinstock G., Scher S.E., Myers E.W., Gibbs R.A., Rubin G.M.;
RT "Finishing a whole-genome shotgun: Release 3 of the Drosophila
melanogaster euchromatic genome sequence."
RN Genome Biol. 3:RESEARCH0079-RESEARCH0079(2002).
[3]
SEQUENCE FROM N.A.
RX MEDLINE=22426070; PubMed=12537573;
RA Kaminker J.S., Bergman C.M., Krommiller B., Carlson J., Svirskaas R.,
RA Patel S., Friese E., Wheeler D.A., Lewis S.E., Rubin G.M.,
RA Ashburner M., Celniker S.E.;
RT "The transposable elements of the Drosophila melanogaster euchromatin:
a genomics perspective."
RN Genome Biol. 3:RESEARCH0084-RESEARCH0084(2002).
[4]
SEQUENCE FROM N.A.
RX MEDLINE=22426069; PubMed=12537572;
RA Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
RA Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochnik S.E.,
RA Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Berman B.P.,
RA Bettencourt B.R., Celniker S.E., de Grey A.D., Drysdale R.A.,
RA Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,
RA Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
RA Lewis S.E.;
RT "Annotation of the Drosophila melanogaster euchromatic genome: a
systematic review."
RN Genome Biol. 3:RESEARCH0083-RESEARCH0083(2002).
[5]
SEQUENCE FROM N.A.
RX FlyBase;
RG FlyBase;
RN Submitted (SEP-2002) to the EMBL/GenBank/DBSJ databases.
[6]
SEQUENCE FROM N.A.
RX FlyBase;
RG FlyBase;
RN Submitted (MAR-2004) to the EMBL/GenBank/DBSJ databases.
CC -L- SIMILARITY: Contains 12 BPTI/Kunitz inhibitor domains.
DR EMBL; AF003765; AAF56795.3; -.
DR HSB; F10646; IAD2.
DR GO; GO:0004867; P:serine-type endopeptidase inhibitor activity; IEA.
DR InterPro; IPR010294; ADAM spacer1.
DR InterPro; IPR006209; EGF_Like.
DR InterPro; IPR003599; IG_Like.
DR InterPro; IPR007110; IG_Like.
DR InterPro; IPR003598; IG_c2.
DR InterPro; IPR010909; PLAC.
DR InterPro; IPR002223; Prot_Inh_Kunz-m.
DR InterPro; IPR000884; TSP1.
DR InterPro; IPR008197; WAP.
DR Pfam; PF05986; ADAM_spacer1; 1.
DR Pfam; PF00047; IG; 2.
DR Pfam; PF00014; Kunitz_BPTI; 12.
DR Pfam; PF00090; TSP_1; 5.
DR Pfam; PF00095; WAP; 1.
DR PRINTS; PR00003; ADISULPHCORE.
DR PRINTS; PR00759; BASICPTASE.
DR ProDom; PD000222; Prot_Inh_Kunz-m; 12.
DR SMART; SM00409; IG; 3.
DR SMART; SM00408; IGC2; 3.
DR SMART; SM00131; KU; 12.
DR SMART; SM00209; TSP1; 7.
DR SMART; SM00217; WAP; 1.
DR PROSITE; PS00317; 4-DISULFIDE_CORE; 1.
DR PROSITE; PS00280; BPTI_KUNITZ_1; 11.
DR PROSITE; PS0279; BPTI_KUNITZ_2; 12.
DR PROSITE; PS00022; EGF_1; UNKNOWN_1.
DR PROSITE; PS00835; IG_Like; 3.
DR PROSITE; PS00900; PLAC; 1.
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Db 4 KRDI CRLPPEOGPC KGRIPRYFYNPASRMCESEIYGGCKGNQNFKTAECV RACR 59

RESULT 16	
Q22685	PRELIMINARY; PRT; 988 AA.
ID	Q22685
AC	Q22685;
DT	01-NOV-1996 (TrEMBLrel. 01, Created)
DT	01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT	01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE	Hypochemical protein T22F7.3.
GN	Names=T22F7.3; ORFNames=T22F7.3;
OS	Caenorhabditis elegans.
OC	Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC	Rhabditidae; Peloderinae; Caenorhabditis.
OX	NCBI_TaxID=6239;
OX	[1]
RN	SEQUENCE FROM N.A.
RP	STRAIN=Bristol N2;
RC	STRAIN=Bristol N2;
RX	MEDLINE=99069613; PubMed=9851916;
RG	WormBase Consortium;
RT	"Genome sequence of the nematode C. elegans: a platform for
RT	investigating biology. The C. elegans Sequencing Consortium.";
RL	Science 282:2012-2018(1998).
[2]	
RN	SEQUENCE FROM N.A.
RP	STRAIN=Bristol N2;
RC	STRAIN=Bristol N2;
RA	Macri C.;
RT	"The sequence of C. elegans cosmid T22F7.";
RL	Submitted (NOV-1994) to the EMBL/GenBank/DBJ databases.
[3]	
RN	SEQUENCE FROM N.A.
RP	STRAIN=Bristol N2;
RC	STRAIN=Bristol N2;
RA	Waterston R.;
RL	Submitted (NOV-2002) to the EMBL/GenBank/DBJ databases.
[4]	
RN	SEQUENCE FROM N.A.
RP	STRAIN=Bristol N2;
RC	STRAIN=Bristol N2;
RG	WormBase Consortium;
RL	Submitted (SEP-2004) to the EMBL/GenBank/DBJ databases.
CC	-1- SIMILARITY: Contains 5 BPTI/Kunitz inhibitor domains.
DR	EMBL; U13071; AAL65793.1; --
DR	HSP; P10646; IADZ.
DR	IntAct; Q22685; --
DR	WormBase; WBGene00020702; T22F7.3.
DR	WormPep; T22F7.3; CE30304.
DR	GO; GO:0004867; F:serine-type endopeptidase inhibitor activity; IEA.
DR	InterPro; IPR006149; EB region.
DR	InterPro; IPR002223; Prot_Inh_Kunz-m.
DR	InterPro; IPR006150; Worm_repeat_1.
DR	Pfam; PF01683; EB; 1.
DR	Pfam; PF00014; Kunitz_BPTI; 5.
DR	PRINTS; PR00759; BASICPTASE.
DR	ProDom; PD000222; Prot_Inh_Kunz-m; 5.
DR	SMART; SM00131; KU; 5.
DR	SMART; SM00289; WRI; 8.
DR	PROSITE; PS00280; BPTI_KUNITZ_1; 3.
DR	PROSITE; PS02079; BPTI_KUNITZ_2; 5.
DR	HYPOTHETICAL protein.
DR	SEQUENCE 988 AA; 108702 MW; 6F62DAPB898C306B CRC64;
QY	Query Match 29.5%; Score 184.5; DB 2; Length 988;
DB	Best Local Similarity 34.3%; Fred. No. 1.9e-09;
DB	Matches 35; Conservative 14; Mismatches 44; Indels 9; Gaps 2;
QY	12 KVECE-----VSEIDCTKPRCCPENMKCPFSCGKKCLDFRDKICSMQPEAGPCLAS 64
DB	402 KLVCENGPNPLGHEWQRCETNADCPSSHSC--QGSHKVCCTPQAGSLCTQPKRLGDC TSA 459
QY	65 IPHWYNNKTKICEFYVGGCGGNNNNFQTEAICLVTCCKVH 106
DB	460 VRRVYVNAATSCBWFYTGCGNDNNNTLMAQQCKGRGTH 501

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RESULT 17
Q7TQN3 PRELIMINARY; PRT; 571 AA.
AC Q7TQN3;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Growth and differentiation factor-associated serum protein 1.
GN Name=Gaspl;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RS SEQUENCE FROM N.A.
RC STRAIN=BALB/c;
RX MEDLINE=22656519; PubMed=12595574; DOI=10.1210/me.2002-0366;
RA Hall J.J., Qiu Y., Hewick R.M., Wolfman N.M.;
RT "Regulation of myostatin-1: a novel protein with protease inhibitor
RT associated serum protein-1: a novel protein with protease inhibitor
RT and follistatin domains.";
RL Mol. Endocrinol. 17:1144-1154(2003).
CC -1- SIMILARITY: Contains 2 BPTI/Kunitz inhibitor domains.
DR EMBL; AY308804; AAP72503.1; -.
DR HSP; P00974; IK09.
DR GO; GO:000515; F:protein binding; IPI.
DR GO; GO:0007179; P:transforming growth factor beta receptor si. .; IDA.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003598; Ig_c2.
DR InterPro; IPR001134; Netrin_C.
DR InterPro; IPR002350; Prot_Inh_Kazal.
DR InterPro; IPR011497; Prot_Inh_Kazal_2.
DR InterPro; IPR002223; Prot_Inh_Kunz-m.
DR InterPro; IPR008993; TIMP_like.
DR InterPro; IPR008197; WAP_.
DR Pfam; PF07648; Kazal_2; 1.
DR Pfam; PF00014; Kunitz_BPTI; 2.
DR Pfam; PF00095; WAP; 1.
DR ProDom; PD000222; Prot_Inh_Kunz-m; 2.
DR SMART; SM00408; IGC2; 1.
DR SMART; SM00280; KAZAL; 1.
DR SMART; SM00131; KU; 2.
DR SMART; SM00217; WAP; 1.
DR PROSITE; PS00317; 4 DISULFIDE CORE; 1.
DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
DR PROSITE; PS50279; BPTI_KUNITZ_2; 2.
DR PROSITE; PS50835; IG_LIKE; 1.
DR PROSITE; PS50189; NTR; 1.
SQ SEQUENCE 571 AA; 63321 MW; B28E676B3DC71256 CRC64;

Query Match 29.2%; Score 182.5; DB 2; Length 571;
Best Local Similarity 31.8%; Pred. No. 1.8e-09;
Matches 35; Conservative 12; Mismatches 34; Indels 29; Gaps 3;

Qy 22 QCTKP---RDCPENM-----KCCPF-----SCGKKCLDFRDKIC 52
Db 322 ECLKPPDSGCGEQTRHFDQAQNCLTTFGCHHNLNHFYEAACMLACMSGPLATC 381

Qy 53 SMOEAGCPCLASPHWYNNKTKICSFYGGCGGNNNFQTEAICLVTC 102
Db 382 SLPALQGPCKAYVPRWAYNSQTGLCOSFVYGGCEGNGNPFESREACBESC 431

RESULT 18
Q7PXZ1 PRELIMINARY; PRT; 2419 AA.
AC Q7PXZ1;
DT 01-MAR-2004 (TrEMBLrel. 26, Created)
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE AgCP12609 (Fragment).

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GN Name=agCG49342; ORFName=ENSANGG00000019572;
OS Anopheles gambiae str. PEST.
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Anopheles.
OX NCBI_TaxID=180454;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=PEST;
RA Anopheles Genome Sequencing Consortium;
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: Contains 9 BPTI/Kunitz inhibitor domains.
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; AA0801008987; EAA01339.1; -.
DR HSP; P10646; IINH.
DR GO; GO:0004867; F:serine-type endopeptidase inhibitor activity; IEA.
DR InterPro; IPR010294; ADAM spacer1.
DR InterPro; IPR006209; EGF Like.
DR InterPro; IPR007110; Ig_Like.
DR InterPro; IPR001090; PLAC.
DR InterPro; IPR002223; Prot_Inh_Kunz-m.
DR InterPro; IPR000884; TSP1.
DR InterPro; IPR008197; WAP.
DR Pfam; PF05986; ADAM spacer1; 1.
DR Pfam; PF00014; Kunitz_BPTI; 9.
DR Pfam; PF00090; TSP_1; 7.
DR Pfam; PF00095; WAP; 1.
DR PRINTS; PR00003; 4DISULPHCORE.
DR PRINTS; PR00759; BASICPTASE.
DR ProDom; PD000222; Prot_Inh_Kunz-m; 9.
DR PROSITE; PS00317; 4 DISULFIDE CORE; 1.
DR PROSITE; PS00280; BPTI_KUNITZ_1; 8.
DR PROSITE; PS02079; BPTI_KUNITZ_2; 9.
DR PROSITE; PS00022; EGF 1; UNKNOWN_1.
DR PROSITE; PS00835; IG LIKE; 2.
DR PROSITE; PS09000; PLAC; 1.
DR PROSITE; PS00092; TSP1; 5.
FT NON_TER 1
SQ SEQUENCE 2419 AA; 260249 MW; 58078660983946 CRC64;

Query Match 29.1%; Score 182; DB 2; Length 2419;
Best Local Similarity 33.9%; Pred. No. 7.9e-09;
Matches 39; Conservative 12; Mismatches 32; Indels 32; Gaps 4;

Qy 21 DOCTKPR-----DCPENMKCCPFSCG-----KKC-----LDPK 49
Db 1515 DVCHLPKISGPTGHHNMYDYDAERNM-CAQFTYGGCLGNMRPESQECKALCSVDDSK 1573
Qy 50 DICSMPOAGCLASIPHHWYNNKTKICSEFIYGGCGGNNNNFQTEAICLVTCCK 104
Db 1574 PPCQPMAGPCNGTFFERWYDKETDACHPFYFGCGKGNKNYPTFASCGYHCKR 1628

RESULT 19
Q8TEU8 PRELIMINARY; PRT; 576 AA.
AC Q8TEU8;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Multivalent protease inhibitor protein.
GN Name=WFIKNRP;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21173622; PubMed=11274388; DOI=10.1073/pnas.061028398;
RA Trexler M., Banyai L., Pathy L.;
RT "A human protein containing multiple types of protease-inhibitory
modules."

Proc. Natl. Acad. Sci. U.S.A. 98:3705-3709 (2001).
[2]
RN SEQUENCE FROM N.A.
RP Trexler M., Banyai L., Pathy L.;
RA "Distinct expression pattern of two related human proteins containing
multiple types of protease-inhibitory modules.";
RT Biol. Chem. 383:0-0 (2002).
RL -!- SIMILARITY: Contains 2 BPTI/Kunitz inhibitor domains.
CC EMBL; AF468657; AAL77058.1; -.
DR HSP; P00974; IKO9.
DR GO; GO:0008233; F:peptidase activity; IEA.
DR GO; GO:0004867; F:serine-type endopeptidase inhibitor activity; IEA.
DR InterPro; IPR007110; Ig_Like.
DR InterPro; IPR003598; Ig_c2.
DR InterPro; IPR001134; Netrin C.
DR InterPro; IPR002350; Prot_Inh_Kazal.
DR InterPro; IPR011497; Prot_Inh_Kazal_2.
DR InterPro; IPR002223; Prot_Inh_Kunz-m.
DR InterPro; IPR008993; TIMP_Like.
DR InterPro; IPR008197; WAP.
DR Pfam; PF07648; Kazal_2; 1.
DR Pfam; PF00014; Kunitz_BPTI; 2.
DR Pfam; PF00095; WAP; 1.
DR PRINTS; PR00003; 4DISULPHCORE.
DR PRINTS; PR00759; BASICPTASE.
DR ProDom; PD000222; Prot_Inh_Kunz-m; 2.
DR SMART; SM00408; IGc2; 1.
DR SMART; SM00280; KAZAL; 1.
DR SMART; SM00131; KU; 2.
DR SMART; SM00217; WAP; 1.
DR PROSITE; PS00317; 4 DISULFIDE CORE; 1.
DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
DR PROSITE; PS02079; BPTI_KUNITZ_2; 2.
DR PROSITE; PS00835; IG LIKE; 1.
DR PROSITE; PS0189; NTR; 1.
KW Protease.
SQ SEQUENCE 576 AA; 63941 MW; 08B4F2EDBE121F81 CRC64;

Query Match 27.8%; Score 173.5; DB 2; Length 576;
Best Local Similarity 31.8%; Pred. No. 1.4e-08;
Matches 35; Conservative 10; Mismatches 36; Indels 29; Gaps 3;

Qy 22 QCTKP-----RDCPENM-----KCCPF-----SCGKKCLDFRDKIC 52
Db 327 ECLPFPSEDCGEQTRHFDQAQNNCLTTFGCHRNHNHFFIYEACMLACSGSLAAC 386
Qy 53 SMPQAGCLASIPHHWYNNKTKICSEFIYGGCGGNNNNFQTEAICLVTC 102
Db 387 SLPALQGPCKAYAPWAYNSQTQCQSFVYGGCGNGNPFESRACEESC 436

RESULT 20
Q6UXZ9 PRELIMINARY; PRT; 576 AA.
AC Q6UXZ9;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Bikunin hlg.
GN ORFNames=UNQ9235;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22887296; PubMed=12975309; DOI=10.1101/gr.1293003;
RA Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D., Brush J.,
RA Chen J., Chow B., Chui C., Crowley C., Currell B., Deuel B., Dowd P.,
RA Eaton D., Foster J., Grimaldi C., Gu Q., Hass P.E., Heldens S.,
RA Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J.,
RA Lewis L., Liao D., Mark B., Robbie E., Sanchez C., Schoenfeld J.,
RA Seshagiri S., Simmons L., Singh J., Smith V., Stinson J., Vagts A.,

RA Vandlen R., Watanabe C., Wieand D., Woods K., Xie M.H., Yansura D.,
RA Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A., Wood W.I.,
RA Godowski P.;
RT "The secreted protein discovery initiative (SPDI), a large-scale
RT effort to identify novel human secreted and transmembrane proteins: a
RT bioinformatics assessment";
RL Genome Res. 13:2265-2270(2003).
CC -!- SIMILARITY: Contains 2 BPTI/Kunitz inhibitor domains.
DR EMBL; AY358142; AAO88509.1; -;
DR HSSP; P00974; 1K09.
DR GO; GO:0004867; F:serine-type endopeptidase inhibitor activity; IEA.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003598; IG C2.
DR InterPro; IPR001134; Netrin C.
DR InterPro; IPR002223; Prot_inh_Kunz-m.
DR InterPro; IPR008993; TIMP_like.
DR InterPro; IPR008197; WAP.
DR Pfam; PF00014; Kunitz BPTI; 2.
DR Pfam; PF00095; WAP; 1.
DR PRINTS; PR00759; BASICPTASE.
DR ProDom; PD000222; Prot_inh_Kunz-m; 2.
DR SMART; SM00409; IG; 1.
DR SMART; SM00408; IGC2; 1.
DR SMART; SM00131; KU; 2.
DR SMART; SM00217; WAP; 1.
DR PROSITE; PS00317; 4_DISULFIDE_CORE; 1.
DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
DR PROSITE; PS0279; BPTI_KUNITZ_2; 2.
DR PROSITE; PS00835; IG LIKE; 1.
DR PROSITE; PS0189; NTR; 1.
SQ SEQUENCE 576 AA; 63912 MW; 08B42DD50C3CF81 CRC64;

Query Match 27.8%; Score 173.5; DB 2; Length 576;
Best Local Similarity 31.8%; Pred. No. 1.4e-08;
Matches 35; Conservative 10; Mismatches 36; Indels 29; Gaps 3;

QY 22 QCTKP---RDCPENM-----KCCPF-----SCGKKCLDFRKDIC 52
DB 327 ECLKPPDSDECGEETRWFDAQANNCLTFTGCHRNLNHFETAEACLMACMSGPLAAC 386

QY 53 SMPQAGPCLASIPHWYNNKTKICSEFYGGCGQNNNNFQTEAICLVTC 102
DB 387 SLPALQGPCKAYAPWAYNSQTGCQSFYVYGCENGNFNESREACEESC 436

RESULT 21
Q9U8G8 PRELIMINARY; PRT; 3198 AA.
AC Q9U8G8;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAY-2000 (TrEMBLrel. 26, Last annotation update)
DE Lacunin precursor.
OS Manduca sexta (Tobacco hawkmoth) (Tobacco hornworm).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia; Sphingioidea;
OC Sphingidae; Sphinginae; Manduca.
OX NCBI_TaxID=7130;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99457716; PubMed=10528409; DOI=10.1016/S0965-1748(99)00064-8;
RA Nardi J.B., Martos R., Walden K.K., Lampe D.J., Robertson H.M.;
RT "Expression of lacunin, a large multidomain extracellular matrix
RT protein, accompanies morphogenesis of epithelial monolayers in Manduca
RT sexta.";
RL Insect Biochem. Mol. Biol. 29:893-897(1999).
RN [2]
RP SEQUENCE FROM N.A.
RA Nardi J., Martos R., Walden K., Lampe D., Robertson H.;
RL Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: Contains 10 BPTI/Kunitz inhibitor domains.

DR EMBL; AF078161; AAP04457.1; -;
DR HSSP; P12111; 1KTH.
DR GO; GO:0004867; F:serine-type endopeptidase inhibitor activity; IEA.
DR InterPro; IPR010294; ADAM spacer1.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003598; IG C2.
DR InterPro; IPR010909; PLAC.
DR InterPro; IPR004094; Prot_inh_antistn.
DR InterPro; IPR002223; Prot_inh_Kunz-m.
DR InterPro; IPR000884; TSP1.
DR InterPro; IPR008197; WAP.
DR Pfam; PF05986; ADAM spacer1; 1.
DR Pfam; PF02822; Anticasin; 4.
DR Pfam; PF00014; Kunitz BPTI; 10.
DR Pfam; PF00090; TSP_1; 5.
DR Pfam; PF00095; WAP; 1.
DR PRINTS; PR00003; 4DISULPHCORE.
DR PRINTS; PR00759; BASICPTASE.
DR SMART; SM00408; IGC2; 2.
DR SMART; SM00131; KU; 10.
DR SMART; SM00209; TSP1; 7.
DR SMART; SM00217; WAP; 1.
DR PROSITE; PS00317; 4_DISULFIDE_CORE; 1.
DR PROSITE; PS00280; BPTI_KUNITZ_1; 8.
DR PROSITE; PS0279; BPTI_KUNITZ_2; 10.
DR PROSITE; PS00835; IG LIKE; 2.
DR PROSITE; PS00900; PLAC; 1.
DR PROSITE; PS00092; TSP1; 5.
KW Signal.
FT SIGNAL.
SQ SEQUENCE 3198 AA; 349366 MW; ABACDA59C0D9134 CRC64;

Query Match 27.8%; Score 173.5; DB 2; Length 3198;
Best Local Similarity 34.4%; Pred. No. 6.8e-08;
Matches 31; Conservative 15; Mismatches 33; Indels 5; Gaps 1;

QY 14 BCEVEIDQCTKPRDCPENMKCCPFSCGKKCLDFRKDICSHPOAGPCLASIPHWYNNK 73
DB 2230 KCVTFEYGGCGGNRNPNFTBECYQYCGT-----AQDICQLPMRSGPCTSLMRWFYDPS 2284

QY 74 TKICSEFYGGCGQNNNNFQTEAICLVTC 103
DB 2285 SDSCSQFTYGGCGDGNDRFTRDDCESRCR 2314

RESULT 22
Q6AX20 PRELIMINARY; PRT; 587 AA.
ID Q6AX20
AC Q6AX20;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE APL2 A protein.
GN Name=apl2 A;
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RX TISSUE=Kidney;
RX MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;
RA Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
RA Richardson P.,
RA "Genetic and genomic tools for Xenopus research: The NIH Xenopus
RT initiative";
RL Dev. Dyn. 225:384-391(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Kidney;
RX PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Derge J.G.,


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RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RG WormBase Consortium;
RL Submitted (SEP-2004) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Contains 5 BPTI/Kunitz inhibitor domains.
DR EMBL; U290936; AAG68408.1; -.
DR PIR; T16210; T16210.
DR HSSP; P10646; IADZ.
DR IntAct; Q09983; -.
DR WormBase; WBGene00017937; F30H5.3.
DR WormPep; F30H5.3; CE01927.
DR GO; GO:0004867; F:serine-type endopeptidase inhibitor activity; IEA.
DR InterPro; IPR002198; ADH short.
DR InterPro; IPR006149; EB region.
DR InterPro; IPR006210; IEGF.
DR InterPro; IPR002223; Prot_Inh_Kunz-m.
DR InterPro; IPR006150; Worm_repeat_1.
DR Pfam; PF01683; EB; 3.
DR Pfam; PF00014; Kunitz BPTI; 5.
DR PRINTS; PR00759; BASICPTASE.
DR SMART; SM00181; EGF; 1.
DR SMART; SM00131; KU; 5.
DR SMART; SM00289; WRI; 15.
DR PROSITE; PS00061; ADH_SHORT; UNKNOWN 1.
DR PROSITE; PS00280; BPTI_KUNITZ_1; 2.
DR PROSITE; PS0279; BPTI_KUNITZ_2; 5.
KW Hypothetical protein.
SQ SEQUENCE 1599 AA; 171658 MW; AB5E6A1D86E9880D CRC64;

Query Match 27.6%; Score 172.5; DB 2; Length 1599;
Best Local Similarity 35.4%; Pred. NO. 4.4e-08;
Matches 35; Conservative 13; Mismatches 42; Indels 9; Gaps 2;

QY 12 KVECEV-----EEIDQTKPRDCPNMKCFPGGKCLDFRDKICSMPOEAGPCLAS 64
DB 518 KLQCKYGTPLKIGSSNQRCASADCFSTHEC--QSDHNVCCPRQAICSPQLRLGDCQKS 575

QY 65 IPHWYNNKTKICSEFIYGGCGNNNNFQTEAICLVTK 103
DB 576 VRYWYNATRACEIFDYTGCGNDNNFETLLEQNTCE 614

RESULT 25
IBPC BOVIN STANDARD; PRT; 67 AA.
AC P00976;
DT 21-JUL-1986 (Rel. 01, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Colostrum trypsin inhibitor (Colostrum BPI).
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE.
RA Cechova D., Jonakova V., Sorm F.;
RT "Primary structure of trypsin inhibitor from cow colostrum (component B2).";
RL Collect. Czech. Chem. Commun. 36:3342-3357(1971).
RN [2]
RP DISULFIDE BONDS.
RA Cechova D., Ber E.;
RT "Disulfide bonds of trypsin inhibitor from cow colostrum.";
RL Collect. Czech. Chem. Commun. 39:680-688(1974).
RN [3]
RP CHARACTERIZATION.
RX PubMed=11947537;
RA Cechova D., Muszynska G.;
RT "Role of lysine 18 in active center of cow colostrum trypsin inhibitor.";
RL FEBS Lett. 8:84-86(1970).

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CC -1- SUBCELLULAR LOCATION: Secreted.
CC PIR; A01207; TIBOC.
DR HSSP; P02760; 1BIK.
DR InterPro; IPR002223; Prot_Inh_Kunz-m.
DR Pfam; PF00014; Kunitz BPTI; 1.
DR PRINTS; PR00759; BASICPTASE.
DR ProDom; PD000222; Prot_Inh_Kunz-m; 1.
DR SMART; SM00131; KU; 1.
DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
DR PROSITE; PS0279; BPTI_KUNITZ_2; 1.
KW Direct protein sequencing; Glycoprotein; Serine protease inhibitor.
FT SITE 18 19 Reactive bond for trypsin.
FT DISULFID 8 58
FT DISULFID 17 41
FT DISULFID 33 54
FT CARBOHYD 27 27 N-linked (GlcNAc...).
SQ SEQUENCE 67 AA; 7511 MW; E2B2093B7CD207CD CRC64;

Query Match 27.5%; Score 172; DB 1; Length 67;
Best Local Similarity 48.1%; Pred. NO. 2.5e-09;
Matches 26; Conservative 11; Mismatches 17; Indels 0; Gaps 0;

QY 50 DICSMPOEAGPCLASIPHWYNNKTKICSEFIYGGCGNNNNFQTEAICLVTK 103
DB 6 DLQQLPOARGPCAKALLFYFNSTNACEPFTYGGCGNNBNFETMCLRCIE 59

RESULT 26
QSDJB6 PRELIMINARY; PRT; 750 AA.
AC Q6DJB6;
DT 25-OCT-2004 (TReMBLrel. 28, Created)
DT 25-OCT-2004 (TReMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TReMBLrel. 28, Last annotation update)
DE App-prov prov.
GN Name=app-prov;
OS Xenopus tropicalis (Western clawed frog) (Silurana tropicalis).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8364;
RN [1]
RP SEQUENCE FROM N.A.
RX TISSUE=Whole body;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.F., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.P., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mollany S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RX TISSUE=Whole body;
RA Klein S., Gerhard D.S.;
RA Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.
DB EMBL; BC075266; AAH75266.1; -.

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CC kallikrein. May play a role in blocking blood coagulation during
CC the larvae fixation on cattle.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: Contains 2 BPTI/Kunitz inhibitor domains.
DR InterPro: IPR002223; Kunitz_BPTI.
DR PRINTS; PR00759; BASICTPTASE.
DR SMART; PD000222; Prot_Inh_Kunz-m; 2.
DR SMART; SM00131; KU; 2.
DR PROSITE; PS00280; BPTI_KUNITZ_1; 2.
DR PROSITE; PS0279; BPTI_KUNITZ_2; 2.
KW Direct protein sequencing; Repeat; Serine protease inhibitor.
FT DOMAIN 10 60 BPTI/Kunitz inhibitor 1.
FT 62 112 BPTI/Kunitz inhibitor 2.
FT DISULFID 10 60 By similarity.
FT DISULFID 35 56 By similarity.
FT NON CONS 69 70 By similarity.
FT DISULFID 71 121 By similarity.
FT DISULFID 80 104 By similarity.
FT DISULFID 96 117 By similarity.
FT SITE 19 20 Reactive bond (By similarity).
FT SITE 71 72 Reactive bond (By similarity).
FT NON TER 122 122
SQ SEQUENCE 122 AA; 13736 MW; 8F5B1F48E10C566F CRC64;

Query Match 27.3%; Score 170.5; DB 1; Length 122;
Best Local Similarity 46.7%; Pred. No. 6.1e-09;
Matches 35; Conservative 7; Mismatches 18; Indels 15; Gaps 3;

QY 36 CFPSC-----GKKCLDFRKDCSMPQAGCLASIPHWYNNKTKICSEFYGGCGCN 88
DB 56 CKASCKPETYEAKKCL-----ARP-ESGCLAYMPMGVDLSKQCQCFEYGGCGCN 107
QY 89 NNNFQTEAICLVTK 103
DB 108 DNKYTTEEBCLSK 122

RESULT 29
Q6ITB9 PRELIMINARY; PRT; 83 AA.
AC Q6ITB9;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Mulgin-3.
OS Pseudechis australis (Mulga snake) (King brown snake).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidodonta; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC Elapidae; Acanthophinae; Pseudechis.
OX NCBI_TaxID=8670;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Venom Gland;
RA Filippovich I.V., Sorokina N.I.;
RL Submitted (MAY-2004) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.
DR EMBL; AY626926; AAT45402.1; -.
DR HSSP; Q16019; IAA.
DR GO; GO:0004867; F:serine-type endopeptidase inhibitor activity; IEA.
DR InterPro; IPR002223; Prot_Inh_Kunz-m.
DR Pfam; PF00014; Kunitz_BPTI; 1.
DR PRINTS; PR00759; BASICTPTASE.
DR ProDom; PD000222; Prot_Inh_Kunz-m; 1.
DR SMART; SM00131; KU; 1.
DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
DR PROSITE; PS0279; BPTI_KUNITZ_2; 1.
SQ SEQUENCE 83 AA; 9103 MW; 315C361D8EC89221 CRC64;

Query Match 27.28%; Score 170; DB 2; Length 83;
Best Local Similarity 52.78%; Pred. No. 4.8e-09;
Matches 29; Conservative 5; Mismatches 21; Indels 0; Gaps 0;

QY 48 RKDICSMPQAGCLASIPHWYNNKTKICSEFYGGCGGNNTFQTEAICLVTC 102
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DB 27 RPDFCELPAATGTCRVGFPFYPNDEKKCLEFFYGGCGGNNTFQTECESTC 81

RESULT 30
Q6ITB5 PRELIMINARY; PRT; 83 AA.
AC Q6ITB5;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Microlepidin-1.
OS Oxyuranus microlepidotus (Inland taipan).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidodonta; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC Elapidae; Acanthophinae; Oxyuranus.
OX NCBI_TaxID=111177;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Venom gland;
RA Filippovich I.V., Sorokina N.I.;
RL Submitted (MAY-2004) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.
DR EMBL; AY626930; AAT45405.1; -.
DR HSSP; F10646; IADZ.
DR GO; GO:0004867; F:serine-type endopeptidase inhibitor activity; IEA.
DR InterPro; IPR002223; Prot_Inh_Kunz-m.
DR Pfam; PF00014; Kunitz_BPTI; 1.
DR PRINTS; PR00759; BASICTPTASE.
DR ProDom; PD000222; Prot_Inh_Kunz-m; 1.
DR SMART; SM00131; KU; 1.
DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
DR PROSITE; PS0279; BPTI_KUNITZ_2; 1.
DR PROSITE; PS0279; BPTI_KUNITZ_2; 1.
SQ SEQUENCE 83 AA; 9040 MW; CB4F5E17570CF94C CRC64;

Query Match 27.0%; Score 169; DB 2; Length 83;
Best Local Similarity 50.9%; Pred. No. 6e-09;
Matches 28; Conservative 7; Mismatches 20; Indels 0; Gaps 0;

QY 48 RKDICSMPQAGCLASIPHWYNNKTKICSEFYGGCGGNNTFQTEAICLVTC 102
DB 27 RPDFCELPAATGTCRVGFPFYPNDEKKCLEFFYGGCGGNNTFQTECESTC 81

RESULT 31
Q9NOX7 PRELIMINARY; PRT; 169 AA.
AC Q9NOX7;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Trophoblast Kunitz domain protein 2.
GN Name=TKDPI;
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=breed Simmental X Hereford;
RA Green J.A., Maclean J.A. II, Gan X., Xie S., Roberts R.M.;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.
DR EMBL; AF241777; AAF61248.1; -.
DR HSSP; P00974; IK09.
DR GO; GO:0004867; F:serine-type endopeptidase inhibitor activity; IEA.
DR InterPro; IPR002223; Prot_Inh_Kunz-m.
DR Pfam; PF00014; Kunitz_BPTI; 1.
DR PRINTS; PR00759; BASICTPTASE.
DR ProDom; PD000222; Prot_Inh_Kunz-m; 1.
DR SMART; SM00131; KU; 1.
DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
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DR PROSITE; PS50279; BPTI_KUNITZ_2; 1.
SQ SEQUENCE 169 AA; 18855 MW; B65C16F4DF0BA3D CRC64;

Query Match 27.0%; Score 169; DB 2; Length 169;
Best Local Similarity 47.3%; Pred. No. 1.2e-08;
Matches 26; Conservative 11; Mismatches 16; Indels 0; Gaps 0;

Qy 48 RKDICSMPOEAGPCLASIPHHWYNNKTKICSEFIYGGCGGNNNFQTEAICLVTC 102
Db 108 KPECFMEPLGPKQDMTRIFYNAKTRICFPFYVGCGEGNNKNNFQTLUSHCIVTC 162

RESULT 32
Q7T363 PRELIMINARY; PRT; 516 AA.
AC Q7T363
DT 01-OCT-2003 (TRENBLrel. 25, Created)
DT 01-OCT-2003 (TRENBLrel. 25, Last sequence update)
DT 01-MAR-2004 (TRENBLrel. 26, Last annotation update)
DE Zgc:64075.
GN ORNames=zgc:64075;
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Kidney;
RX MEDLINE=2238257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Brownstein M.J., Ustin T.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Stapleton M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bobak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smallus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RN Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RP [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Kidney;
RA Strausberg R.;
RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: Contains 2 BPTI/Kunitz inhibitor domains.
DR EMBL; BC053239; AAH53239.1; -.
DR HSPF; F10846; IADZ.
DR ZFIN; ZDB-GENE-040426-2169; zgc:64075.
DR GO; GO:0004867; F:serine-type endopeptidase inhibitor activity; IEA.
DR InterPro; IPR002048; EF-hand.
DR InterPro; IPR002172; LDL_receptor_A.
DR InterPro; IPR011106; MAN5C_N.
DR InterPro; IPR000601; PKD.
DR InterPro; IPR002223; Prot_Inh_Kunz-m.
DR Pfam; PF00014; Kunitz_BPTI; 2.
DR Pfam; PF00057; Ldl_recept_a; 1.
DR Pfam; PF07502; MAN5C; 1.
DR ProDom; PD000222; Prot_Inh_Kunz-m; 2.
DR SMART; SM00131; KU; 2.
DR SMART; SM00192; LDLA; 1.
DR SMART; SM00089; PKD; 1.
DR PROSITE; PS00280; BPTI_KUNITZ_1; 2.

DR PROSITE; PS50279; BPTI_KUNITZ_2; 2.
DR PROSITE; PS00018; EF_HAND; UNKNOWN_1.
DR PROSITE; PS01209; LDLRA_1; 1.
DR PROSITE; PS50069; LDLRA_2; 1.
SQ SEQUENCE 516 AA; 57695 MW; 20B0A4CSB270DE16 CRC64;

Query Match 27.0%; Score 169; DB 2; Length 516;
Best Local Similarity 26.6%; Pred. No. 3.3e-08;
Matches 37; Conservative 13; Mismatches 41; Indels 48; Gaps 4;

Qy 4 LGKPCPKIKVEC-EVEIDQCTPRDCPENKKCCP--FSGKKKCL----- 45
Db 297 IGSAPHPSGRIGRIDAVEQCRRP-----CSPEHFTCDNKKCCIGKDLVCDKEKQCS 348

Qy 46 -----DFKDCISMPQEGPCLASIPHHWYNNKTKICSEFIY 83
Db 349 GSDEKECDKWDYDLVKURGISPDVSKARCVKPPVTGTCPGSGTQKWTNPNKRLCYRNYG 408

Qy 84 GCGGNNNNFQTEAICLVTC 102
Db 409 GCEGNQRFETEACGCTFC 427

RESULT 33
Q9GPI5 PRELIMINARY; PRT; 86 AA.
AC Q9GPI5
DT 01-MAR-2001 (TRENBLrel. 16, Created)
DT 01-MAR-2001 (TRENBLrel. 16, Last sequence update)
DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)
DE Hypothetical protein.
OS Ixodes ricinus (Sheep tick).
OC Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Acari;
OC Parasitiformes; Ixodida; Ixodidae; Ixodes.
OX NCBI_TaxID=34613;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Salivary glands;
RX MEDLINE=22134277; PubMed=12139212;
RA Lehoulle G., Rochez C., Louahed J., Rutti B., Brossard M., Bollen A.,
RA Godfroid E.;
RT "Isolation of Ixodes ricinus salivary gland mRNA encoding factors
induced during the blood feeding process.";
RL Am. J. Trop. Med. Hyg. 66:225-233(2002).
CC -!- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.
DR EMBL; AJ269641; CA855816.1; -.
DR HSPF; P12111; IKNF.
DR GO; GO:0004867; F:serine-type endopeptidase inhibitor activity; IEA.
DR InterPro; IPR002223; Prot_Inh_Kunz-m.
DR Pfam; PF00014; Kunitz_BPTI; 1.
DR PRINTS; PR00759; BASIGPTASE.
DR ProDom; PD000222; Prot_Inh_Kunz-m; 1.
DR SMART; SM00131; KU; 1.
DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
DR PROSITE; PS50279; BPTI_KUNITZ_2; 1.
KW Hypothetical protein.
SQ SEQUENCE 86 AA; 9727 MW; 9473B1794A055F0 CRC64;

Query Match 26.9%; Score 168; DB 2; Length 86;
Best Local Similarity 48.1%; Pred. No. 7.7e-09;
Matches 25; Conservative 11; Mismatches 16; Indels 0; Gaps 0;

Qy 52 CSMPQEGPCLASIPHHWYNNKTKICSEFIYGGCGGNNNFQTEAICLVTC 103
Db 31 CKLPDDGPCNRPISYIFDKTKTKCFWYMGCGEGNNNFENITTCQECR 82

RESULT 34
Q21418 PRELIMINARY; PRT; 922 AA.
AC Q21418
DT 01-NOV-1996 (TRENBLrel. 01, Created)
DT 01-NOV-1996 (TRENBLrel. 01, Last sequence update)
```

DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
DE ORFNames=K10D3.4;
GN Caenorhabditis elegans.
OS Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]_TaxID=6239;
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RX MEDLINE=99069613; PubMed=9851916;
RA none;
RT "Genome sequence of the nematode C.elegans: A platform for
RT investigating biology.";
RL Science 282:2012-2018(1998).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RA Bradshaw-Cordum H.; Leonard S.; Graves T.;
RT "The sequence of C. elegans cosmid Y55F3BR.";
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RA Waterston R.H.;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RA Waterston R.;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RN [5]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RA Waterston R.;
RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
RN [6]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RA Waterston R.;
RL Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.
RN [7]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RA Waterston R.;
RL Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.
RN [8]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RA Waterston R.;
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
RN [9]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RA Waterston R.;
RL Submitted (AUG-2002) to the EMBL/GenBank/DBJ databases.
RN [10]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RA Waterston R.;
RL Submitted (NOV-2002) to the EMBL/GenBank/DBJ databases.
RN [11]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RA Waterston R.;
RL Submitted (NOV-2002) to the EMBL/GenBank/DBJ databases.
RN [12]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RA Waterston R.;
RL Submitted (DEC-2002) to the EMBL/GenBank/DBJ databases.
RN [13]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RA Waterston R.;
RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
RN [14]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RA Wilson R.;
RL Submitted (JUL-2003) to the EMBL/GenBank/DBJ databases.
RN [15]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RG WormBase Consortium;
RT "Genome sequence of the nematode C. elegans: a platform for
RT investigating biology. The C. elegans Sequencing Consortium.";
RL Science 282:2012-2018(1998).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RA Bradshaw-Cordum H.; Leonard S.; Graves T.;
RT "The sequence of C. elegans cosmid Y55F3BR.";
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RA Waterston R.H.;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RA Waterston R.;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RN [5]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RA Waterston R.;
RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
RN [6]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RA Waterston R.;
RL Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.
RN [7]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RA Waterston R.;
RL Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.
RN [8]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RA Waterston R.;
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
RN [9]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RA Waterston R.;
RL Submitted (AUG-2002) to the EMBL/GenBank/DBJ databases.
RN [10]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RA Waterston R.;
RL Submitted (NOV-2002) to the EMBL/GenBank/DBJ databases.
RN [11]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RA Waterston R.;
RL Submitted (NOV-2002) to the EMBL/GenBank/DBJ databases.
RN [12]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RA Waterston R.;
RL Submitted (DEC-2002) to the EMBL/GenBank/DBJ databases.
RN [13]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RA Waterston R.;
RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
RN [14]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RA Wilson R.;
RL Submitted (JUL-2003) to the EMBL/GenBank/DBJ databases.
RN [15]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RG WormBase Consortium;

QY 32 NMKC-----CP--FSC-----GKCLDFRDKICSMPOEAGPCLASIPHHWYN 71
Db 371 NMECSPTGSGANSCPSSTHSCSTSGSTTFGVCPRPQYVCKLPREQGCGTYSNRWFFN 430
QY 72 KTKTICSEFIYGGCGGNNNFOTEATCLVTCK 103
Db 431 AKTGNCBEEFIYSGCGGNANNFETKECQDYCR 462

RESULT 35
Q9N343 PRELIMINARY; PRT; 1297 AA.
AC Q9N343;
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Hypothetical protein Y55F3BR.2.
GN Name=Y55F3BR.2; ORFNames=Y55F3BR.2;
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OX Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RX MEDLINE=99069613; PubMed=9851916;
RG WormBase Consortium;

Query Match 26.9%; Score 168; DB 2; Length 922;
Best Local Similarity 38.0%; Pred. No. 7.2e-08;
Matches 35; Conservative 8; Mismatches 29; Indels 20; Gaps 3;
QY 32 NMKC-----CP--FSC-----GKCLDFRDKICSMPOEAGPCLASIPHHWYN 71
Db 371 NMECSPTGSGANSCPSSTHSCSTSGSTTFGVCPRPQYVCKLPREQGCGTYSNRWFFN 430
QY 72 KTKTICSEFIYGGCGGNNNFOTEATCLVTCK 103
Db 431 AKTGNCBEEFIYSGCGGNANNFETKECQDYCR 462

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RL Submitted (SEP-2004) to the EMBL/GenBank/DBSJ databases.
RN [16]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RG wormBase Consortium;
RL Submitted (SEP-2004) to the EMBL/GenBank/DBSJ databases.
CC -1- SIMILARITY: Contains 4 BPTI/Kunitz inhibitor domains.
DR EMBL; AC024830; AAF59608.3; -.
DR GO; GO:0004867; F:serine-type endopeptidase inhibitor activity; IEA.
KW Hypothetical protein.
SQ SEQUENCE 1297 AA; 142370 MW; 7C8FAA75CE07ED8C CRC64;

Query Match      26.8%; Score 167.5; DB 2; Length 1297;
Best Local Similarity 28.0%; Pred. No. 1.1e-07;
Matches 35; Conservative 13; Mismatches 34; Indels 43; Gaps 3;

Qy 22 QCTPRDCP-----ENMKCCPFS-----CGKKCLDFR----- 48
Db 673 RCARDTDCPSTHTCAMEHQVCCPTPPHREIQFKYKHDLVSSSLKIVGSRHENYRPRGFV 732
Qy 49 -----KDISCMPOEAGPCLASIPHHWYNNKTKICSEFYGGCGGNNNNFQTEAIC 98
Db 733 ARPRLFIEETKLTCTEPLRVGDKQSVRFQWYNAETKTCESFLYTGCQGNRRFNSLNEC 792
Qy 99 LVTCK 103
Db 793 QSYCK 797

RESULT 36
Q8T3S7 PRELIMINARY; PRT; 80 AA.
AC Q8T3S7;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Toxin 1.
OS Araneus ventricosus.
OC Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Araneae;
OC Araneomorphae; Entelegynae; Araneioidea; Araneidae; Araneus.
OX NCBI_TaxID=182803;
RN [1]
RP SEQUENCE FROM N.A.
RA Jung E.H., Lee K.S., Han J.H., Je Y.H., Chang J.H., Roh J.Y.,
RA Sohn H.D., Jin B.R.;
RT "Molecular cloning of two cDNAs encoding an insecticidal toxin from
RT the spider, Araneus ventricosus, and construction of a recombinant
RT baculovirus expressing a spider toxin.";
RL Int. J. Ind. Entomol. 4:43-49(2002).
RN [2]
RP SEQUENCE FROM N.A.
RA Chung E.H., Lee K.S., Han J.H., Sohn H.D., Jin B.R.;
RL Submitted (MAR-2002) to the EMBL/GenBank/DBSJ databases.
CC -1- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.
DR EMBL; AY091482; AAM14403.1; -.
DR HSSP; P12111; 1KTH.
DR GO; GO:0004867; F:serine-type endopeptidase inhibitor activity; IEA.
DR InterPro; IPR002223; Prot_Inh_Kunz-m.
DR Pfam; PF00014; Kunitz_BPTI; 1.
DR PRINTS; PR00759; BASICTPASE.
DR SMART; SM00131; KU; 1.
DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
DR PROSITE; PS0279; BPTI_KUNITZ_2; 1.
SQ SEQUENCE 80 AA; 9275 MW; D07F5F9AC6B7BC10 CRC64;

Query Match      26.7%; Score 167; DB 2; Length 80;
Best Local Similarity 51.9%; Pred. No. 9e-09;
Matches 28; Conservative 9; Mismatches 17; Indels 0; Gaps 0;

Qy 49 KDICSMPOEAGPCLASIPHHWYNNKTKICSEFYGGCGGNNNNFQTEAICLVTC 102
Db 24 KDRCLLPVGTGCKASLTRYDYDKTACVFEFYGGCGGNNRRNFKRDKCEKAC 77
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RESULT 37
Q6ITB4 PRELIMINARY; PRT; 83 AA.
AC Q6ITB4;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Microlepidin-2.
OS Oxyuranus microlepidotus (Inland taipan).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC Elapidae; Acanthophinae; Oxyuranus.
OX NCBI_TaxID=111177;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Venom gland;
RA Filippovich I.V., Sorokina N.I.;
RL Submitted (MAY-2004) to the EMBL/GenBank/DBSJ databases.
CC -1- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.
DR EMBL; AY626931; AAT45407.1; -.
DR HSSP; P10646; IADZ.
DR GO; GO:0004867; F:serine-type endopeptidase inhibitor activity; IEA.
DR InterPro; IPR002223; Prot_Inh_Kunz-m.
DR Pfam; PF00014; Kunitz_BPTI; 1.
DR PRINTS; PR00759; BASICTPASE.
DR ProDom; PD000222; Prot_Inh_Kunz-m; 1.
DR SMART; SM00131; KU; 1.
DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
DR PROSITE; PS0279; BPTI_KUNITZ_2; 1.
SQ SEQUENCE 83 AA; 9074 MW; 3145E51757014221 CRC64;

Query Match      26.7%; Score 167; DB 2; Length 83;
Best Local Similarity 50.9%; Pred. No. 9.3e-09;
Matches 28; Conservative 6; Mismatches 21; Indels 0; Gaps 0;

Qy 48 RKDICSMPOEAGPCLASIPHHWYNNKTKICSEFYGGCGGNNNNFQTEAICLVTC 102
Db 27 RPDFCELPADTGPCRVGFPSFYFNPDEKKCLEFYGGCGGNNNNFITKECESTC 81

RESULT 38
Q6ITB6 PRELIMINARY; PRT; 83 AA.
AC Q6ITB6;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Scutellin-2.
OS Oxyuranus scutellatus.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC Elapidae; Acanthophinae; Oxyuranus.
OX NCBI_TaxID=8668;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Venom gland;
RA Filippovich I.V., Sorokina N.I.;
RL Submitted (MAY-2004) to the EMBL/GenBank/DBSJ databases.
CC -1- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.
DR EMBL; AY626929; AAT45405.1; -.
DR HSSP; P10646; IADZ.
DR GO; GO:0004867; F:serine-type endopeptidase inhibitor activity; IEA.
DR InterPro; IPR002223; Prot_Inh_Kunz-m.
DR Pfam; PF00014; Kunitz_BPTI; 1.
DR PRINTS; PR00759; BASICTPASE.
DR ProDom; PD000222; Prot_Inh_Kunz-m; 1.
DR SMART; SM00131; KU; 1.
DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
DR PROSITE; PS0279; BPTI_KUNITZ_2; 1.
SQ SEQUENCE 83 AA; 9074 MW; 3145E51757014221 CRC64;

Query Match      26.7%; Score 167; DB 2; Length 83;
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Best Local Similarity 50.9%; Pred. No. 9.3e-09;
Matches 28; Conservative 6; Mismatches 21; Indels 0; Gaps 0;

QY 48 RXDSCMPQAGPCLASIPHHWYNNKTKICSEFYGGCGGNNNNFOTEAICLVTC 102
DB 27 RPDCELPAATGFCRVGFFSYNPDKCLCFIYGGCGGNNNNFITEECSTC 81

RESULT 39

Q6T6S5 PRELIMINARY; PRT; 90 AA.
AC Q6T6S5;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Kunitz protease inhibitor 2.
OS Bitis gabonica (Gaboon viper).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC Viperidae; Viperinae; Bitis.
OX NCBI_TaxID=8694;
RN [1]
RP SEQUENCE FROM N.A.
RX PubMed=15276202; DOI=10.1016/j.gene.2004.03.024;
RA Francischetti I.M., My-Pham V., Harrison J., Garfield M.K.,
RA Ribeiro J.M.;
RT "Bitis gabonica (Gaboon viper) snake venom gland: toward a catalog for
RT the full-length transcripts (cDNA) and proteins.";
RL Gene 337:55-69(2004).
RN [2]
RP SEQUENCE FROM N.A.
RA Francischetti I.M.B., Pham V.M., Garfield M.K., Ribeiro J.M.C.;
RL Submitted (OCT-2003) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.
DR EMBL; AY430413; AAK24535.1; -;
DR HSP; Q16019; 1AAP.
DR GO; GO:0008233; F:peptidase activity; IEA.
DR GO; GO:004867; F:serine-type endopeptidase inhibitor activity; IEA.
DR InterPro; IPR002223; Prot_Inh_Kunz-m.
DR Pfam; PF00014; Kunitz_BPTI; 1.
DR PRINTS; PR00759; BASICPTASE.
DR ProDom; PD000222; Prot_Inh_Kunz-m; 1.
DR SMART; SM00131; KU; 1.
DR PROSITE; PS00280; BPTI_KUNITZ_1; 2.
DR PROSITE; PS00279; BPTI_KUNITZ_2; 2.
DR PROSITE; PS00018; EP_HAND; UNKNOWN_1.
DR PROSITE; PS01209; LDFA_1; 1.
DR PROSITE; PS00668; LDFA_2; 1.
DR PROSITE; PS50093; PKD; 1.
KW Protease.

Query Match 26.7%; Score 167; DB 2; Length 90;
Best Local Similarity 45.2%; Pred. No. 1e-08;
Matches 28; Conservative 10; Mismatches 20; Indels 4; Gaps 1;

QY 41 GKCLDFRDKICSMPOEAGPCLASIPHHWYNNKTKICSEFYGGCGGNNNNFOTEAICLV 100
DB 24 GK-...RPDFCYLPADTGCMANFRFYDVSASCKKFTYGGCHGNANNNFETRECK 79

QY 101 TC 102

DB 80 KC 81

QY SEQUENCE 90 AA; 10006 MW; 2BEDCID2020852AF CRC64;

Query Match 26.7%; Score 167; DB 2; Length 90;
Best Local Similarity 45.2%; Pred. No. 1e-08;
Matches 28; Conservative 10; Mismatches 20; Indels 4; Gaps 1;

QY 41 GKCLDFRDKICSMPOEAGPCLASIPHHWYNNKTKICSEFYGGCGGNNNNFOTEAICLV 100
DB 24 GK-...RPDFCYLPADTGCMANFRFYDVSASCKKFTYGGCHGNANNNFETRECK 79

QY 101 TC 102

DB 80 KC 81

QY SEQUENCE 90 AA; 10006 MW; 2BEDCID2020852AF CRC64;

RESULT 40

Q6DRJ1 PRELIMINARY; PRT; 515 AA.
AC Q6DRJ1;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Serine protease inhibitor HGFAI.
OS Brachydanio rerio (zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.

OX NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RX PubMed=15256591; DOI=10.1073/pnas.0403292011;
RA Amsterdam A., Nissen R.M., Sun Z., Swindell E.C., Farrington S.,
RA Hopkins N.;
RT "Identification of 315 genes essential for early zebrafish
RT development.";
RL Proc. Natl. Acad. Sci. U.S.A. 101:12792-12797(2004).
CC -!- SIMILARITY: Contains 2 BPTI/Kunitz inhibitor domains.
DR EMBL; AY648768; AAT68086.1; -;
DR GO; GO:0008233; F:peptidase activity; IEA.
DR GO; GO:004867; F:serine-type endopeptidase inhibitor activity; IEA.
DR InterPro; IPR002048; EF-hand.
DR InterPro; IPR002172; LDL_receptor_A.
DR InterPro; IPR011106; MANSC_N.
DR InterPro; IPR000601; PKD.
DR InterPro; IPR002223; Prot_Inh_Kunz-m.
DR Pfam; PF00014; Kunitz_BPTI; 2.
DR Pfam; PF00057; Ldl_recept_a; 1.
DR Pfam; PF07502; MANSC; 1.
DR PRINTS; PR00759; BASICPTASE.
DR ProDom; PD000222; Prot_Inh_Kunz-m; 2.
DR SMART; SM00131; KU; 2.
DR SMART; SM00192; LDFA; 1.
DR SMART; SM00089; PKD; 1.
DR PROSITE; PS00280; BPTI_KUNITZ_1; 2.
DR PROSITE; PS00279; BPTI_KUNITZ_2; 2.
DR PROSITE; PS00018; EP_HAND; UNKNOWN_1.
DR PROSITE; PS01209; LDFA_1; 1.
DR PROSITE; PS00668; LDFA_2; 1.
DR PROSITE; PS50093; PKD; 1.
KW Protease.
SQ SEQUENCE 515 AA; 57579 MW; AF948A7B0EE46DB4 CRC64;

Query Match 26.6%; Score 166.5; DB 2; Length 515;
Best Local Similarity 27.2%; Pred. No. 5.8e-08;
Matches 34; Conservative 12; Mismatches 32; Indels 47; Gaps 3;

QY 17 VEEIQCTKPRDCPENMKCCP--FSCGKKCL-----FSCGKKCL----- 45
DB 311 IDAVEQCQDRP-----CSPEHFTCDNKKCKGKLVCDKEKQSGDSDEKCDKWDYL 362

QY 46 -----DFRKDICSMPOEAGPCLASIPHHWYNNKTKICSEFYGGCGGNNNNFOTEA 97
DB 363 IKLRGISPDVSKARCVKPPVTGTCPSQTKWYNNKRLCYRFNYGCGGNNRFFETAG 422

QY 98 CLVTC 102

DB 423 CMTFC 427

QY SEQUENCE 515 AA; 57579 MW; AF948A7B0EE46DB4 CRC64;

RESULT 41

Q90WAI PRELIMINARY; PRT; 83 AA.
AC Q90WAI;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Textlinin.
OS Pseudonaja textilis textilis.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC Elapidae; Acanthophiinae; Pseudonaja.
OX NCBI_TaxID=169397;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Venom gland;
RA Masci P.P., Lavin M.F., Gaffney P.J., Sorokina I.N., Flippovich I.V.;
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Venom gland;


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Q7YRQ8
ID Q7YRQ8 PRELIMINARY; PRT; 234 AA.
AC Q7YRQ8;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Tissue factor pathway inhibitor-2.
OS Bos taurus (Bovine)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovinae; Bos.
OC NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22802738; PubMed=12921785; DOI=10.1016/S0003-9861(03)00332-1;
RA Du X., Deng F.M., Chand H.S., Kisiel W.;
RT "Molecular cloning, expression, and characterization of bovine tissue
factor pathway inhibitor-2.";
RL Arch. Biochem. Biophys. 417:96-104 (2003).
[2]
RP SEQUENCE FROM N.A.
RA Deng F.-M., Kisiel W., Sun T.-T.;
RL Submitted (FEB-2003) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: Contains 3 BPTI/Kunitz inhibitor domains.
DR EMBL; AY234861; AAO84035.1; -.
DR HSSP; P00981; 1DTK.
DR GO; GO:0004867; F:serine-type endopeptidase inhibitor activity; IEA.
DR InterPro; IPR002223; Prot_Inh_Kunz-m.
DR Pfam; PF00014; Kunitz_BPTI; 3.
DR ProDom; PD000222; Prot_Inh_Kunz-m; 3.
DR SMART; SM00131; KU; 3.
DR PROSITE; PS00280; BPTI_KUNITZ_1; 3.
DR PROSITE; PS0279; BPTI_KUNITZ_2; 3.
DR PROSITE; PS50279; BPTI_KUNITZ_2; 3.
SQ SEQUENCE 234 AA; 26575 MW; 401EEC84D589B422 CRC64;

Query Match 26.4%; Score 165; DB 2; Length 234;
Best Local Similarity 49.1%; Pred. No. 3.9e-08;
Matches 27; Conservative 11; Mismatches 17; Indels 0; Gaps 0;

QY 50 DICSMQEQAGPCPLASIPHWYKTKICSEFYGGCGGNNNFQTEAICLVTCCK 104
DB 34 EICLLPDDGFCRAPISYYIDRYTOSCFREFMYGGCGGNANFNTEACNEACWK 88

RESULT 45
ID Q6ZNI4 PRELIMINARY; PRT; 283 AA.
AC Q6ZNI4;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein FLJ16032.
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
OC NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Tongue;
RA Ninomiya K., Wagatsuma M., Kanda K., Kondo H., Yokoi T., Kodaira H.,
RA Furuya T., Takahashi M., Kikkawa E., Omura Y., Abe K., Kamiyama K.,
RA Katsuta N., Sato K., Tanikawa M., Yamazaki M., Sugiyama T., Irie R.,
RA Otsuki T., Sato H., Wakamatsu A., Ishii S., Yamamoto J., Isono Y.,
RA Kawai-Hio Y., Saito K., Nishikawa T., Kimura K., Yamashita H.,
RA Matsuo K., Nakamura Y., Sekine M., Kikuchi H., Murakawa K.,
RA Kanehori K., Takahashi-Fujii A., Oshima K., Sugiyama A., Kawakami B.,
RA Suzuki Y., Sugano S., Nagahara K., Masuho Y., Nagai K., Isogai T.;
RL Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.
DR EMBL; AK131196; BA018391.1; -.
DR HSSP; P00974; 1K09.
DR GO; GO:0004867; F:serine-type endopeptidase inhibitor activity; IEA.
DR InterPro; IPR001134; Netrin_C.
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DR InterPro; IPR002223; Prot_Inh_Kunz-m.
DR InterPro; IPR008993; TIMP-like.
DR Pfam; PF00014; Kunitz_BPTI; 2.
DR PRINTS; PR00759; BASICTPASE.
DR ProDom; PD000222; Prot_Inh_Kunz-m; 2.
DR SMART; SM00131; KU; 1.
DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
DR PROSITE; PS0279; BPTI_KUNITZ_2; 1.
DR PROSITE; PS50189; NTR; 1.
SQ SEQUENCE 283 AA; 31291 MW; 86206E7309866D30 CRC64;

Query Match 26.4%; Score 165; DB 2; Length 283;
Best Local Similarity 42.2%; Pred. No. 4.6e-08;
Matches 27; Conservative 9; Mismatches 28; Indels 0; Gaps 0;

QY 39 SCGKCLDFRKDICSMQEQAGPCPLASIPHWYKTKICSEFYGGCGGNNNFQTEAIC 98
DB 80 ACWLACMSGLAACSLPALQGFQKAVAPRWAYNSGTQGCQSFYGGCGGNFNFSREAC 139

QY 99 LVTC 102
DB 140 BESS 143

RESULT 46
ID Q7SZ46 PRELIMINARY; PRT; 342 AA.
AC Q7SZ46;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Ambp-prov protein.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;
OC Xenopodinae; Xenopus.
OC NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Whole;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heich F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Rana S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Pahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.B.,
RA Jones S.J., Marra M.A.;
RP "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
[2]
RP SEQUENCE FROM N.A.
RC TISSUE=Whole;
RX MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;
RA Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
RA Richardson P.;
RT "Genetic and genomic tools for Xenopus research: The NIH Xenopus
initiative.";
RL Dev. Dyn. 225:384-391 (2002).
[3]
RP SEQUENCE FROM N.A.
RC TISSUE=Whole;
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DR	EMBL; AF099018; AAF02490.1; -.	
DR	HSP; P31713; ISHP.	
DR	MGI; MG1:1338033; Spintl.	
DR	InterPro; IPR002172; LDL_receptor_A.	
DR	InterPro; IPR001106; MANSC_N.	
DR	InterPro; IPR002223; Prot_Inh_Kunz-m.	
DR	Pfam; PF00014; Kunitz_BPTI_2	
DR	Pfam; PF00057; Ldl_recept_a; 1.	
DR	Pfam; PF07502; MANSC; 1.	
DR	PRINTS; PR00759; BASICPTASE.	
DR	ProDom; PD000222; Prot_Inh_Kunz-m; 2.	
DR	SMART; SM00131; KU; 2.	
DR	SMART; SM00192; LDLa; 1.	
DR	PROSITE; PS00280; BPTI_KUNITZ_1; 2.	
DR	PROSITE; PS00279; BPTI_KUNITZ_2; 2.	
DR	PROSITE; PS01209; LDLRA_1; FALSE_NEG.	
DR	PROSITE; PS00068; LDLRA_2; 1.	
DR	PROSITE; PS0986; MANSC; 1.	
KW	Glycoprotein; Repeat; Serine protease inhibitor; Signal.	
FT	SIGNAL 1 29 Potential.	
FT	CHAIN 30 507 Kunitz-type protease inhibitor 1.	
FT	DOMAIN 51 134 MANSC.	
FT	DOMAIN 244 294 BPTI/Kunitz inhibitor 1.	
FT	DOMAIN 312 348 LDL_receptor class A.	
FT	DOMAIN 369 419 BPTI/Kunitz inhibitor 2.	
FT	SITE 254 255 Reactive bond (By similarity).	
FT	SITE 379 380 Reactive bond (By similarity).	
FT	DISULFID 244 294 By similarity.	
FT	DISULFID 253 277 By similarity.	
FT	DISULFID 269 290 By similarity.	
FT	DISULFID 369 419 By similarity.	
FT	DISULFID 378 402 By similarity.	
FT	DISULFID 394 415 By similarity.	
FT	CARBOHYD 229 229 N-linked (GlcNAc..) (Potential).	
FT	CARBOHYD 501 501 N-linked (GlcNAc..) (Potential).	
SQ	SEQUENCE 507 AA; 56676 MW; 20CB5DECF46AA7 CRC64;	
Query Match 26.4%; Score 165; DB 1; Length 507;		
Best Local Similarity 32.3%; Pred.No. 8e-08;		
Matches 32; Conservative 15; Mismatches 40; Indels 12; Gaps 2;		
QY	15 CEVEEDQCTKPDCCPENMKCCPFSGKKCLDP-----RKDICSMPQAGPCLAS 64	
DB	324 CSIDGFECDTDPDCPDGSD--EATCEKYSTGDFELQNHFLSDKGYCAELPDITGFCKEN 381	
QY	65 IPHWYNTKTKICSEFIYGGCGGNNNFQTEAICLVTK 103	
DB	382 IPRWYNPTSFRCARTYGGCYGNKNFEEQQCLSCR 420	
RESULT 48		
O62504	PRELIMINARY; PRT; 1474 AA.	
ID	O62504	
AC	O62504;	
DT	01-AUG-1998 (TrEMBLrel. 07, Created)	
DT	01-AUG-1998 (TrEMBLrel. 07, Last sequence update)	
DT	01-JUN-2003 (TrEMBLrel. 24, Last annotation update)	
DE	Hypothetical protein ZC84.6.	
GN	ORFNames=ZC84.6;	
OS	Caenorhabditis elegans.	
OC	Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;	
OC	Rhabditidae; Peloderinae; Caenorhabditis.	
OX	NCBI_TaxID=6239;	
RN	[1]	
RP	SEQUENCE FROM N.A.	
RC	STRAIN=Bristol N2;	
RX	MEDLINE=99069613; PubMed=9851916;	
RA	none;	
RT	"Genome sequence of the nematode C.elegans: A platform for	
RL	investigating biology.";	
RL	Science 282:2012-2018(1998).	
RN	[2]	
RP	SEQUENCE FROM N.A.	


```

Qy      45 LDFRKDICSMPQAGPCLASIPHHWYNNKTKICSEFIYGGCGGNNNNFQTEAICLVTC 102
       :|::||::||::||::||::||::||::||::||::||::||::||::||::||::||
Db      2 VDFDKQ-CVPTADGPCKGFMPMWMWNIFTSQCBEFIYGGCGGNDNRYRTKEBCDKC 58

RESULT 50
Q708Y9 PRELIMINARY; PRT; 750 AA.
ID Q708Y9 AC Q708Y9
DT 05-JUL-2004 (TtEMBLrel. 27, Created)
DT 05-JUL-2004 (TtEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TtEMBLrel. 27, Last annotation update)
DE Amyloid-beta-like protein B precursor.
GN Name=aplp2 B;
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidea; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxId=8355;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RA Collin R.W.J., van Strien D., Leunissen J.A., Martens G.J.M.;
RL Submitted (NOV-2003) to the EMBL/GenBank/DBJ databases.
CC -I- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.
DR EMBL; AJ508933; CAS75663.1; -.
DR HSP; Q16019; IAA.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0005488; F:binding; IEA.
DR GO; GO:0004867; F:serine-type endopeptidase inhibitor activity; IEA.
DR InterPro; IPR008155; A4_APP.
DR InterPro; IPR008154; A4_extra.
DR InterPro; IPR002223; Prot_Inh_Kunz-m.
DR Pfam; PF02177; A4_EXTRA; 1.
DR Pfam; PF00014; Kunitz_BPTI; 1.
DR PRINTS; PR00203; AMYOIDA4.
DR PROSITE; PS00759; BASICPTASE.
DR ProDom; PD000223; Prot_Inh_Kunz-m; 1.
DR SMART; SM00006; A4_EXTRA; 1.
DR SMART; SM00331; KU; 1.
DR PROSITE; PS00320; A4_INTRIA; 1.
DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
DR PROSITE; PS50279; BPTI_KUNITZ_2; 1.
KW Signal.
FT SIGNAL 1 20 Potential.
FT CHAIN 21 750 amyloid-beta-like protein B.
SQ SEQUENCE 750 AA; 85363 MW; 7118763E7A763689 CRC64;

Query Match 26.2%; Score 163.5; DB 2; Length 750;
Best Local Similarity 34.6%; Pred. No. 1.6e-07;
Matches 36; Conservative 12; Mismatches 37; Indels 19; Gaps 3

Qy      16 EVERBI-DQCTKPRDC-----PENMKCFPGCGKCLDPFRKDICSMPQAG 59
Db      242 EEIEIEDEVVEDRYYYDNEDYNENPTPEPNERQL---SGKDIITDVKSVCQEAVTG 298

Qy      60 PCLASIPHHWYNNKTKICSEFIYGGCGGNNNNFQTEAICLVTC 103
Db      299 PCRAMPRRWYFDLGKKCVRFYIGGCGGNNRNPFSADYCMVACK 342

Search completed: September 21, 2005, 16:40:10
Job time : 59.472 secs

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OM protein - protein search, using sw model

Run on: September 21, 2005, 14:52:13 ; Search time 31.8938 Seconds
(without alignments)
618.452 Million cell updates/sec

Title: US-10-807-204-1_COPY_77_127

Perfect score: 302

Sequence: 1 CSMPQAGPCLASIPHWYN.....GGCQGNNNFQTEAICLVTC 51

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 50 summaries

Database : A_Geneseq_16Dec04:*
1: Geneseqp1980s:*
2: Geneseqp1990s:*
3: Geneseqp2000s:*
4: Geneseqp2001s:*
5: Geneseqp2002s:*
6: Geneseqp2003as:*
7: Geneseqp2003bs:*
8: Geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	302	100.0	106	7	ADAL19801 Mature fo
2	302	100.0	131	7	ADAL19800 Engineere
3	302	100.0	131	7	ADAL19811 Engineere
4	292	96.7	131	7	ADAL19814 Human DJ1
5	224	74.2	136	7	ADAL19815 Mouse DJ1
6	219	72.5	51	2	Aaw75257 Fragment
7	219	72.5	51	5	Aae27025 Human gen
8	219	72.5	51	5	Aae27163 Human gen
9	219	72.5	51	8	ADG89845 Human sec
10	219	72.5	58	4	Aae13084 Human ser
11	219	72.5	58	4	Aae60630 Kunitz do
12	219	72.5	58	7	ADFL1997 Human CAB
13	219	72.5	58	8	ADL16838 Human Kun
14	219	72.5	58	8	ADL89980 Human CAB
15	219	72.5	64	4	Aae13093 Human ser
16	219	72.5	102	5	Aae27095 Human sec
17	219	72.5	102	5	Aae28009 Human gen
18	219	72.5	102	6	ABU65039 Human sec
19	219	72.5	102	8	ADG89848 Human sec
20	219	72.5	117	5	Aae27094 Human sec
21	219	72.5	117	5	Aae27165 Human gen
22	219	72.5	117	6	ABU65038 Human sec
23	219	72.5	117	8	ADG89847 Human sec
24	219	72.5	133	2	Aaw75219 Human sec
25	219	72.5	133	5	Aae26982 Human gen

26	219	72.5	133	5	Aae27120 Human gen
27	219	72.5	133	6	ABU64993 Human sec
28	219	72.5	133	7	ADAL19812 Human EPP
29	219	72.5	133	8	ADG89802 Human pro
30	219	72.5	164	3	AAY70010 Human pro
31	219	72.5	179	8	ABM85103 Human dia
32	188	62.3	134	7	ADAL19813 Mouse EPP
33	170	56.3	43	4	ADAL19813 Mouse EPP
34	169	56.0	571	7	Aae13096 Human ser
35	169	56.0	571	7	Aae39459 Mouse GDF
36	169	56.0	571	7	ADD93670 Mouse GDF
37	167	55.3	58	2	AAR99146 Aprotinin
38	166	55.0	54	4	Aae13092 Trypsin i
39	166	55.0	86	4	ABAB48380 I. ficinu
40	161	53.3	51	2	Aaw25929 Anti-tryp
41	161	53.3	55	2	AAR25931 RPDF-Kun1
42	161	53.3	58	2	AAR27402 Human neu
43	161	53.3	58	2	AAR99160 Genetical
44	161	53.3	58	2	AAR99159 Genetical
45	161	53.3	58	2	AAR99158 Genetical
46	161	53.3	58	8	ADF71964 Kallikrei
47	161	53.3	58	8	ADF71963 Kallikrei
48	161	53.3	58	8	ADF71962 Kallikrei
49	161	53.3	124	2	Aaw25933 New prote
50	161	53.3	124	2	Aaw25932 New prote

ALIGNMENTS

RESULT 1

ADAL19801

ID ADAL19801 standard; protein; 106 AA.

AC ADAL19801;

DT 20-NOV-2003 (first entry)

DE Mature form of engineered human DJ11 protein SEQ ID NO:2.

XX DJ11; Kunitz-type protease inhibitor domain; antiinflammatory;
KW antiallergic; thrombolytic; anticoagulant; cardiant; vasotropic;
KW antibacterial; immunosuppressive; antirheumatic; antiarthritic;
KW nephrotropic; antipsoriatic; vulnery; protease inhibitor; gene therapy;
KW acute pancreatitis; pulmonary injury; allergy-induced protease release;
KW deep vein thrombosis; myocardial infarction; shock; septic shock;
KW hyperfibrinolytic haemorrhage; inflammatory disorder; emphysema;
KW idiopathic pulmonary fibrosis; rheumatoid arthritis; glomerulonephritis;
KW chronic inflammatory bowel disease; psoriasis.

OS Synthetic.

XX Homo sapiens.

Key Location/Qualifiers

FT Disulfide-bond 8..36 /note = predicted disulfide bond

FT Disulfide-bond 15..40 /note = predicted disulfide bond

FT Disulfide-bond 23..35 /note = predicted disulfide bond

FT Disulfide-bond 29..44 /note = predicted disulfide bond

FT Domain 52..102 /note = predicted disulfide bond

FT Disulfide-bond 52..102 /note = Kunitz domain predicted by pfscan

FT Disulfide-bond 61..85 /note = predicted disulfide bond

FT Disulfide-bond 77..98 /note = predicted disulfide bond

FT Disulfide-bond /note = predicted disulfide bond

WO2003070770-A2.

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PD 28-AUG-2003.
XX
XX 18-FEB-2003; 2003WO-EP001629.
XX
XX 21-FEB-2002; 2002US-0358683P.
XX
XX (GENE-) GENEPROT INC.
XX
XX Bougueleret L, Bairoch A, Niknejad A;
XX
XX WPI; 2003-663849/62.
DR
XX
XX New engineered human Kunitz-type protease inhibitor for diagnosing,
XX preventing or treating conditions associated with excessive proteinase
XX activity, e.g. inflammation, pulmonary injuries, myocardial infarction or
XX hemorrhage.
XX
XX Claim 5; Page 71; 87pp; English.
PS
XX
XX The present invention describes an isolated, purified or recombinant DJ11
XX polypeptide comprising a Kunitz-type protease inhibitor domain or its
XX biologically active portion. The polypeptide comprises at least 98 %
XX identity to residues 77-127 of a 131 amino acid sequence (S1, see
XX ADA19800), or to residues 52-102 of a 106 amino acid sequence (S2, see
XX ADA19801). DJ11 has antiinflammatory, antiallergic, thrombolytic,
XX anticoagulant, cardiatic, vasotropic, antibacterial, immunosuppressive,
XX antirheumatic, antiarthritic, nephrotropic, antipsoriatic and vulnary
XX activities, and can be used as a protease inhibitor and in gene therapy.
XX Composition and methods from the present invention can be used in
XX diagnosing, preventing or treating conditions associated with excessive
XX proteinase activity, such as acute pancreatitis, pulmonary injury,
XX allergy-induced protease release, deep vein thrombosis, myocardial
XX infarction, shock (including septic shock), hyperfibrinolytic
XX haemorrhage, and especially, inflammatory disorders (e.g. emphysema,
XX idiopathic pulmonary fibrosis, rheumatoid arthritis, glomerulonephritis,
XX chronic inflammatory bowel disease or psoriasis). The DJ11 proteins may
XX be used in preserving platelet function, organ preservation or in wound
XX healing. The polynucleotide sequence encoding DJ11 may be used as
XX hybridisation probes, in chromosome and gene mapping, in the generation
XX of antisense RNA and DNA, and as targets for pharmaceutical intervention.
XX The present sequence represents the mature form of an engineered human
XX DJ11 protein from the present invention.
XX
XX Sequence 106 AA;
SQ
Query Match 100.0%; Score 302; DB 7; Length 106;
Best Local Similarity 100.0%; Pred. No. 3.2e-30;
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 CSMPQAGPCPLASIPHHWYKTKICSEFIYGGCGNNNFQTEAICLVTC 51
Db 52 CSMPQAGPCPLASIPHHWYKTKICSEFIYGGCGNNNFQTEAICLVTC 102
RESULT 2
ADA19800
ID ADA19800 standard; protein; 131 AA.
XX
XX ADA19800;
AC
XX
XX 20-NOV-2003 (first entry)
DT
XX
XX Engineered human DJ11 protein SEQ ID NO:1.
DE
XX
XX DJ11; Kunitz-type protease inhibitor domain; antiinflammatory;
KW antiallergic; thrombolytic; anticoagulant; cardiatic; vasotropic;
KW antibacterial; immunosuppressive; antirheumatic; antiarthritic;
KW nephrotropic; antipsoriatic; vulnary; protease inhibitor; gene therapy;
KW acute pancreatitis; pulmonary injury; allergy-induced protease release;
KW deep vein thrombosis; myocardial infarction; shock; septic shock;
KW hyperfibrinolytic haemorrhage; inflammatory disorder; emphysema;
KW idiopathic pulmonary fibrosis; rheumatoid arthritis; glomerulonephritis;
KW chronic inflammatory bowel disease; psoriasis.

```

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XX
OS Synthetic.
OS Homo sapiens.
XX
XX Key Location/Qualifiers
FH Misc-difference 1..131
FT /note= "eppin-like precursor"
FT Peptide 1..25
FT /label= signal
FT Protein 26..131
FT /note= "mature DJ11 protein"
FT Disulfide-bond 33..61
FT /note = predicted disulfide bond
FT Disulfide-bond 40..65
FT /note = predicted disulfide bond
FT Disulfide-bond 48..60
FT /note = predicted disulfide bond
FT Disulfide-bond 54..69
FT /note = predicted disulfide bond
FT Domain 77..127
FT /note = Kunitz domain predicted by pfscan
FT Disulfide-bond 77..127
FT /note = predicted disulfide bond
FT Disulfide-bond 86..110
FT /note = predicted disulfide bond
FT Disulfide-bond 102..123
FT /note = predicted disulfide bond
XX
XX WO2003070770-A2.
XX
XX 28-AUG-2003.
XX
XX 18-FEB-2003; 2003WO-EP001629.
XX
XX 21-FEB-2002; 2002US-0358683P.
XX
XX (GENE-) GENEPROT INC.
XX
XX Bougueleret L, Bairoch A, Niknejad A;
XX
XX WPI; 2003-663849/62.
DR
XX
XX N-PSDB; ADA19810.
XX
XX New engineered human Kunitz-type protease inhibitor for diagnosing,
XX preventing or treating conditions associated with excessive proteinase
XX activity, e.g. inflammation, pulmonary injuries, myocardial infarction or
XX hemorrhage.
XX
XX Claim 5; Page 69-70; 87pp; English.
XX
XX The present invention describes an isolated, purified or recombinant DJ11
XX polypeptide comprising a Kunitz-type protease inhibitor domain or its
XX biologically active portion. The polypeptide comprises at least 98 %
XX identity to residues 77-127 of a 131 amino acid sequence (S1, see
XX ADA19800), or to residues 52-102 of a 106 amino acid sequence (S2, see
XX ADA19801). DJ11 has antiinflammatory, antiallergic, thrombolytic,
XX anticoagulant, cardiatic, vasotropic, antibacterial, immunosuppressive,
XX antirheumatic, antiarthritic, nephrotropic, antipsoriatic and vulnary
XX activities, and can be used as a protease inhibitor and in gene therapy.
XX Composition and methods from the present invention can be used in
XX diagnosing, preventing or treating conditions associated with excessive
XX proteinase activity, such as acute pancreatitis, pulmonary injury,
XX allergy-induced protease release, deep vein thrombosis, myocardial
XX infarction, shock (including septic shock), hyperfibrinolytic
XX haemorrhage, and especially, inflammatory disorders (e.g. emphysema,
XX idiopathic pulmonary fibrosis, rheumatoid arthritis, glomerulonephritis,
XX chronic inflammatory bowel disease or psoriasis). The DJ11 proteins may
XX be used in preserving platelet function, organ preservation or in wound
XX healing. The polynucleotide sequence encoding DJ11 may be used as
XX hybridisation probes, in chromosome and gene mapping, in the generation
XX of antisense RNA and DNA, and as targets for pharmaceutical intervention.
XX The present sequence represents an engineered human DJ11 protein from the
XX present invention.

```

XX SQ Sequence 131 AA;
 Query Match 100.0%; Score 302; DB 7; Length 131;
 Best Local Similarity 100.0%; Pred. No. 4.1e-30;
 Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CSMPOEAGPCLASIPHHWYNNKTKICSEFIYGGCGGNNNFQTEAICLVTC 51
 |||||
 DB 77 CSMPOEAGPCLASIPHHWYNNKTKICSEFIYGGCGGNNNFQTEAICLVTC 127
 |||||

RESULT 3
 ADA19811
 ID ADA19811 standard; protein; 131 AA.
 XX AC ADA19811;
 XX DT 20-NOV-2003 (first entry)
 XX Engineered human DJ11 protein SEQ ID NO:12.
 XX DJ11; Kunitz-type protease inhibitor domain; antiinflammatory;
 KW antiallergic; thrombolytic; anticoagulant; cardiant; vasotropic;
 KW antibacterial; immunosuppressive; antirheumatic; antiarthritic;
 KW nephrotropic; antipsoriatic; vulnary; protease inhibitor; gene therapy;
 KW acute pancreatitis; pulmonary injury; allergy-induced protease release;
 KW deep vein thrombosis; myocardial infarction; shock; septic shock;
 KW hyperfibrinolytic haemorrhage; inflammatory disorder; emphysema;
 KW idiopathic pulmonary fibrosis; rheumatoid arthritis; glomerulonephritis;
 KW chronic inflammatory bowel disease; psoriasis.
 XX Synthetic.
 OS Homo sapiens.
 OS WO2003070770-A2.
 XX PN 28-AUG-2003.
 XX PF 18-FEB-2003; 2003WO-EP001629.
 XX PR 21-FEB-2002; 2002US-0358683P.
 XX PA (GENE-) GENEPROT INC.
 XX PI Bougueleret L, Bairoch A, Niknejad A;
 XX WPI; 2003-663849/62.
 XX New engineered human Kunitz-type protease inhibitor for diagnosing,
 PT preventing or treating conditions associated with excessive proteinase
 PT activity, e.g. inflammation, pulmonary injuries, myocardial infarction or
 PT hemorrhage.
 XX Disclosure; Page 84; 87pp; English.

XX The present invention describes an isolated, purified or recombinant DJ11
 CC polypeptide comprising a Kunitz-type protease inhibitor domain or its
 CC biologically active portion. The polypeptide comprises at least 98 %
 CC identity to residues 77-127 of a 131 amino acid sequence (S1, see
 CC ADA19800), or to residues 52-102 of a 106 amino acid sequence (S2, see
 CC ADA19801). DJ11 has antiinflammatory, antiallergic, immunosuppressive,
 CC anticoagulant, cardiant, vasotropic, antibacterial, immunosuppressive,
 CC antirheumatic, antiarthritic, nephrotropic, antipsoriatic and vulnary
 CC activities, and can be used as a protease inhibitor and in gene therapy.
 CC protease activity, such as acute pancreatitis, pulmonary injury,
 CC allergy-induced protease release, deep vein thrombosis, myocardial
 CC infarction, shock (including septic shock), hyperfibrinolytic
 CC haemorrhage, and especially, inflammatory disorders (e.g. emphysema,
 CC idiopathic pulmonary fibrosis, rheumatoid arthritis, glomerulonephritis,
 CC chronic inflammatory bowel disease or psoriasis). The DJ11 proteins may

CC be used in preserving platelet function, organ preservation or in wound
 CC healing. The polynucleotide sequence encoding DJ11 may be used as
 CC hybridisation probes, in chromosome and gene mapping, in the generation
 CC of antisense RNA and DNA, and as targets for pharmaceutical intervention.
 CC The present sequence represents an engineered human DJ11 protein from the
 CC present invention.

XX SQ Sequence 131 AA;

Query Match 100.0%; Score 302; DB 7; Length 131;
 Best Local Similarity 100.0%; Pred. No. 4.1e-30;
 Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CSMPOEAGPCLASIPHHWYNNKTKICSEFIYGGCGGNNNFQTEAICLVTC 51
 |||||
 DB 77 CSMPOEAGPCLASIPHHWYNNKTKICSEFIYGGCGGNNNFQTEAICLVTC 127
 |||||

RESULT 4
 ADA19814
 ID ADA19814 standard; protein; 131 AA.
 XX AC ADA19814;
 XX DT 20-NOV-2003 (first entry)
 XX Human DJ11 protein SEQ ID NO:15.

XX DJ11; Kunitz-type protease inhibitor domain; antiinflammatory;
 KW antiallergic; thrombolytic; anticoagulant; cardiant; vasotropic;
 KW antibacterial; immunosuppressive; antirheumatic; antiarthritic;
 KW nephrotropic; antipsoriatic; vulnary; protease inhibitor; gene therapy;
 KW acute pancreatitis; pulmonary injury; allergy-induced protease release;
 KW deep vein thrombosis; myocardial infarction; shock; septic shock;
 KW hyperfibrinolytic haemorrhage; inflammatory disorder; emphysema;
 KW idiopathic pulmonary fibrosis; rheumatoid arthritis; glomerulonephritis;
 KW chronic inflammatory bowel disease; psoriasis.

XX OS Homo sapiens.

XX PN WO2003070770-A2.

XX XX 28-AUG-2003.

XX PF 18-FEB-2003; 2003WO-EP001629.

XX PR 21-FEB-2002; 2002US-0358683P.

XX PA (GENE-) GENEPROT INC.

XX PI Bougueleret L, Bairoch A, Niknejad A;

XX WPI; 2003-663849/62.

XX New engineered human Kunitz-type protease inhibitor for diagnosing,
 PT preventing or treating conditions associated with excessive proteinase
 PT activity, e.g. inflammation, pulmonary injuries, myocardial infarction or
 PT hemorrhage.

XX Disclosure; Fig 1; 87pp; English.

XX The present invention describes an isolated, purified or recombinant DJ11
 CC polypeptide comprising a Kunitz-type protease inhibitor domain or its
 CC biologically active portion. The polypeptide comprises at least 98 %
 CC identity to residues 77-127 of a 131 amino acid sequence (S1, see
 CC ADA19800), or to residues 52-102 of a 106 amino acid sequence (S2, see
 CC ADA19801). DJ11 has antiinflammatory, antiallergic, immunosuppressive,
 CC anticoagulant, cardiant, vasotropic, antibacterial, immunosuppressive,
 CC antirheumatic, antiarthritic, nephrotropic, antipsoriatic and vulnary
 CC activities, and can be used as a protease inhibitor and in gene therapy.
 CC protease activity, such as acute pancreatitis, pulmonary injury,
 CC allergy-induced protease release, deep vein thrombosis, myocardial
 CC infarction, shock (including septic shock), hyperfibrinolytic
 CC haemorrhage, and especially, inflammatory disorders (e.g. emphysema,
 CC idiopathic pulmonary fibrosis, rheumatoid arthritis, glomerulonephritis,
 CC chronic inflammatory bowel disease or psoriasis). The DJ11 proteins may

CC allergy-induced protease release, deep vein thrombosis, myocardial
 CC infarction, shock (including septic shock), hyperfibrinolytic
 CC haemorrhage, and especially, inflammatory disorders (e.g. emphysema,
 CC idiopathic pulmonary fibrosis, rheumatoid arthritis, glomerulonephritis,
 CC chronic inflammatory bowel disease or psoriasis). The DJ11 proteins may
 CC be used in preserving platelet function, organ preservation or in wound
 CC healing. The polynucleotide sequence encoding DJ11 may be used as
 CC hybridisation probes, in chromosome and gene mapping, in the generation
 CC of antisense RNA and DNA, and as targets for pharmaceutical intervention.
 CC The present sequence represents a human DJ11 protein given in comparison
 CC with DJ11 proteins in the exemplification of the present invention.

XX Sequence 131 AA;

Query Match 96.7%; Score 292; DB 7; Length 131;
 Best Local Similarity 98.0%; Pred. No. 7.5e-29;
 Matches 50; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 1 CSMPEAGPCLASIPHHWYNNKTKICSEFIYGGCGGNNNFQTEAICLVTC 51
 Db 77 CSMPEAGPCLASIPHHWYNNKTKICSEFIYGGCGGNNNFQTEAICLVTC 127

RESULT 5
 ADA19815
 ID ADA19815 standard; protein; 136 AA.

XX ADA19815;

XX 20-NOV-2003 (first entry)

XX Mouse DJ11 protein SEQ ID NO:16.

XX DJ11; Kunitz-type protease inhibitor domain; antiinflammatory;
 KW antiallergic; thrombolytic; anticoagulant; cardiant; vasotropic;
 KW antibacterial; immunosuppressive; antirheumatic; antiarthritic;
 KW nephrotropic; antipsoriatic; vulnery; protease inhibitor; gene therapy;
 KW acute pancreatitis; pulmonary injury; allergy-induced protease release;
 KW deep vein thrombosis; myocardial infarction; shock; septic shock;
 KW hyperfibrinolytic haemorrhage; inflammatory disorder; emphysema;
 KW idiopathic pulmonary fibrosis; rheumatoid arthritis; glomerulonephritis;
 KW chronic inflammatory bowel disease; psoriasis.

XX Mus musculus.

XX WO2003070770-A2.

XX 28-AUG-2003.

XX 18-FEB-2003; 2003WO-EP001629.

XX 21-FEB-2002; 2002US-0358683P.

XX (GENE-) GENEPROT INC.

XX Bougueleret L, Bairoch A, Niknejad A;

XX WPI; 2003-663849/62.

XX New engineered human Kunitz-type protease inhibitor for diagnosing,
 FT preventing or treating conditions associated with excessive proteinase
 PT activity, e.g. inflammation, pulmonary injuries, myocardial infarction or
 PT hemorrhage.

XX Disclosure; Fig 1; 87pp; English.

XX The present invention describes an isolated, purified or recombinant DJ11
 CC polypeptide comprising a Kunitz-type protease inhibitor domain or its
 CC biologically active portion. The polypeptide comprises at least 98 %
 CC identity to residues 77-127 of a 131 amino acid sequence (SI, see
 CC ADA19800), or to residues 52-102 of a 106 amino acid sequence (S2, see
 CC ADA19801). DJ11 has antiinflammatory, antiallergic, thrombolytic,
 CC anticoagulant, cardiant, vasotropic, antibacterial, immunosuppressive,

CC antirheumatic, antiarthritic, nephrotropic, antipsoriatic and vulnery
 CC activities, and can be used as a protease inhibitor and in gene therapy.
 CC Composition and methods from the present invention can be used in
 CC diagnosing, preventing or treating conditions associated with excessive
 CC proteinase activity, such as acute pancreatitis, pulmonary injury,
 CC allergy-induced protease release, deep vein thrombosis, myocardial
 CC infarction, shock (including septic shock), hyperfibrinolytic
 CC haemorrhage, and especially, inflammatory disorders (e.g. emphysema,
 CC idiopathic pulmonary fibrosis, rheumatoid arthritis, glomerulonephritis,
 CC chronic inflammatory bowel disease or psoriasis). The DJ11 proteins may
 CC be used in preserving platelet function, organ preservation or in wound
 CC healing. The polynucleotide sequence encoding DJ11 may be used as
 CC hybridisation probes, in chromosome and gene mapping, in the generation
 CC of antisense RNA and DNA, and as targets for pharmaceutical intervention.
 CC The present sequence represents a mouse DJ11 protein given in comparison
 CC with DJ11 proteins in the exemplification of the present invention.

XX Sequence 136 AA;

Query Match 74.2%; Score 224; DB 7; Length 136;
 Best Local Similarity 66.7%; Pred. No. 3.2e-20;
 Matches 34; Conservative 8; Mismatches 9; Indels 0; Gaps 0;

Oy 1 CSMPEAGPCLASIPHHWYNNKTKICSEFIYGGCGGNNNFQTEAICLVTC 51
 Db 77 CSLPQDPGCLAYLPWWYNNQETDLCTEFYGGCGGNNNFPGEGICTVVC 127

RESULT 6

AAW75257

ID AAW75257 standard; protein; 51 AA.

XX AAW75257;

XX 29-JAN-1999 (first entry)

XX Fragment of human secreted protein encoded by gene 24.

XX Human; secreted protein; fusion protein; gene therapy; protein therapy;
 KW diagnosis; tissue; cancer; tumour; neurodegenerative disorder; leukaemia;
 KW developmental abnormality; foetal deficiency; blood; allergy; renal;
 KW immune system; asthma; lymphocytic disease; brain; hepatic; lymphoma;
 KW inflammation; ischaemic shock; Alzheimer's disease; restenosis; AIDS;
 KW cognitive disorder; schizophrenia; prostate; obesity; osteoclast; thymus;
 KW osteoporosis; arthritis; testis; lung; thyroiditis; thyroid; digestion;
 KW endocrine; metabolism; regulation; malabsorption; gastritis; neoplasm.

XX Homo sapiens.

XX WO9840483-A2.

XX 17-SEP-1998.

XX 12-MAR-1998; 98WO-US004858.

XX 14-MAR-1997; 97US-0040710P.

XX 14-MAR-1997; 97US-0040762P.

XX 30-MAY-1997; 97US-0048100P.

XX 30-MAY-1997; 97US-0048189P.

XX 30-MAY-1997; 97US-0048357P.

XX 30-MAY-1997; 97US-0050934P.

XX 06-JUN-1997; 97US-0048970P.

XX 05-SEP-1997; 97US-005765P.

XX 19-DEC-1997; 97US-0068368P.

XX (HUMA-) HUMAN GENOME SCI INC.

XX Ruben SM, Rosen CA, Li Y, Zeng Z, Kyaw H, Fischer CL, Li H;

XX Soppet DR, Gentz RL, Wei YF, Moore PA, Young PE, Greene JM;

XX Ferrie AW;

XX WPI; 1998-520811/44.

XX N-PSDB; AAV34309.

PT New polypeptides and nucleic acid molecules for diagnosing, preventing or
 PT treating diseases associated with aberrant expression or activity of the
 PT polypeptide, e.g. cancer, asthma, AIDS, Parkinson's disease or diabetes.
 XX
 PS Disclosure; SEQ ID NO 118; 320pp; English.

XX The invention relates to an isolated nucleic acid molecule encoding a
 CC secreted protein that is at least 95% identical to a polynucleotide
 CC fragment of any of the nucleotide sequences listed in table 1A of the
 CC specification, which is hybridisable to the nucleotide sequences, a
 CC polynucleotide encoding a polypeptide (or a polypeptide fragment, domain
 CC or epitope of any of the amino acid sequences) listed in table 1A of the
 CC specification, a polynucleotide which is an (allelic) variant of the
 CC nucleotide sequences listed in the specification, a polynucleotide which
 CC encodes a species homologue of the above amino acid sequences, a
 CC polynucleotide capable of hybridising under stringent conditions to any
 CC of the above polynucleotides, where the polynucleotide does not hybridise
 CC under stringent conditions to a nucleic acid molecule having a nucleotide
 CC sequence of only A or T residues. Also included are a recombinant host
 CC comprising the above nucleic acid molecule, making a recombinant host
 CC cell comprising the above nucleic acid molecule, an isolated polypeptide
 CC comprising a sequence that is at least 95% identical to the polypeptide
 CC (or its fragment, domain, epitope, secreted form, (allelic) variant or
 CC homologue) encoded by the above nucleic acid molecule, an isolated
 CC antibody that binds specifically to the above polypeptide, a recombinant
 CC host cell produced by the above method and that expresses the above
 CC polypeptide, making an isolated polypeptide, preventing, treating or
 CC ameliorating a medical condition, diagnosing a pathological condition or
 CC a susceptibility to a pathological condition in a subject, identifying a
 CC binding partner to the above polypeptide, the gene corresponding to the
 CC cDNA sequence given in the specification, and identifying an activity in
 CC a biological assay. The nucleic acid molecule and polypeptide are useful
 CC in diagnosing, preventing, prognosing or treating diseases or disorders
 CC associated with aberrant expression and/or activity of the above
 CC polypeptide, such as neural disorders, immune system disorders, muscular
 CC disorders, reproductive disorders, gastrointestinal disorders, pulmonary
 CC disorders, cardiovascular disorders, renal disorders, proliferative
 CC disorders and/or cancers. In particular, these diseases are systemic
 CC lupus erythematosus, rheumatoid arthritis, multiple sclerosis,
 CC thyroiditis, anaemia, Grave's disease, diabetes, hepatitis, asthma,
 CC allergies, nephritis, Parkinson's disease, Alzheimer's disease,
 CC atherosclerosis, myocardial infarction, AIDS and infections. The methods
 CC may be used for identifying agonists and antagonists of the
 CC polynucleotide and polypeptide. The present sequence is a protein from
 CC one of the 28 disclosed secreted protein genes, it is not clear whether
 CC this is an alternative expressed protein or a fragment of one of the
 CC claimed proteins.

XX Sequence 51 AA;

Query Match 72.5%; Score 219; DB 8; Length 51;
 Best Local Similarity 68.6%; Pred. No. 4.7e-20;
 Matches 35; Conservative 5; Mismatches 11; Indels 0; Gaps 0;

QY 1 CSMPQAGPCLASIPHHWYKTKICSEFIYGGCGNNNNFQTEAICLVTC 51
 DB 1 CEMPKEGTCLAYFLHWYDKDNTCSMFVYGGCGNNNNFQSKANCLNTC 51

RESULT 10

AAE13084

ID AAE13084 standard; peptide; 58 AA.

XX AAE13084;

XX 28-JAN-2002 (first entry)

DE Human serine proteinase inhibitor BTL.009 peptide.

XX Human; BTL.009 protein; serine proteinase inhibitor; cytostatic;
 KW nephrotropic; idiopathic pulmonary fibrosis; cystic fibrosis; emphysema;
 KW rheumatoid arthritis; adult respiratory distress syndrome; angioedema;
 KW blood coagulation; glomerulonephritis; prophylactic; platelet activation;

KW neutrophil; monocyte; granulocyte; organ failure; inflammatory disease;
 KW elastase inhibitor; chymotrypsin inhibitor; lung injury; vascular injury;
 KW therapeutic.

XX Homo sapiens.

XX US6294648-B1.

XX 25-SEP-2001.

XX 20-JUL-1999; 99US-00358569.

XX 20-JUL-1999; 99US-00358569.

XX (FARB) BAYER CORP.

XX Delaria K, Roczniak S, Davies C;

XX WPI; 2001-662224/76.

XX New isolated protein for inhibiting human serine proteinase activity in the
 PT treatment of e.g. emphysema and adult respiratory distress syndrome.

XX Claim 1; Col 15-16; 16pp; English.

XX The invention relates to human BTL.009 protein, a serine proteinase
 CC inhibitor of the Kunitz family that exhibits greater potency towards
 CC neutral serine proteinases. BTL.009 protein is found to inhibit leukocyte
 CC elastase, chymotrypsin-like protease and trypsin-like protease. BTL.009
 CC protein is useful for treating emphysema, idiopathic pulmonary fibrosis,
 CC adult respiratory distress syndrome, cystic fibrosis, rheumatoid
 CC arthritis, organ failure, glomerulonephritis, other inflammatory diseases
 CC and diseases involving lung and vascular injury. BTL.009 is also useful
 CC for preventing neutrophil and monocyte activation and formation of active
 CC oxygen species during the oxidative burst of stimulated granulocytes.
 CC BTL.009 is useful for reducing platelet activation and blood coagulation
 CC and for the prophylactic or therapeutic treatment of patients undergoing
 CC angioplasty. The present sequence is human serine proteinase inhibitor
 CC BTL.009 peptide corresponding to Kunitz domain used in the
 CC exemplification of the invention. Note: The present sequence shown in
 CC column 14 and sequence listing of the specification lacks 3 amino acid
 CC residues at the C-terminal end

XX Sequence 58 AA;

Query Match 72.5%; Score 219; DB 4; Length 58;
 Best Local Similarity 68.6%; Pred. No. 5.4e-20;
 Matches 35; Conservative 5; Mismatches 11; Indels 0; Gaps 0;

QY 1 CSMPQAGPCLASIPHHWYKTKICSEFIYGGCGNNNNFQTEAICLVTC 51
 DB 5 CEMPKEGTCLAYFLHWYDKDNTCSMFVYGGCGNNNNFQSKANCLNTC 55

RESULT 11

AAE60630

ID AAE60630 standard; protein; 58 AA.

XX AAE60630;

XX 27-APR-2001 (first entry)

DE Kunitz domain, SEQ ID NO:8, used to identify BTL.010 protein.

XX Human BTL.010; neutral serine proteinase inhibitor; elastase inhibitor;
 KW proteinase-3 inhibitor; Kunitz domain; emphysema;
 KW idiopathic pulmonary fibrosis; adult respiratory distress syndrome;
 KW cystic fibrosis; rheumatoid arthritis; organ failure; glomerulonephritis;
 KW platelet activation; blood coagulation; neutrophil activation;
 KW monocyte activation; angioedema; inflammatory disease; lung injury;
 KW vascular injury; nephrotropic; anti-rheumatic; antiarthritic.

XX Unidentified.

XX US6180607-B1.
 XX 30-JAN-2001.
 PD
 XX
 XX 05-AUG-1999; 99US-00369494.
 XX
 XX 05-AUG-1999; 99US-00369494.
 XX
 XX (DAVI/) DAVIES C.
 XX (CHEN/) CHEN D.
 XX (ROCZ/) ROCZNIK S.
 XX
 XX Davies C, Chen D, Rocznik S;
 XX WPI; 2001-190860/19.
 DR
 XX
 XX Novel serine proteinase inhibitor of the Kunitz family, BTL.010 useful
 XX for treating emphysema, cystic fibrosis, adult respiratory distress
 XX syndrome, rheumatoid arthritis, organ failure and glomerulonephritis.
 XX
 XX Disclosure; Col 6; 17pp; English.
 XX
 XX The invention relates to a novel human serine protease inhibitor of the
 XX Kunitz family, BTL.010 (fragments given in AAB60623, AAB60631 and
 XX AAB60634). The BTL.010 protein is thought to preferentially inhibit
 XX neutral serine proteases such as elastase and proteinase-3, relative to
 XX trypsin-like and chymotrypsin-like proteases. A substantial proportion of
 XX the BTL.010 protein Kunitz domain (AAB60631) was identified via homology
 XX searching in the GenBank high throughput genomic (HTG) DNA sequence
 XX database using the Kunitz domain sequences AAB60630, and was confirmed as
 XX being novel using the Kunitz domain sequences AAB60632, and AAB60633.
 XX This sequence information was extended to provide a larger region of
 XX BTL.010 protein sequence data (AAB60634) by identifying an open reading
 XX frame (ORF) which comprised DNA encoding the BTL.010 Kunitz domain
 XX fragment in a 399 bp fragment of human genomic DNA (AAF59750),
 XX corresponding to bases 16016-16414 of GenBank accession number AC004846.
 XX The entire BTL.010 Kunitz domain sequence (AAB60623) was obtained from
 XX the BTL.010 ORF-encoded sequence. The BTL.010 protein, and pharmaceutical
 XX compositions comprising it, may be used for inhibiting protease activity,
 XX particularly that of leukocyte elastase, in the prevention, treatment or
 XX amelioration of medical conditions such as emphysema, idiopathic
 XX pulmonary fibrosis, adult respiratory distress syndrome, cystic fibrosis,
 XX rheumatoid arthritis, organ failure or glomerulonephritis. BTL.010
 XX compositions of the invention modulate at least one physiological
 XX condition such as platelet activation, blood coagulation, neutrophil
 XX activation, or monocyte activation. BTL.010 is also useful for the
 XX prophylactic or therapeutic treatment of patients undergoing angioplasty,
 XX and for the treatment of inflammatory diseases and diseases involving
 XX lung and vascular injury. The present sequence represents a Kunitz domain
 XX sequence used to identify the BTL.010 protein

XX Sequence 58 AA;
 Query Match 72.5%; Score 219; DB 4; Length 58;
 Best Local Similarity 68.6%; Pred. No. 5.4e-20;
 Matches 35; Conservative 5; Mismatches 11; Indels 0; Gaps 0;

Oy 1 CSMPEAGPCLASIPHHWYKTKICSEFIYGGCGGNNNNFQTEAICLVTC 51
 |||:||||| |||:| |||:|||||:|:|
 Db 5 CEMPKETGPCLAYFLHWYDKDKNTCSMFYVYGGCGGNNNNFQSKANCLNTC 55

RESULT 12
 ADP41997
 ID ADP41997 standard; protein; 58 AA.
 XX
 XX AC ADP41997;
 XX
 XX DT 12-FEB-2004 (first entry)
 XX
 XX DE Human CAB37 Kunitz domain peptide.
 XX

KW albumin fusion; Kunitz domain; cytostatic; haemostatic;
 KW hereditary angioedema; cancer; bleeding; gene therapy; human; CAB37.
 XX
 XX OS Homo sapiens.
 XX
 XX PN WO2003066824-A2.
 XX
 XX PD 14-AUG-2003.
 XX
 XX 07-FEB-2003; 2003WO-US003616.
 XX
 XX 07-FEB-2002; 2002US-0355547P.
 XX
 XX (AVET) AVENTIS BEHRING GMBH.
 XX (AVET) AVENTIS BEHRING LLC.
 XX (DELZ) DELTA BIOTECHNOLOGY LTD.
 XX (DYAX-) DYAX CORP.
 XX
 XX Hauser H, Weimer T, Romberg V, Kee SM, Sleep D, Ladner RC;
 XX Ley AC;
 XX WPI; 2003-731497/69.
 DR
 XX
 XX Albumin fusion protein comprising a Kunitz domain peptide and an albumin,
 XX useful for preparing a composition for treating a patient with hereditary
 XX angioedema or angioedema-related disease, cancer or bleeding disorder.
 XX
 XX Disclosure; Page 20; 110pp; English.
 XX
 XX The invention relates to a novel albumin fusion protein comprising a
 XX Kunitz domain peptide or its fragment or variant and an albumin or its
 XX fragment or variant. The fusion protein of the invention demonstrates a
 XX cycostatic and haemostatic activities and may be useful for preparing a
 XX composition for treating a patient with hereditary angioedema, an
 XX angioedema-related disease, cancer, a cancer-related disease or a
 XX bleeding disorder, as well as during gene therapy procedures. The current
 XX sequence is that of the human Kunitz domain peptide of the invention.

XX Sequence 58 AA;
 Query Match 72.5%; Score 219; DB 7; Length 58;
 Best Local Similarity 68.6%; Pred. No. 5.4e-20;
 Matches 35; Conservative 5; Mismatches 11; Indels 0; Gaps 0;

Oy 1 CSMPEAGPCLASIPHHWYKTKICSEFIYGGCGGNNNNFQTEAICLVTC 51
 |||:||||| |||:| |||:|||||:|:|
 Db 5 CEMPKETGPCLAYFLHWYDKDKNTCSMFYVYGGCGGNNNNFQSKANCLNTC 55

RESULT 13
 ADL16838
 ID ADL16838 standard; peptide; 58 AA.
 XX
 XX AC ADL16838;
 XX
 XX DT 06-MAY-2004 (first entry)
 XX
 XX DE Human Kunitz domain (KD) peptide.
 XX
 XX BTL.010 protein; serine proteinase inhibitor; Kunitz domain; emphysema;
 XX idiopathic pulmonary fibrosis; adult respiratory distress syndrome;
 XX cystic fibrosis; rheumatoid arthritis; organ failure; glomerulonephritis;
 XX inflammatory disease; oxidative burst; blood coagulation; gene therapy; human; KD.
 XX
 XX OS Homo sapiens.
 XX
 XX PN US6689582-B1.
 XX
 XX PD 10-FEB-2004.
 XX
 XX 12-MAY-2000; 2000US-00569670.
 XX
 XX PF Human CAB37 Kunitz domain peptide.
 XX

```
PR 05-AUG-1999; 99US-00369494.
XX (FARB ) BAYER PHARM CORP.
PA
PI Davies C, Chen D, Rocznia S;
XX
XX WPI; 2004-141424/14.
DR
XX New isolated polynucleotide encoding BTL.010 serine proteinase, useful
PT for treating e.g. emphysema, idiopathic pulmonary fibrosis, adult
PT respiratory distress syndrome, cystic fibrosis, rheumatoid arthritis or
XX glomerulonephritis.
XX
PS Disclosure; SEQ ID NO 8; 17pp; English.
XX
XX The invention relates to BTL.010, a human serine proteinase inhibitor of
CC the Kunitz family and its corresponding nucleic acid sequence. The
CC sequences of the invention are useful for treating diseases, e.g.
CC emphysema, idiopathic pulmonary fibrosis, adult respiratory distress
CC syndrome, cystic fibrosis, rheumatoid arthritis, organ failure,
CC glomerulonephritis or inflammatory diseases. The BTL.010 protein is also
CC useful for preventing neutrophil and monocyte activation and formation of
CC active oxygen species during the oxidative burst of stimulated
CC granulocytes. It is also useful for reducing platelet activation and
CC blood coagulation. BTL.010 DNA is useful in gene therapy. The present
CC sequence is human Kunitz domain (KD) peptide.
XX
XX Sequence 58 AA;
SQ
Query Match 72.5%; Score 219; DB 8; Length 58;
Best Local Similarity 68.6%; Pred. NO. 5.4e-20;
Matches 35; Conservative 5; Mismatches 11; Indels 0; Gaps 0;
QY 1 CSMPOEAGPCLASIPHHWYNNKTKICSEFIYGGCGGNNNNFQTEAICLVTC 51
DB 5 CEMPKEGTCLAYFLHWWYDKDNTCSMFVYGGCGGNNNNFQSKANCLNTC 55
RESULT 15
AAE13093
ID AAE13093 standard; peptide; 64 AA.
XX
XX AAE13093;
AC
XX
XX 28-JAN-2002 (first entry)
DT
XX
XX Human serine proteinase inhibitor BTL.009 C-terminal peptide.
DE
XX
XX Human; BTL.009 protein; serine proteinase inhibitor; cytostatic;
KW nephrotropic; idiopathic pulmonary fibrosis; cystic fibrosis; emphysema;
KW rheumatoid arthritis; adult respiratory distress syndrome; angioedema;
KW blood coagulation; glomerulonephritis; prophylactic; platelet activation;
KW neutrophil; monocyte; granulocyte; organ failure; inflammatory disease;
KW elastase inhibitor; chymotrypsin inhibitor; lung injury; vascular injury;
KW therapeutic.
XX
XX Homo sapiens.
OS
XX
XX US6294648-B1.
PN
XX
XX 25-SEP-2001.
PD
XX
XX 20-JUL-1999; 99US-00358569.
PP
XX
XX 20-JUL-1999; 99US-00358569.
PR
XX
XX (FARB ) BAYER CORP.
PA
XX
XX Delaria K, Rocznia S, Davies C;
PI
XX
XX WPI; 2001-662224/76.
DR
XX
XX New isolated protein for inhibiting human serine protease activity in the
PT treatment of e.g. emphysema and adult respiratory distress syndrome.
PT
XX
XX Disclosure; Col 6; 16pp; English.
PS
XX
XX The invention relates to human BTL.009 protein, a serine proteinase
CC inhibitor of the Kunitz family that exhibits greater potency towards
CC neutral serine proteinases. BTL.009 protein is found to inhibit leukocyte
CC elastase, chymotrypsin-like protease and trypsin-like protease. BTL.009
CC protein is useful for treating emphysema, idiopathic pulmonary fibrosis,
CC adult respiratory distress syndrome, cystic fibrosis, rheumatoid
CC arthritis, organ failure, glomerulonephritis, other inflammatory diseases
CC and diseases involving lung and vascular injury. BTL.009 is also useful
CC for preventing neutrophil and monocyte activation and formation of active
CC oxygen species during the oxidative burst of stimulated granulocytes.
CC BTL.009 is useful for reducing platelet activation and blood coagulation
CC
```

```
ADR89980
ID ADR89980 standard; peptide; 58 AA.
XX
XX ADR89980;
AC
XX
XX 18-NOV-2004 (first entry)
DT
XX
XX Human CAB37 protein kunitz domain peptide.
DE
XX
XX Kunitz domain peptide; cystic fibrosis; cystic fibrosis related disease;
KW hereditary angioedema; cancer; chronic obstructive pulmonary disease;
KW asthma; bronchitis; acute respiratory syndrome; pneumonia; bleeding;
KW cytostatic; haemostatic; CAB37 protein; human.
XX
XX Homo sapiens.
OS
XX
XX US2004171794-A1.
PN
XX
XX 02-SEP-2004.
PD
XX
XX 07-FEB-2003; 2003US-00361997.
PP
XX
XX 07-FEB-2003; 2003US-00361997.
PR
XX
XX (LADN/) LADNER R C.
PA
XX (LEYA/) LEY A C.
PA
XX
XX Ladner RC, Ley AC;
PI
XX
XX WPI; 2004-625120/60.
DR
XX
XX New kunitz domain peptide useful as human neutrophil elastase inhibitor
PT for the treatment of e.g. cystic fibrosis and related disease.
PT
XX
```


XX 02-FEB-2001; 2001US-0265583P.
PR (RUBE/) RUBEN S M.
PA (ROSE/) ROSEN C A.
PA (LIYY/) LI Y.
PA (ZENG/) ZENG Z.
PA (KYAW/) KYAW H.
PA (FISC/) FISCHER C L.
PA (LIHH/) LI H.
PA (SOPP/) SOPPET D R.
PA (GENTZ/) GENTZ R L.
PA (WEIY/) WEI Y.
PA (MOOR/) MOORE P A.
PA (YOUN/) YOUNG P E.
PA (GREE/) GREENE J M.
PA (FERR/) FERRIE A M.
XX
PI Ruben SM, Rosen CA, Li Y, Zeng Z, Kyaw H, Fischer CL, Li H;
PI Soppet DR, Gentz RL, Wei Y, Moore PA, Young PE, Greene JM;
PI Ferrie AM;
XX
DR WPI; 2002-574454/61.
XX
XX New nucleic acid molecules encoding 28 human secreted proteins, useful
PT for diagnosing, preventing, treating or ameliorating medical conditions
PT and as food additives or preservatives.
XX
XX Disclosure; Page 17; 209pp; English.
XX
CC AAD44854-AAD44984 represent cDNAs corresponding to 28 human secreted
CC protein genes, and AAE27097-AAE27137 represent the proteins they encode.
CC AAE27138-AAE27164 represent human secreted protein fragments. The genes
CC and their corresponding secreted proteins are useful for preventing,
CC treating or ameliorating medical conditions, e.g., by protein or gene
CC therapy. Secreted protein sequences of the invention are useful for the
CC diagnosis or treatment of disorders such as autoimmune diseases (e.g.
CC rheumatoid arthritis), hyperproliferative disorders (e.g. neoplasms of
CC the breast or liver), cerebrovascular disorders (e.g. cerebral ischaemia,
CC angioneurosis), cardiovascular disorders (e.g. cardiac arrest), nervous
CC system disorders (e.g. Alzheimer's disease), infections caused by fungi,
CC bacteria and viruses and ocular disorders (e.g. corneal infection). The
CC polypeptides can also be used to aid wound healing and epithelial cell
CC proliferation, to prevent skin aging due to sunburn, to maintain organs
CC before transplantation, for supporting cell culture of primary tissues,
CC to regenerate tissues and in chemotaxis. They can also be used as food
CC additives or preservative to increase or decrease storage capabilities,
CC fat content, lipid, protein, carbohydrate, vitamins, minerals, cofactors
CC and other nutritional components. The present sequence represents a human
CC secreted protein fragment referred to in the disclosure of the invention
XX
XX Sequence 102 AA;
SQ
Query Match 72.5%; Score 219; DB 5; Length 102;
Best Local Similarity 68.6%; Pred. No. 1e-19;
Matches 35; Conservative 5; Mismatches 11; Indels 0; Gaps 0;
QY 1 CSMQAGCLASIPHWYNNKTKICSEFIYGCQGNNNNFTQETALCLVTC 51
DB 46 CEMPKEGPCFLYFLHWYDKNDKTCMSFVYGCQGNNNNFSKANCCLNTC 96
RESULT 18
ABU65039
ID ABU65039 standard; peptide; 102 AA.
XX
AC ABU65039;
XX
DT 15-MAY-2003 (first entry)
XX
DE Human secreted protein gene 24, protein #3.
XX
KW Secreted protein; immunodeficiency; multiple sclerosis;

KW severe combined immunodeficiency; autoimmune disorder; cancer;
KW rheumatoid arthritis; diabetes mellitus; haematopoietic disorder;
KW inflammatory condition; septic shock; inflammatory bowel disease;
KW Crohn's disease; respiratory disorder; asthma; allergy; stroke;
KW gastrointestinal disorder; central nervous system disorder;
KW ischaemic brain injury; neurodegenerative disorder; Parkinson's disease;
KW Alzheimer's disease; cardiovascular disorder; atherosclerosis;
KW blood-related disorder; thrombosis; atherosclerosis; renal disorder;
KW hyperproliferative disorder; acute glomerulonephritis; Addison's disease;
KW endocrine disorder; liver disease; reproductive system disorder;
KW endometriosis; infectious disease; pancreatic disorder; vaccine;
KW wound repair; angiogenesis; lymphatic disorder; hair loss; body weight;
KW body height; hair colour; human.
XX
XX Homo sapiens.
OS
XX
XX US2002172994-A1.
PN
XX
XX 21-NOV-2002.
PD
XX
XX 11-MAY-2001; 2001US-00852797.
PF
XX
XX 14-MAR-1997; 97US-0040710P.
PR 14-MAR-1997; 97US-0040762P.
PR 30-MAY-1997; 97US-0048100P.
PR 30-MAY-1997; 97US-0048189P.
PR 30-MAY-1997; 97US-0048357P.
PR 30-MAY-1997; 97US-0050934P.
PR 06-JUN-1997; 97US-0048970P.
PR 05-SEP-1997; 97US-0057765P.
PR 19-DEC-1997; 97US-0068368P.
PR 12-MAR-1998; 98WO-US004858.
PR 11-SEP-1998; 98US-0015206P.
PR 02-FEB-2001; 2001US-0265583P.
XX
XX (RUBE/) RUBEN S M.
PA (ROSE/) ROSEN C A.
PA (LIYY/) LI Y.
PA (ZENG/) ZENG Z.
PA (KYAW/) KYAW H.
PA (FISC/) FISCHER C L.
PA (LIHH/) LI H.
PA (SOPP/) SOPPET D R.
PA (GENTZ/) GENTZ R L.
PA (WEIY/) WEI Y.
PA (MOOR/) MOORE P A.
PA (YOUN/) YOUNG P E.
PA (GREE/) GREENE J M.
PA (FERR/) FERRIE A M.
XX
PI Ruben SM, Rosen CA, Li Y, Zeng Z, Kyaw H, Fischer CL, Li H;
PI Soppet DR, Gentz RL, Wei Y, Moore PA, Young PE, Greene JM;
PI Ferrie AM;
XX
XX WPI; 2003-310989/30.
XX
XX New human secreted polypeptides and polynucleotides for diagnosing,
PT prognosing, preventing and treating immune, hyperproliferative, liver,
PT kidney, reproductive disorders and for identifying modulators of
PT therapeutic use.
XX
XX Disclosure; Page 16; 209pp; English.
XX
XX The invention relates to an isolated polypeptide comprising an amino acid
CC sequence at least 95% identical to sequence of 28 human secreted
CC proteins, their fragment, polypeptide domain, epitope, secreted form,
CC variant, allelic variant, or species homologue, or the encoded sequence
CC included in ATCC 97921 and 97922. Also included are the encoding nucleic
CC acids, recombinant vectors, host cells, antibodies, and genes. The
CC proteins and nucleic acids are useful for diagnosing, preventing,
CC treating, prognosing or ameliorating a medical condition e.g.
CC immunodeficiencies (e.g. X-linked agammaglobulinaemia, B cell
CC immunodeficiencies, severe combined immunodeficiencies), autoimmune

disorders (e.g. systemic erythematosis, rheumatoid arthritis, multiple sclerosis, autoimmune thyroiditis, autoimmune haemolytic anaemia, Goodpasture's syndrome, Grave's disease, diabetes mellitus, dermatitis), haematopoietic disorders, inflammatory conditions (e.g. septic shock, sepsis, reperfusion injury, inflammatory bowel disease, Crohn's disease), respiratory disorders (e.g. asthma and allergy), gastrointestinal disorders, cancers (e.g. gastric, ovarian, lung, bladder, liver and breast), central nervous system (CNS) disorders (e.g. ischaemic brain injury and/or stroke, traumatic brain injury), neurodegenerative disorders (e.g. Parkinson's disease and Alzheimer's disease, AIDS-related dementia, and prion disease), cardiovascular disorders (e.g. atherosclerosis, myocarditis, cardiovascular disease, and cardiopulmonary bypass complications), inflammation (e.g. hepatitis, gout, trauma, pancreatitis, sarcoidosis, dermatitis, allogenic transplant rejection), blood-related disorders (thrombosis, arterial thrombosis), hyperproliferative disorders, renal disorders (e.g. acute glomerulonephritis), endocrine disorders (e.g. Addison's disease, hyperthyroidism, hypothyroidism), liver diseases and disorders, reproductive system disorders (e.g. endometriosis), infectious diseases, and pancreatic disorders. Many other diseases and disorders are listed in the specification. They also useful as a vaccine adjuvant. Further they are useful to enhance or inhibit complement mediated cell lysis, for stimulating wound and tissue repair, angiogenesis, and the repair of vascular or lymphatic diseases or disorders. They are also useful to prevent hair loss, to modulate mammalian characteristics such as body height, weight, hair colour, and to increase or decrease storage capabilities, fat content, lipid, protein, carbohydrate, vitamins, minerals, cofactors or other nutritional components. The proteins are also useful for identifying binding partners. The present sequence represents a secreted protein of the invention

Sequence 102 AA;

Query Match 72.5%; Score 219; DB 6; Length 102;
 Best Local Similarity 68.6%; Pred. No. 1e-19;
 Matches 35; Conservative 5; Mismatches 11; Indels 0; Gaps 0;

1 CSMPQAGPCPLASIPHWYNNKTKICSEFIYGGCGNNNNFQTRACILVTC 51
 46 CEMPRTGPCLAYFLHWDYKDKTCSMFYGGCGNNNNFQSRANCLNTC 96

RESULT 19
 ADG89848
 ID ADG89848 standard; protein; 102 AA.

AC ADG89848;

DT 11-MAR-2004 (first entry)

DE Human secreted protein gene 24 protein #6.

Secreted protein; gene therapy; neural disorder; immune system disorders; muscular disorder; reproductive disorder; gastrointestinal disorder; pulmonary disorder; cardiovascular disorder; renal disorder; proliferative disorder; cancer; systemic lupus erythematosis; rheumatoid arthritis; multiple sclerosis; thyroiditis; anaemia; Grave's disease; diabetes; hepatitis; asthma; allergy; nephritis; myocardial infarction; AIDS; infection; human.

OS Homo sapiens.

XX US20032225009-A1.

PD 04-DEC-2003.

XX 30-JAN-2002; 2002US-00058993.

PR 14-MAR-1997; 97US-0040710P.

PR 14-MAR-1997; 97US-0040762P.

PR 30-MAY-1997; 97US-0048100P.

PR 30-MAY-1997; 97US-0048189P.

30-MAY-1997; 97US-00483537P.
 30-MAY-1997; 97US-0050934P.
 06-JUN-1997; 97US-0048970P.
 05-SEP-1997; 97US-0057765P.
 19-DEC-1997; 97US-0068368P.
 12-MAR-1998; 98WO-US0004858.
 11-SEP-1998; 98WO-00152060.
 02-FEB-2001; 2001US-0265583P.
 11-MAY-2001; 2001US-00852659.
 11-MAY-2001; 2001US-00852797.
 11-MAY-2001; 2001US-00853161.

(ROSE/) ROSEN C A.
 (RUBE/) RUBEN S M.
 (LIYU/) LI Y.
 (ZENG/) ZENG Z.
 (KIYAW/) KIYAW H.
 (FISC/) FISCHER C L.
 (LIHH/) LI H.
 (SOPP/) SOPPET D R.
 (GENT/) GENTZ R L.
 (WEIY/) WEI Y.
 (MOOR/) MOORE P A.
 (YOUN/) YOUNG P E.
 (GREE/) GREENE J M.
 (FERR/) FERRIE A M.
 (HAST/) HASTINGS G A.

Rosen CA, Ruben SM, Li Y, Zeng Z, Kyaw H, Fischer CL, Li H;
 Soppet DR, Gentz RL, Wei Y, Moore PA, Young PE, Greene JM;
 Ferrie AM, Hastings GA;
 WPI; 2004-042167/04.

New polypeptides and nucleic acid molecules for diagnosing, preventing or treating diseases associated with aberrant expression or activity of the polypeptide, e.g. cancer, asthma, AIDS, Parkinson's disease or diabetes.
 Disclosure; SEQ ID NO 121; 320pp; English.

The invention relates to an isolated nucleic acid molecule encoding a secreted protein that is at least 95% identical to a polynucleotide fragment of any of the nucleotide sequences listed in table 1A of the specification, which is hybridisable to the nucleotide sequences, a polynucleotide encoding a polypeptide (or a polypeptide fragment, domain or epitope of any of the amino acid sequences) listed in table 1A of the specification, a polynucleotide which is an (allelic) variant of the nucleotide sequences listed in the specification, a polynucleotide which encodes a species homologue of the above amino acid sequences, a polynucleotide capable of hybridising under stringent conditions to any of the above polynucleotides, where the polynucleotide does not hybridise under stringent conditions to a nucleic acid molecule having a nucleotide sequence of only A or T residues. Also included are a recombinant vector comprising the above nucleic acid molecule, making a recombinant host cell comprising the above nucleic acid molecule, an isolated polypeptide comprising a sequence that is at least 95% identical to the polypeptide (or its fragment, domain, epitope, secreted form, (allelic) variant or homologue) encoded by the above nucleic acid molecule, an isolated antibody that binds specifically to the above polypeptide, a recombinant host cell produced by the above method and that expresses the above polypeptide, making an isolated polypeptide, preventing, treating or ameliorating a medical condition, diagnosing a pathological condition or a binding partner to the above polypeptide, the gene corresponding to the cDNA sequence given in the specification, and identifying an activity in a biological assay. The nucleic acid molecule and polypeptide are useful in diagnosing, preventing, prognosing or treating diseases or disorders associated with aberrant expression and/or activity of the above polypeptide, such as neural disorders, immune system disorders, muscular disorders, reproductive disorders, gastrointestinal disorders, pulmonary disorders, cardiovascular disorders, renal disorders, proliferative disorders and/or cancers. In particular, these diseases are systemic lupus erythematosis, rheumatoid arthritis, multiple sclerosis,

CC thyroiditis, anaemia, Grave's disease, diabetes, hepatitis, asthma,
 CC allergies, nephritis, Parkinson's disease, Alzheimer's disease,
 CC atherosclerosis, myocardial infarction, AIDS and infections. The methods
 CC may be used for identifying agonists and antagonists of the
 CC polynucleotide and polypeptide. The present sequence is a protein from
 CC one of the 28 disclosed secreted protein genes, it is not clear whether
 CC this is an alternative expressed protein or a fragment of one of the
 CC claimed proteins.

XX Sequence 102 AA;
 SQ

Query Match 72.5%; Score 219; DB 8; Length 102;
 Best Local Similarity 68.6%; Pred. No. 1e-19;
 Matches 35; Conservative 5; Mismatches 11; Indels 0; Gaps 0;

QY 1 CSMPOEAGPCLASIPHHWYNNKTKICSEFIYGGCGNNNNFOTEICLVTC 51
 DB 46 CEMPXETGPCLAYFLHWYDKDNTCSMFYGGCGNNNNFQSKANCLNTC 96

RESULT 20
 AAE27094
 ID AAE27094 standard; protein; 117 AA.
 AC AAE27094;
 XX
 DT 13-DEC-2002 (first entry)
 XX
 DE Human secreted protein #1.
 XX
 KW Human; immunodeficiency; X-linked agammaglobulinaemia; septic shock;
 KW autoimmune disorder; rheumatoid arthritis; multiple sclerosis; cancer;
 KW Grave's disease; diabetes mellitus; haematopoietic disorder; stroke;
 KW respiratory disorder; asthma; allergy; gastrointestinal disorder;
 KW inflammatory bowel disease; neurodegenerative disorder; hepatitis;
 KW Parkinson's disease; Alzheimer's disease; cardiovascular disorder;
 KW atherosclerosis; myocarditis; renal disorder; fungicide; virucide;
 KW hyperproliferative disorder; acute glomerulonephritis; tonsillitis;
 KW respiratory disorder; rhinitis; sinusitis; neurological disease;
 KW endocrine disorder; Addison's disease; reproductive system disorder;
 KW endometriosis; vasotrophic; vulnerary; cytostatic; nootropic; cardiant;
 KW anti-HIV; tranquiliser; gout; antiparasitic.

XX Homo sapiens.
 OS
 XX US2002077287-A1.
 XX
 PD 20-JUN-2002.
 XX
 PF 11-MAY-2001; 2001US-00852659.
 XX
 PR 11-SEP-1998; 98US-00152060.
 XX
 PA (RUBE/) RUBEN S M.
 PA (ROSE/) ROSEN C A.
 PA (LIYV/) LI Y.
 PA (ZENG/) ZENG Z.
 PA (KYAW/) KYAW H.
 PA (FISC/) FISCHER C L.
 PA (LIHH/) LI H.
 PA (SOPP/) SOPPET D R.
 PA (GENT/) GENTZ R L.
 PA (WEIY/) WEI Y.
 PA (MOOR/) MOORE P A.
 PA (YOUN/) YOUNG P E.
 PA (GREE/) GREENE J M.
 PA (FERR/) FERRIE A M.

XX Ruben SM, Rosen CA, Li Y, Zeng Z, Kyaw H, Fischer CL, Li H;
 PI Soppet DR, Gentz RL, Wei Y, Moore PA, Young PE, Greene JM;
 PI Ferrie AM;
 XX
 DR WPI; 2002-598780/64.

XX Novel human secreted polypeptides and polynucleotides for diagnosing,
 PT preventing, treating immune, hyperproliferative, cardiovascular, of
 PT neurological, reproductive disorders and identifying modulators of
 PT therapeutic use.
 XX
 PS Disclosure; Page 16; 209pp; English.
 XX
 AAD44636-AAD44676 represent cDNAs corresponding to 28 human secreted
 CC protein genes, and AAE26959-AAE26999 represent the proteins they encode.
 CC AAE27000-AAE27025 represent human secreted protein fragments or their
 CC variants. The secreted proteins and genes are useful for preventing,
 CC treating or ameliorating medical conditions, e.g., by protein or gene
 CC therapy. Specific uses are described for each of the 28 genes, based on
 CC the tissues in which they are most highly expressed and include
 CC developing products for the diagnosis or treatment of immunodeficiencies,
 CC e.g., X-linked agammaglobulinaemia, B cell immunodeficiencies, severe
 CC combined immunodeficiencies, autoimmune disorders e.g., systemic lupus
 CC erythematosus, rheumatoid arthritis, multiple sclerosis, autoimmune
 CC thyroiditis, autoimmune haemolytic anaemia, Goodpasture's syndrome,
 CC Grave's disease, diabetes mellitus, dermatitis, inflammatory conditions
 CC including septic shock, sepsis, reperfusion injury, inflammatory bowel
 CC disease, Crohn's disease, haematopoietic disorders, respiratory disorders
 CC e.g., asthma and allergy, gastrointestinal disorders e.g., inflammatory
 CC bowel disease), cancers e.g., gastric, ovarian, lung, liver, bladder and
 CC breast), central nervous system (CNS) disorders e.g., ischaemic brain
 CC injury and/or stroke, neurodegenerative disorders e.g., Parkinson's
 CC disease and Alzheimer's disease, AIDS-related dementia and prion disease,
 CC cardiovascular disorders e.g., myocarditis, arrhythmias, atherosclerosis,
 CC inflammatory disorders e.g., hepatitis, gout, trauma, pancreatitis,
 CC sarcoidosis and allogenic transplant rejection, blood-related disorder
 CC (thrombosis, arterial thrombosis, atherosclerosis), hyperproliferative
 CC disorders, respiratory disorders e.g. rhinitis, sinusitis, tonsillitis,
 CC lung cancer, allergic disorders, pneumonitis, renal disorders e.g. acute
 CC glomerulonephritis, neurological diseases, liver disorders, endocrine
 CC disorders e.g., hyperthyroidism, Addison's disease, hyperpituitarism,
 CC infectious diseases and reproductive system disorders e.g. endometriosis.
 CC The present sequence represents a human secreted protein of the invention
 XX
 SQ Sequence 117 AA;
 Query Match 72.5%; Score 219; DB 5; Length 117;
 Best Local Similarity 68.6%; Pred. No. 1.2e-19;
 Matches 35; Conservative 5; Mismatches 11; Indels 0; Gaps 0;

QY 1 CSMPOEAGPCLASIPHHWYNNKTKICSEFIYGGCGNNNNFOTEICLVTC 51
 DB 61 CEMPXETGPCLAYFLHWYDKDNTCSMFYGGCGNNNNFQSKANCLNTC 111

RESULT 21
 AAE27165
 ID AAE27165 standard; protein; 117 AA.
 AC AAE27165;
 XX
 DT 13-DEC-2002 (first entry)
 XX
 DE Human gene 24 encoded secreted protein fragment #1.
 XX
 KW Human; secreted protein; autoimmune disease; hyperproliferative disorder;
 KW rheumatoid arthritis; neoplasm; cerebrovascular disorder; angiodenesis;
 KW cerebral ischaemia; cardiovascular disorder; nervous system disorder;
 KW cardiac arrest; Alzheimer's disease; ocular disorder; wound healing;
 KW infection; corneal infection; skin aging; food additive; preservative;
 KW tissue regeneration; immunosuppressive; antiproliferative; cytostatic;
 KW cardiant; vasotrophic; cerebroprotective; nootropic; neuroprotective;
 KW antibacterial; virucide; fungicide; ophthalmological; gene therapy;
 KW vulnerary.
 XX
 OS Homo sapiens.
 XX
 PN US2002076756-A1.

```
XX PD 20-JUN-2002.
XX PF 11-MAY-2001; 2001US-00853161.
XX PR 02-FEB-2001; 2001US-0265583P.
XX PA (RUBE//) RUBEN S M.
XX PA (ROSE//) ROSEN C A.
XX PA (LIYY//) LI Y.
XX PA (ZENG//) ZENG Z.
XX PA (KYAW//) KYAW H.
XX PA (FISC//) FISCHER C L.
XX PA (LIHH//) LI H.
XX PA (SOPP//) SOPPET D R.
XX PA (GENT//) GENTZ R L.
XX PA (WEIY//) WEI Y.
XX PA (MOOR//) MOORE P A.
XX PA (YOUN//) YOUNG P E.
XX PA (GREE//) GREENE J M.
XX PA (FERR//) FERRIE A M.
XX PI Ruben SM, Rosen CA, Li Y, Zeng Z, Kyaw H, Fischer CL, Li H;
PI Soppet DR, Gentz RL, Wei Y, Moore PA, Young PE, Greene JM;
XX PF Ferrie AM;
XX XX WPI; 2002-574454/61.
XX DR New nucleic acid molecules encoding 28 human secreted proteins, useful
XX PT for diagnosing, preventing, treating or ameliorating medical conditions
XX PT and as food additives or preservatives.
XX PS Disclosure; Page 17; 209pp; English.
XX CC AAD44854-AAD44984 represent cDNAs corresponding to 28 human secreted
XX CC protein genes, and AAE27097-AAE27137 represent the proteins they encode.
XX CC AAE27138-AAE27164 represent human secreted protein fragments. The genes
XX CC and their corresponding secreted proteins are useful for preventing,
XX CC treating or ameliorating medical conditions, e.g., by protein or gene
XX CC therapy. Secreted protein sequences of the invention are useful for the
XX CC diagnosis or treatment of disorders such as autoimmune diseases (e.g.
XX CC rheumatoid arthritis), hyperproliferative disorders (e.g. neoplasms of
XX CC the breast or liver), cerebrovascular disorders (e.g. cerebral ischaemia,
XX CC angiogenesis), cardiovascular disorders (e.g. cardiac arrest), nervous
XX CC system disorders (e.g. Alzheimer's disease), infections caused by fungi,
XX CC bacteria and viruses and ocular disorders (e.g. corneal infection). The
XX CC polypeptides can also be used to aid wound healing and epithelial cell
XX CC proliferation, to prevent skin aging due to sunburn, to maintain organs
XX CC before transplantation, for supporting cell culture of primary tissues,
XX CC to regenerate tissues and in chemotaxis. They can also be used as food
XX CC additives or preservative to increase or decrease storage capabilities,
XX CC fat content, lipid, protein, carbohydrate, vitamins, minerals, cofactors
XX CC and other nutritional components. The present sequence represents a human
XX CC secreted protein fragment referred to in the disclosure of the invention
XX SQ Sequence 117 AA;
XX Query Match 72.5%; Score 219; DB 5; Length 117;
XX Best Local Similarity 68.6%; Pred. NO. 1.2e-19;
XX Matches 35; Conservative 5; Mismatches 11; Indels 0; Gaps 0;
Qy 1 CSMPOEAGPCLASIPHHVYNNKTKICSEFIYGGCGNNNNFQTEAICLVTC 51
Db 61 CEMPKEPTGCLAYFLHWDYDKDNTCSMPVYVYGGCGNNNNFQSKANCLNTC 111
RESULT 22
ABU65038
ID ABU65038 standard; protein; 117 AA.
XX AC ABU65038;
XX DT 15-MAY-2003 (first entry)
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XX DE Human secreted protein gene 24, protein #4.
XX KW Secreted protein; immunodeficiency; multiple sclerosis;
KW severe combined immunodeficiency; autoimmune disorder; cancer;
KW rheumatoid arthritis; diabetes mellitus; haematopoietic disorder;
KW inflammatory condition; septic shock; inflammatory bowel disease;
KW Crohn's disease; respiratory disorder; asthma; allergy; stroke;
KW gastrointestinal disorder; central nervous system disorder;
KW ischaemic brain injury; neurodegenerative disorder; Parkinson's disease;
KW Alzheimer's disease; cardiovascular disorder; atherosclerosis;
KW blood-related disorder; thrombosis; atherosclerosis; renal disorder;
KW hyperproliferative disorder; acute glomerulonephritis; Addison's disease;
KW endocrine disorder; liver disease; reproductive system disorder;
KW endometriosis; infectious disease; pancreatic disorder; vaccine;
KW wound repair; angiogenesis; lymphatic disorder; hair loss; body weight;
XX KW body height; hair colour; human.
XX OS Homo sapiens.
XX PN US2002172994-A1.
XX XX 21-NOV-2002.
XX PF 11-MAY-2001; 2001US-00852797.
XX XX 14-MAR-1997; 97US-0040710P.
PR 14-MAR-1997; 97US-0040762P.
PR 30-MAY-1997; 97US-0048100P.
PR 30-MAY-1997; 97US-0048189P.
PR 30-MAY-1997; 97US-0048357P.
PR 30-MAY-1997; 97US-0050934P.
PR 06-JUN-1997; 97US-0048970P.
PR 05-SEP-1997; 97US-0057765P.
PR 19-DEC-1997; 97US-0068368P.
PR 12-MAR-1998; 98WO-US004858.
PR 11-SEP-1998; 98US-00152060.
PR 02-FEB-2001; 2001US-0265583P.
XX (RUBE//) RUBEN S M.
PA (ROSE//) ROSEN C A.
PA (LIYY//) LI Y.
PA (ZENG//) ZENG Z.
PA (KYAW//) KYAW H.
PA (FISC//) FISCHER C L.
PA (LIHH//) LI H.
PA (SOPP//) SOPPET D R.
PA (GENT//) GENTZ R L.
PA (WEIY//) WEI Y.
PA (MOOR//) MOORE P A.
PA (YOUN//) YOUNG P E.
PA (GREE//) GREENE J M.
PA (FERR//) FERRIE A M.
XX Ruben SM, Rosen CA, Li Y, Zeng Z, Kyaw H, Fischer CL, Li H;
PI Soppet DR, Gentz RL, Wei Y, Moore PA, Young PE, Greene JM;
PI Ferrie AM;
XX WPI; 2003-310989/30.
XX PT New human secreted polypeptides and polynucleotides for diagnosing,
XX PT prognosing, preventing and treating immune, hyperproliferative, liver,
XX PT kidney, reproductive disorders and for identifying modulators of
XX PT therapeutic use.
XX PS Disclosure; Page 16; 209pp; English.
XX CC The invention relates to an isolated polypeptide comprising an amino acid
XX CC sequence at least 95% identical to sequence of 28 human secreted
XX CC proteins, their fragment, polypeptide domain, epitope, secreted form,
XX CC variant, allelic variant, or species homologue, or the encoded sequence
XX CC included in ATCC 97921 and 97922. Also included are the encoding nucleic
XX CC acids, recombinant vectors, host cells, antibodies, and genes. The
```


CC disorders, reproductive disorders, gastrointestinal disorders, pulmonary
 CC disorders, cardiovascular disorders, renal disorders, proliferative
 CC disorders and/or cancers. In particular, these diseases are systemic
 CC lupus erythematosus, rheumatoid arthritis, multiple sclerosis,
 CC thyroiditis, anaemia, Grave's disease, diabetes, hepatitis, asthma,
 CC allergies, nephritis, Parkinson's disease, Alzheimer's disease,
 CC atherosclerosis, myocardial infarction, AIDS and infections. The methods
 CC may be used for identifying agonists and antagonists of the
 CC polynucleotide and polypeptide. The present sequence is a protein from
 CC one of the 28 disclosed secreted protein genes, it is not clear whether
 CC this is an alternative expressed protein or a fragment of one of the
 CC claimed proteins.

XX Sequence 117 AA;

Query Match 72.5%; Score 219; DB 8; Length 117;
 Best Local Similarity 68.6%; Pred. No. 1.2e-19;
 Matches 35; Conservative 5; Mismatches 11; Indels 0; Gaps 0;

Oy 1 CSMPOEAGPCLASIPHHWYKTKICSEFIYGGCGNNNFQTEAICLVTC 51
 Db 61 CEMPKEGTGCLAYFLHWWYDKKNTCSMFVYGGCGNNNFQSKANCLNTC 111

RESULT 24
 AAU75219
 ID AAU75219 standard; protein; 133 AA.

XX AC AAU75219;

XX DT 29-JAN-1999 (first entry)

XX DE Human secreted protein encoded by gene 24 clone HTEBY11.

XX Human; secreted protein; fusion protein; gene therapy; protein therapy;
 KW diagnosis; tissue; cancer; tumour; neurodegenerative disorder; leukaemia;
 KW developmental abnormality; foetal deficiency; blood; allergy; renal;
 KW immune system; asthma; lymphocytic disease; brain; hepatic; lymphoma;
 KW inflammation; ischaemic shock; Alzheimer's disease; restenosis; AIDS;
 KW cognitive disorder; schizophrenia; prostate; obesity; osteoclast; thymus;
 KW osteoporosis; arthritis; testis; lung; thyroiditis; thyroid; digestion;
 KW endocrine; metabolism; regulation; malabsorption; gastritis; neoplasm.

XX OS Homo sapiens.

XX PN WO9804083-A2.

XX PD 17-SEP-1998.

XX PF 12-MAR-1998; 98WO-US004858.

XX PR 14-MAR-1997; 97US-0040710P.

XX PR 14-MAR-1997; 97US-0040762P.

XX PR 30-MAY-1997; 97US-0048100P.

XX PR 30-MAY-1997; 97US-0048189P.

XX PR 30-MAY-1997; 97US-0048357P.

XX PR 30-MAY-1997; 97US-0050934P.

XX PR 06-JUN-1997; 97US-0048970P.

XX PR 05-SEP-1997; 97US-0057765P.

XX PR 19-DEC-1997; 97US-0068369P.

XX PA (HUMA-) HUMAN GENOME SCI INC.

XX PI Ruben SM, Rosen CA, Li Y, Zeng Z, Kyaw H, Fischer CL, Li H;

PI Soppet DR, Gentz RL, Wei YF, Moore PA, Young PE, Greene JM;

PI Ferrie AM;

XX DR WPI; 1998-520811/44.

XX DR N-PSDB; AAV34309.

XX Isolated human polynucleotide(s) encoding secretory peptide(s) - used to
 FT develop products for the diagnosis and treatment of e.g. inflammation,
 FT cancers, CNS disorders or immune system disorders.

XX Claim 1; Page 167-168; 20ipp; English.

XX This sequence represents a secreted human protein encoded by the gene
 CC clone detailed in the descriptor line. The gene can be used to generate
 CC fusion proteins by linking to the gene to a human immunoglobulin Fc
 CC portion (e.g. AAV34277) for increasing the stability of the fused protein
 CC as compared to the human protein only. The invention relates to 28 novel
 CC genes and their fragments (nucleic acid sequences: AAV34286-V34325; amino
 CC acid sequences AAV5196-W5235) which are useful for preventing, treating
 CC or ameliorating medical conditions e.g. by protein or gene therapy. Also,
 CC pathological conditions can be diagnosed by determining the amount of the
 CC new polypeptides in a sample or by determining the presence of mutations
 CC in the new polynucleotides. Specific uses are described for each of the
 CC 28 polynucleotides, based on which tissues they are most highly expressed
 CC in (see AAV34286 for described uses)

XX SQ Sequence 133 AA;

Query Match 72.5%; Score 219; DB 2; Length 133;
 Best Local Similarity 68.6%; Pred. No. 1.3e-19;
 Matches 35; Conservative 5; Mismatches 11; Indels 0; Gaps 0;

Oy 1 CSMPOEAGPCLASIPHHWYKTKICSEFIYGGCGNNNFQTEAICLVTC 51
 Db 77 CEMPKEGTGCLAYFLHWWYDKKNTCSMFVYGGCGNNNFQSKANCLNTC 127

RESULT 25

AAE26982

ID AAE26982 standard; protein; 133 AA.

XX AC AAE26982;

XX DT 13-DEC-2002 (first entry)

XX DE Human gene 24 encoded secreted protein HTEBY11, SEQ ID NO:34.

XX Human; immunodeficiency; X-linked agammaglobulinemia; septic shock;
 KW autoimmune disorder; rheumatoid arthritis; multiple sclerosis; cancer;
 KW Grave's disease; diabetes mellitus; haematopoietic disorder; stroke;
 KW respiratory disorder; asthma; allergy; gastrointestinal disorder;
 KW inflammatory bowel disease; neurodegenerative disorder; hepatitis;
 KW Parkinson's disease; Alzheimer's disease; cardiovascular disorder;
 KW atherosclerosis; myocarditis; renal disorder; fungicide; virucide;
 KW hyperproliferative disorder; acute glomerulonephritis; tonsillitis;
 KW respiratory disorder; rhinitis; sinusitis; neurological disease;
 KW endocrine disorder; Addison's disease; reproductive system disorder;
 KW endometriosis; vasotropic; vulnery; cytostatic; nootropic; cardiant;
 KW anti-HIV; tranquilliser; gout; antiparasitic.

XX OS Homo sapiens.

XX PF Key Location/Qualifiers

XX Peptide 1..21

XX Protein /label= signal_peptide

XX 22..133

XX /note= "Human mature secreted protein"

XX US2002077287-A1.

XX 20-JUN-2002.

XX 11-MAY-2001; 2001US-00852659.

XX 11-SEP-1998; 98US-00152060.

XX (RUBE/) RUBEN S M.

XX (ROSE/) ROSEN C A.

XX (LIY/) LI Y.

XX (ZENG/) ZENG Z.

XX (KYAW/) KYAW H.

XX (FISC/) FISCHER C L.

PA (LIHH//) LI H.
 PA (SOPP//) Soppet D R.
 PA (GENTZ//) GENTZ R L.
 PA (WEIY//) WEI Y.
 PA (MOOR//) MOORE P A.
 PA (YOUN//) YOUNG P E.
 PA (GREE//) GREENE J M.
 PA (FERR//) FERRIE A M.
 XX
 PI Ruben SM, Rosen CA, Li Y, Zeng Z, Kyaw H, Fischer CL, Li H;
 PI Soppet DR, Gentz RL, Wei Y, Moore PA, Young PE, Greene JM;
 PI Ferrie AM;
 XX
 DR WPI: 2002-598780/64.
 DR N-PSDB; AAD44659.
 XX
 PT Novel human secreted polypeptides and polynucleotides for diagnosing,
 PT preventing, treating immune, hyperproliferative, cardiovascular, of
 PT neurological, reproductive disorders and identifying modulators of
 PT therapeutic use.
 PT
 XX
 PS Claim 11; Page 185-186; 209pp; English.
 XX
 CC AAD44636-AAD44676 represent cDNAs corresponding to 28 human secreted
 CC protein genes, and AAE26959-AAE26999 represent the proteins they encode.
 CC AAE27000-AAE27025 represent human secreted protein fragments or their
 CC variants. The secreted proteins and genes are useful for preventing,
 CC treating or ameliorating medical conditions, e.g. by protein or gene
 CC therapy. Specific uses are described for each of the 28 genes, based on
 CC the tissues in which they are most highly expressed and include
 CC developing products for the diagnosis or treatment of immunodeficiencies,
 CC e.g., X-linked agammaglobulinemia, B cell immunodeficiencies, severe
 CC combined immunodeficiencies, autoimmune disorders e.g., systemic lupus
 CC erythematosus, rheumatoid arthritis, multiple sclerosis, autoimmune
 CC thyroiditis, autoimmune haemolytic anaemia, Goodpasture's syndrome,
 CC Grave's disease, diabetes mellitus, dermatitis, inflammatory conditions
 CC including septic shock, sepsis, reperfusion injury, inflammatory bowel
 CC disease, Crohn's disease, haematopoietic disorders, respiratory disorders
 CC e.g., asthma and allergy, gastrointestinal disorders e.g., inflammatory
 CC bowel disease), cancers e.g., gastric, ovarian, lung, liver, bladder and
 CC breast), central nervous system (CNS) disorders e.g., ischaemic brain
 CC injury and/or stroke, neurodegenerative disorders e.g., Parkinson's
 CC disease and Alzheimer's disease, AIDS-related dementia and prion disease,
 CC cardiovascular disorders e.g., myocarditis, arrhythmias, atherosclerosis,
 CC inflammatory disorders e.g., hepatitis, gout, trauma, pancreatitis,
 CC sarcoidosis and allogeneic transplant rejection, blood-related disorder
 CC (thrombosis, arterial thrombosis, atherosclerosis), hyperproliferative
 CC disorders, respiratory disorders e.g. rhinitis, sinusitis, tonsillitis,
 CC lung cancer, allergic disorders, pneumonitis, renal disorders. e.g. acute
 CC glomerulonephritis, neurological diseases, liver disorders, endocrine
 CC disorders e.g., hyperthyroidism, Addison's disease, hyperpituitarism,
 CC infectious diseases and reproductive system disorders e.g. endometriosis.
 CC The present sequence represents a human secreted protein of the invention
 XX
 SQ Sequence 133 AA;
 Query Match 72.5%; Score 219; DB 5; Length 133;
 Best Local Similarity 68.6%; Pred. No. 1.3e-19;
 Matches 35; Conservative 5; Mismatches 11; Indels 0; Gaps 0;
 QY 1 CGMPQAGPCLASIPHWYNNKTKICSEFIYGCQGNNNNFQTEAICLVTC 51
 DB 77 CEMPKEGTCLAVFLHWYDKDNTCSMFYGCQGNNNNFQSKANCLNTC 127
 RESULT 26
 AAE27120
 ID AAE27120 standard; protein; 133 AA.
 XX
 AC AAE27120;
 XX
 DT 13-DEC-2002 (first entry)
 XX

Human gene 24 encoded secreted protein HTEBY11, SEQ ID NO:75.

Human; secreted protein; autoimmune disease; hyperproliferative disorder;
 rheumatoid arthritis; neoplasm; cerebrovascular disorder; angiogenesis;
 cerebral ischaemia; cardiovascular disorder; nervous system disorder;
 cardiac arrest; Alzheimer's disease; ocular disorder; wound healing;
 infection; corneal infection; skin aging; food additive; preservative;
 tissue regeneration; immunosuppressive; antiproliferative; cytostatic;
 cardiant; vasotropic; cerebroprotective; nootropic; neuroprotective;
 antibacterial; virucide; fungicide; ophthalmological; gene therapy;
 vulnery.

Homo sapiens.

Key Location/Qualifiers
 Peptide 1..21
 Protein 22..133
 /label= Signal_peptide
 /note= "Mature human secreted protein"

US2002076756-A1.

20-JUN-2002.

11-MAY-2001; 2001US-00853161.

02-FEB-2001; 2001US-0265583P.

(RUBE//) RUBEN S M.
 (ROSE//) ROSEN C A.
 (LIYY//) LI Y.
 (ZENG//) ZENG Z.
 (KYAW//) KYAW H.
 (FISC//) FISCHER C L.
 (LIHH//) LI H.
 (SOPP//) Soppet D R.
 (GENT//) GENTZ R L.
 (WEIY//) WEI Y.
 (MOOR//) MOORE P A.
 (YOUN//) YOUNG P E.
 (GREE//) GREENE J M.
 (FERR//) FERRIE A M.

Ruben SM, Rosen CA, Li Y, Zeng Z, Kyaw H, Fischer CL, Li H;
 Soppet DR, Gentz RL, Wei Y, Moore PA, Young PE, Greene JM;
 Ferrie AM;

WPI: 2002-574454/61.
 N-PSDB; AAD44877.

New nucleic acid molecules encoding 28 human secreted proteins, useful
 for diagnosing, preventing, treating or ameliorating medical conditions
 and as food additives or preservatives.

Claim 11; Page 185-186; 209pp; English.

AAD44854-AAD44984 represent cDNAs corresponding to 28 human secreted
 protein genes, and AAE27097-AAE27137 represent the proteins they encode.
 AAE27138-AAE27164 represent human secreted protein fragments. The genes
 and their corresponding secreted proteins are useful for preventing,
 treating or ameliorating medical conditions, e.g., by protein or gene
 therapy. Secreted protein sequences of the invention are useful for the
 diagnosis or treatment of disorders such as autoimmune diseases (e.g.
 rheumatoid arthritis), hyperproliferative disorders (e.g. neoplasms of
 the breast or liver), cerebrovascular disorders (e.g. cerebral ischaemia,
 angiodysplasia), cardiovascular disorders (e.g. cardiac arrest), nervous
 system disorders (e.g. Alzheimer's disease), infections caused by fungi,
 bacteria and viruses and ocular disorders (e.g. corneal infection). The
 polypeptides can also be used to aid wound healing and epithelial cell
 proliferation, to prevent skin aging due to sunburn, to maintain organs
 before transplantation, for supporting cell culture of primary tissues,
 to regenerate tissues and in chemotaxis. They can also be used as food
 additives or preservative to increase or decrease storage capabilities,

CC The invention relates to an isolated nucleic acid molecule encoding a
CC secreted protein that is at least 95% identical to a polynucleotide
CC fragment of any of the nucleotide sequences listed in table 1A of the
CC specification, which is hybridizable to the nucleotide sequences, a
CC polynucleotide encoding a polypeptide (or a polypeptide fragment, domain
CC or epitope of any of the amino acid sequences) listed in table 1A of the
CC specification, a polynucleotide which is an (allelic) variant of the
CC nucleotide sequences listed in the specification, a polynucleotide which
CC encodes a species homologue of the above amino acid sequences, a
CC polynucleotide capable of hybridizing under stringent conditions to any
CC of the above polynucleotides, where the polynucleotide does not hybridize
CC under stringent conditions to a nucleic acid molecule having a nucleotide
CC sequence of only A or T residues. Also included are a recombinant vector
CC comprising the above nucleic acid molecule, making a recombinant host
CC cell comprising the above nucleic acid molecule, an isolated polypeptide
CC comprising a sequence that is at least 95% identical to the polypeptide
CC (or its fragment, domain, epitope, secreted form, (allelic) variant or
CC homologue) encoded by the above nucleic acid molecule, an isolated
CC antibody that binds specifically to the above polypeptide, a recombinant
CC host cell produced by the above method and that expresses the above
CC polypeptide, making an isolated polypeptide, preventing, treating or
CC ameliorating a medical condition, diagnosing a pathological condition or
CC a susceptibility to a pathological condition in a subject, identifying a
CC binding partner to the above polypeptide, the gene corresponding to the
CC cDNA sequence given in the specification, and identifying an activity in
CC a biological assay. The nucleic acid molecule and polypeptide are useful
CC in diagnosing, preventing, prognosing or treating diseases or disorders
CC associated with aberrant expression and/or activity of the above
CC polypeptide, such as neural disorders, immune system disorders, muscular
CC disorders, reproductive disorders, gastrointestinal disorders, pulmonary
CC disorders, cardiovascular disorders, renal disorders, proliferative
CC disorders and/or cancers. In particular, these diseases are systemic
CC lupus erythematosus, rheumatoid arthritis, multiple sclerosis,
CC thyroditis, anaemia, Grave's disease, diabetes, hepatitis, asthma,
CC allergies, nephritis, Parkinson's disease, Alzheimer's disease,
CC atherosclerosis, myocardial infarction, AIDS and infections. The methods
CC may be used for identifying agonists and antagonists of the
CC polynucleotide and polypeptide. The present sequence is a protein from
CC one of the 28 disclosed secreted protein genes.

XX SQ Sequence 133 AA;

Query Match 72.5%; Score 219; DB 8; Length 133;
Best Local Similarity 68.6%; Pred. No. 1.3e-19;
Matches 35; Conservative 5; Mismatches 11; Indels 0; Gaps 0;

Qy 1 CSMFQEAGPCLASIPHHWYKTKICSEFIYGGCGGNNNNFQTEAICLVTC 51
|||:||||| ||||:| |||:||||| ||||:| |||:||||| ||||:| |||:
Db 77 CEMPKEGTGCLAYFLHWWYDKDNTCSMFYVGGCGGNNNNFQSKANCLNTC 127

RESULT 30
AAAY70010
ID AAY70010 standard; protein; 164 AA.

XX AC AAY70010;

XX DT 05-JUN-2000 (first entry)

XX DE Human Protease and associated protein-4 (PPRG-4).

XX KW Protease and associated protein-4; PPRG-4; anti-PPRG antibody; diagnosis;
KW treatment; cell proliferative disorder; cancer; cirrhosis;
KW arteriosclerosis; atherosclerosis; bursitis; hepatitis; immune disorder;
KW AIDS; Addison's disease; adult respiratory distress syndrome; allergy;
KW ankylosing spondylitis; amyloidosis; cytostatic; antiarteriosclerotic;
KW hepatocarcinoma; antinflammatory; virucide; antipsoriatic; anti-HIV;
KW antiallergic; immunosuppressive; antidiabetic; antianaemic;
KW neuroprotective; human.

XX OS Homo sapiens.

XX FH Key Location/Qualifiers

FT Modified-site 157 /note= "Potential Phosphorylation site"

XX FT WO200009709-A2.

XX PN 24-FEB-2000.

XX PF 06-AUG-1999; 99WO-US017818.

XX PR 10-AUG-1998; 98US-0096114P.

XX PR 11-FEB-1999; 99US-0119768P.

XX PA (INCY-) INCYTE PHARM INC.

XX PI Bandman O, Hillman JL, Baughn MR, Azimzai Y, Guegler KJ;

XX PI Corley NC, Yue H, Tang YT, Reddy R, Patterson C, Au-Young J;

XX PI Shih LL, Lu DM;

XX DR WPI; 2000-224346/19.

XX DR N-PSDB; AAZ50921.

XX PT New human proteases, useful for diagnosis, treatment and prevention of

XX PS cell proliferative disorders such as atherosclerosis.

XX PS Claim 1; Page 77; 114pp; English.

XX CC The present sequence is that of human protease and associated protein-4

XX CC (PPRG-4), which is expressed in reproductive tissues. It is encoded by

XX CC cDNA identified in Incyte clone 2012492 derived from TESTNOT03 CDNA

XX CC library. It has been identified as a protease as it includes a Kunitz

XX CC family signature sequence. Anti-PPRG antibodies can be used as

XX CC therapeutic antagonists, reagents for diagnosis and monitoring diseases

XX CC and for isolating PPRG. PPRG nucleotide sequence can be used as probe or

XX CC primer for diagnosis and monitoring of PPRG-related diseases and gene

XX CC mapping. PPRG can be used in the treatment of cell proliferative

XX CC disorders like cancer, arteriosclerosis, atherosclerosis, bursitis,

XX CC cirrhosis and hepatitis, and immune disorders like AIDS, Addison's

XX CC disease, adult respiratory distress syndrome, allergies, ankylosing

XX CC spondylitis and amyloidosis

XX SQ Sequence 164 AA;

Query Match 72.5%; Score 219; DB 3; Length 164;

Best Local Similarity 68.6%; Pred. No. 1.7e-19;

Matches 35; Conservative 5; Mismatches 11; Indels 0; Gaps 0;

Qy 1 CSMFQEAGPCLASIPHHWYKTKICSEFIYGGCGGNNNNFQTEAICLVTC 51

|||:||||| ||||:| |||:||||| ||||:| |||:||||| ||||:| |||:

Db 108 CEMPKEGTGCLAYFLHWWYDKDNTCSMFYVGGCGGNNNNFQSKANCLNTC 158

RESULT 31

ABM85103

ID ABM85103 standard; protein; 179 AA.

XX AC ABM85103;

XX DT 18-NOV-2004 (first entry)

XX DE Human diagnostic and therapeutic pprotein SEQ ID NO:5352.

XX KW gene therapy; human diagnostic and therapeutic polynucleotide; ditbp.
XX OS Homo sapiens.
XX PN WO2004023973-A2.
XX PD 25-MAR-2004.
XX PF 12-SEP-2003; 2003WO-US028227.
XX PR 12-SEP-2002; 2002US-0410259P.
XX PR 12-SEP-2002; 2002US-0410260P.

XX (INCY-) INCYTE CORP.
XX Schmidt JP, Wright RJ, Bruns CM, Marjanovic MM, Shen F;
PI Harthorne TA, Suchorski MT, Altus CM, Pitts SJ, Elder LV;
PI Mooney EM, Deleane AM, Panesar IS, Banville SC, Reddy TP;
PI Stevens KA, Blanchard JL, Panzer SR, Wang X, Au AP, Gerstin EH;
PI Peralta CH, Anderson SB, Rioux P, Stuve EJ, Wu MC, Stuve LL;
PI Lagace RE, Spiro PA, Stewart EA, Wingrove J, Vitt UA, Kirton ES;
PI Xu Y, Kwong M, Policky JL, Hurwitz BL, Ma Y, Jackson JL, Gietzen D;
PI Patury S, Shi X, Suarez C;
XX WPI; 2004-329368/30.
DR N-PSDB; ACN43755.
XX New diagnostic and therapeutic polynucleotides and polypeptides, useful
PT in diagnosing a condition, disease or disorder associated with human
PT molecules, e.g. autoimmune or inflammatory disorders, in gene therapy or
PT in gene mapping.
XX Claim 27; Page; 190pp; English.
XX The invention relates to novel diagnostic and therapeutic polynucleotides
XX selected from one of the 2722 sequences defined in the specification. A
CC polynucleotide of the invention may have a use in gene therapy. The human
CC diagnostic and therapeutic polynucleotides (dithp) or polypeptides may be
CC used to diagnose a particular condition, disease or disorder associated
CC with human molecules, e.g. cell proliferative disorders,
CC autoimmune/inflammatory disorder, developmental disorder, endocrine
CC disorder, neurological disorders, gastrointestinal disorders, or
CC infections caused by virus, bacteria, fungi or parasite. The dithp
CC molecules may also be used in genetic mapping, in identifying individuals
CC from minute biological samples in detecting single nucleotide
CC polymorphisms, as molecular weight markers, and for somatic or germline
CC gene therapy. The present sequence represents a dithp protein of the
CC invention. Note: The sequence data for this patent is not represented in
CC the printed specification, but was obtained in electronic format directly
CC from WIPO at www.wipo.int/pct/en/sequences/listing.htm
XX Sequence 179 AA;
SQ
Query Match 72.5%; Score 219; DB 8; Length 179;
Best Local Similarity 68.6%; Pred. NO. 1.8e-19;
Matches 35; Conservative 5; Mismatches 11; Indels 0; Gaps 0;
QY 1 CSMQAGAGPCLASIPHWYNNKTKICSEFIYGGCGQNNNNFQTEAICLVTC 51
DB 77 CEMPKETGCPCLAYFLHWYDKDNTCSMFYGGCGQNNNNFQSKANCLNTC 127
RESULT 32
ADA19813
ID ADA19813 standard; protein; 134 AA.
XX ADA19813;
XX 20-NOV-2003 (first entry)
DE Mouse EPPIN protein SEQ ID NO:14.
XX D11; Kunitz-type protease inhibitor domain; antiinflammatory;
KW anti-allergic; thrombolytic; anticoagulant; cardiant; vasotropic;
KW antibacterial; immunosuppressive; antirheumatic; antiarthritic;
KW nephrotropic; antipsoriatic; vulnary; protease inhibitor; gene therapy;
KW acute pancreatitis; pulmonary injury; allergy-induced protease release;
KW deep vein thrombosis; myocardial infarction; shock; septic shock;
KW hyperfibrinolytic haemorrhage; inflammatory disorder; emphysema;
KW idiopathic pulmonary fibrosis; rheumatoid arthritis; glomerulonephritis;
KW chronic inflammatory bowel disease; psoriasis; EPPIN.
XX Mus musculus.
XX W02003070770-A2.
PN

XX 28-AUG-2003.
XX 18-FEB-2003; 2003WO-EP001629.
XX 21-FEB-2002; 2002US-0358683P.
XX (GENE-) GENEPROT INC.
XX Bougueleret L, Bairoch A, Niknejad A;
XX WPI; 2003-663849/62.
XX New engineered human Kunitz-type protease inhibitor for diagnosing,
PT preventing or treating conditions associated with excessive proteinase
PT activity, e.g. inflammation, pulmonary injuries, myocardial infarction or
PT hemorrhage.
XX Disclosure; Fig 1; 87pp; English.
XX The present invention describes an isolated, purified or recombinant D11
CC polypeptide comprising a Kunitz-type protease inhibitor domain or its
CC biologically active portion. The polypeptide comprises at least 98 %
CC identity to residues 77-127 of a 131 amino acid sequence (S1, see
CC ADA19800), or to residues 52-102 of a 106 amino acid sequence (S2, see
CC ADA19801). D11 has antinflammatory, antibacterial, thrombolytic,
CC anticoagulant, cardiant, vasotropic, antirheumatic, antipsoriatic and vulnary
CC activities, and can be used as a protease inhibitor and in gene therapy.
CC Composition and methods from the present invention can be used in
CC diagnosing, preventing or treating conditions associated with excessive
CC proteinase activity, such as acute pancreatitis, pulmonary injury,
CC allergy-induced protease release, deep vein thrombosis, myocardial
CC infarction, shock (including septic shock), hyperfibrinolytic
CC haemorrhage, and especially, inflammatory disorders (e.g. emphysema,
CC idiopathic pulmonary fibrosis, rheumatoid arthritis, glomerulonephritis,
CC chronic inflammatory bowel disease or psoriasis). The D11 proteins may
CC be used in preserving platelet function, organ preservation or in wound
CC healing. The polynucleotide sequence encoding D11 may be used as
CC hybridisation probes, in chromosome and gene mapping, in the generation
CC of antisense RNA and DNA, and as targets for pharmaceutical intervention.
CC The present sequence represents a mouse EPPIN protein given in comparison
CC with D11 proteins in the exemplification of the present invention.
XX Sequence 134 AA;
SQ
Query Match 62.3%; Score 188; DB 7; Length 134;
Best Local Similarity 54.9%; Pred. NO. 1.1e-15;
Matches 28; Conservative 10; Mismatches 13; Indels 0; Gaps 0;
QY 1 CSMQAGAGPCLASIPHWYNNKTKICSEFIYGGCGQNNNNFQTEAICLVTC 51
DB 77 CSLPKDSGYCMAYFRWWFKENSTCQVFIYGGCGQNNNNFQSQICQAC 127
RESULT 33
AAE13096
ID AAE13096 standard; peptide; 43 AA.
XX AAE13096;
XX 28-JAN-2002 (first entry)
XX Human serine proteinase inhibitor BTL.009 peptide fragment #2.
XX Human, BTL.009 protein; serine proteinase inhibitor; cytostatic;
KW nephrotropic; idiopathic pulmonary fibrosis; cystic fibrosis; emphysema;
KW rheumatoid arthritis; adult respiratory distress syndrome; angioplasty;
KW blood coagulation; glomerulonephritis; prophylactic; platelet activation;
KW neutrophil; monocyte; granulocyte; organ failure; inflammatory disease;
KW elastase inhibitor; chymotrypsin inhibitor; lung injury; vascular injury;
KW therapeutic.
XX

KW metabolic disorder; metabolic syndrome; anorexia nervosa; osteoporosis;
KW myotonia; neuroprotective; obesity; immunomodulator; diabetes.
OS Mus sp.
XX
XX
FH Key Location/Qualifiers
FT Domain 105..170
FT /note= "Follistatin domain"
XX
XX US2003162714-A1.
XX
XX 28-AUG-2003.
XX
XX 21-FEB-2003; 2003US-00369736.
XX
XX 21-FEB-2002; 2002US-0357845P.
PR 20-DEC-2002; 2002US-0434644P.
XX
XX (AMHP) WYETH.
XX
XX Hill JJ, Wolfman NM;
XX
XX WPI; 2003-756055/71.
DR N-PSDB; AAD59923.
XX
XX Composition containing growth and differentiation factor-associated serum
PT protein-1, useful for treating e.g. muscular dystrophy or diabetes, also
PT for diagnosis.
XX
XX Disclosure; Fig 6C; Opp; English.
XX
XX The present invention relates to the use of a protein GDF (growth and
CC differentiation factor)-associated serum protein (GASP) 1 comprising
CC at least one follistatin domain to modulate the level or activity of
CC growth and differentiation factor (GDF) -8. Administration of GASP 1 is
CC used to modulate GDF-8 for treatment of muscular disorders such as
CC muscular dystrophy (benign X-linked, limb-girdle, facioscapulohumeral,
CC myotonic, distal, oculopharyngeal, Duchenne or Fukuyama-type congenital),
CC progressive dystrophic ophthalmoplegia, amyotrophic lateral sclerosis,
CC congestive obstructive pulmonary disease, congenital myopathy (myotonia),
CC familial periodic paralysis, paroxysmal myoglobinuria, myasthenia gravis,
CC Eaton-Lambert syndrome, secondary myasthenia, organ atrophy, frailty,
CC carpal tunnel syndrome, paroxysmal muscle atrophy, sarcopaenia, cachexia
CC and other muscle wasting syndromes such as traumatic or chronic injury to
CC muscle, metabolic disorders such as diabetes types 1 or 2, impaired
CC glucose tolerance, hyperglycaemia, metabolic syndrome, insulin resistance
CC induced by trauma and obesity, adipose tissue disorder such as obesity,
CC and bone degenerative conditions such as osteoporosis, osteopaenia,
CC osteoarthritis, low bone mass due to chronic glucocorticoid therapy,
CC premature gonadal failure, vitamin D deficiency, androgen suppression,
CC secondary hyperparathyroidism, nutritional deficiencies and anorexia
CC nervosa. The present sequence is mouse GDF (growth and differentiation
CC factor)-associated serum protein (GASP)
XX
XX Sequence 571 AA;
SQ
Query Match 56.0%; Score 169; DB 7; Length 571;
Best Local Similarity 49.0%; Pred. No. 1.4e-12;
Matches 25; Conservative 9; Mismatches 17; Indels 0; Gaps 0;
QY 1 CSMQBAQPCLASIPHHWYNNKTKICSEFIYGGCGGNNNNFOTEAICLVTC 51
DB 381 CSLPALQGPCKAYVPRWAYNSQTGLCQSFYVGGCGGNNFESREACBESC 431

RESULT 36
ADD93670
ID ADD93670 standard; protein; 571 AA.
XX
XX ADD93670;
AC
XX
XX 29-JAN-2004 (first entry)
DT
XX

DE Mouse GDF-associated serum protein 1 (GASPl).
XX
XX Mouse; GDF-associated serum protein 1; GASPl; antidiabetic; anorectic;
KW osteopathic; gene therapy.
XX
XX Mus sp.
XX
XX Key Location/Qualifiers
FH Peptide 1..29
FT /note= "Signal peptide"
FT Protein 30..571
FT /note= "Mature protein"
FT Domain 105..170
FT /note = Follistatin domain
FT Modified-site 313
FT /note= "potential N-glycosylation site"
FT Modified-site 514
FT /note= "potential N-glycosylation site"
XX
XX WO2003072714-A2.
XX
XX 04-SEP-2003.
XX
XX 21-FEB-2003; 2003WO-US005150.
XX
XX 21-FEB-2002; 2002US-0357846P.
PR 20-DEC-2002; 2002US-0434645P.
XX
XX (AMHP) WYETH.
XX
XX Hill JJ, Wolfman NM;
XX
XX WPI; 2003-812402/76.
DR N-PSDB; ADD93719, ADD93720.
XX
XX New compositions comprising a protein containing at least one follistatin
PT domain, useful for treating muscular dystrophy (e.g. sarcopaenia, and
PT cachexia), metabolic disease (e.g. diabetes or obesity), or bone
PT degenerative diseases.
XX
XX Example 9; Fig 6C; 113pp; English.
XX
XX The present sequence is the protein sequence for mouse GDF-associated
CC serum protein 1 (GASPl), a protein which includes a follistatin domain
CC and which binds to growth and differentiation factor-8 (GDF-8 or
CC myostatin). The invention provides methods for modulating the effects of
CC GDF-8 on cells. These methods involve administering a protein comprising
CC at least one follistatin domain, or a nucleic acid encoding such a
CC protein. The methods are used to treat disorders relating to the level or
CC activity of GDF-8. These include a muscular disorder such as muscular
CC dystrophy (e.g. severe or benign X-linked muscular dystrophy, limb-girdle
CC dystrophy, facioscapulohumeral dystrophy, myotonic dystrophy, distal
CC muscular dystrophy, progressive dystrophic ophthalmoplegia,
CC oculopharyngeal dystrophy, Fukuyama-type congenital muscular dystrophy,
CC congenital myopathy, myotonia congenita, familial periodic paralysis,
CC paroxysmal myoglobinuria, myasthenia gravis, Eaton-Lambert syndrome,
CC secondary myasthenia, denervation atrophy, paroxysmal muscle atrophy,
CC muscle wasting syndrome, sarcopaenia, and cachexia), traumatic or chronic
CC injury to muscle tissue, metabolic disease or disorder (e.g. type 2
CC diabetes, non-insulin-dependent diabetes mellitus, hyperglycaemia, or
CC obesity), adipose tissue disorder (e.g. obesity), and bone degenerative
CC disease (e.g. osteoporosis) (all claimed).
XX
XX Sequence 571 AA;
SQ
Query Match 56.0%; Score 169; DB 7; Length 571;
Best Local Similarity 49.0%; Pred. No. 1.4e-12;
Matches 25; Conservative 9; Mismatches 17; Indels 0; Gaps 0;
QY 1 CSMQBAQPCLASIPHHWYNNKTKICSEFIYGGCGGNNNNFOTEAICLVTC 51
DB 381 CSLPALQGPCKAYVPRWAYNSQTGLCQSFYVGGCGGNNFESREACBESC 431

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RESULT 37
AAR99146
ID AAR99146 standard; protein; 58 AA.
XX
XX AAR99146;
AC
XX
XX 12-FEB-1997 (first entry)
DT
XX
XX Aprotinin-like Kunitz domain.
DE
XX
XX Aprotinin; Kunitz domain; human neutrophil elastase; hNE;
KW connective tissue; alpha 1 protease inhibitor; API; neutrophil;
KW algal antitrypsin; respiratory disorder; cystic fibrosis;
KW smokers emphysema.
XX
XX Synthetic.
OS
XX
XX WO9620278-A2.
PN
XX
XX 04-JUL-1996.
PD
XX
XX 15-DEC-1995; 95WO-US016349.
PF
XX
XX 16-DEC-1994; 94US-00358160.
PR
XX
XX (PROT-) PROTEIN ENG CORP.
PA
XX
XX Ley AC, Ladner RC, Guterman SK, Roberts BL, Markland W, Kent RB;
PI
XX
XX WPI; 1996-321851/32.
DR
XX
XX New engineered inhibitors of human neutrophil elastase - contg. aprotinin
PT -like Kunitz domain for treating, e.g. cystic fibrosis or other
PT respiratory disorders.
XX
XX Example 23; Page 47; 105pp; English.
PS
XX
XX Genetically engineered human derived Kunitz domains can be used to
CC inhibit human neutrophil elastase, an enzyme involved in the elimination
CC of pathogens and the restructuring of connective tissue. In cases of
CC reduction of the circulating alpha-1-protease inhibitor (API or alpha
CC antitrypsin), or the inactivation of API by oxidation (smokers
CC emphysema), extensive destruction of the lung tissue may result from
CC uncontrolled elastolytic activity of human neutrophil elastase. Other
CC respiratory disorders such as cystic fibrosis are thought to be caused by
CC human neutrophil elastase release by neutrophils. The genetically
CC engineered human derived Kunitz domains can be used to treat such
CC respiratory disorders. See AAR99146-R99211
XX
XX Sequence 58 AA;
SQ
Query Match 55.3%; Score 167; DB 2; Length 58;
Best Local Similarity 56.9%; Pred. No. 2.1e-13;
Matches 29; Conservative 5; Mismatches 17; Indels 0; Gaps 0;
Qy 1 CSMPOEAGPCLASIPHHWYKTKICSEFIYGGCGNNNFQTEAICLVTC 51
| : | | | | | | | | | | : | | | | | | | | | | |
Db 5 CLLPAETGPCRAMIPRFYNAKSGKCEPFYIYGGCGNNNFQTEECRRTC 55
RESULT 38
AAE13092
ID AAE13092 standard; peptide; 54 AA.
XX
XX AAE13092;
AC
XX
XX 28-JAN-2002 (first entry)
DT
XX
XX Trypsin inhibitor peptide.
DE
XX
XX BTL.009 protein; serine proteinase inhibitor; cytostatic; therapeutic;
KW nephrotropic; idiopathic pulmonary fibrosis; cystic fibrosis; emphysema;
KW
```

```
KW rheumatoid arthritis; adult respiratory distress syndrome; angioplasty;
KW blood coagulation; glomerulonephritis; prophylactic; platelet activation;
KW neutrophil; monocyte; granulocyte; organ failure; inflammatory disease;
KW elastase inhibitor; chymotrypsin inhibitor; lung injury; vascular injury;
KW trypsin inhibitor.
XX
XX Unidentified.
OS
XX
XX US6294648-B1.
PN
XX
XX 25-SEP-2001.
PD
XX
XX 20-JUL-1999; 99US-00358569.
PF
XX
XX 20-JUL-1999; 99US-00358569.
PR
XX
XX (FARB ) BAYER CORP.
PA
XX
XX Delaria K, Roczniak S, Davies C;
PI
XX
XX WPI; 2001-662224/76.
DR
XX
XX New isolated protein for inhibiting human serine protease activity in the
PT treatment of e.g. emphysema and adult respiratory distress syndrome.
PT
XX
XX Disclosure; Col 5-6; 16pp; English.
PS
XX
XX The invention relates to human BTL.009 protein, a serine proteinase
CC inhibitor of the Kunitz family that exhibits greater potency towards
CC neutral serine proteinases. BTL.009 protein is found to inhibit leukocyte
CC elastase, chymotrypsin-like protease and trypsin-like protease. BTL.009
CC protein is useful for treating emphysema, idiopathic pulmonary fibrosis,
CC adult respiratory distress syndrome, cystic fibrosis, rheumatoid
CC arthritis, organ failure, glomerulonephritis, other inflammatory diseases
CC and diseases involving lung and vascular injury. BTL.009 is also useful
CC for preventing neutrophil and monocyte activation and formation of active
CC oxygen species during the oxidative burst of stimulated granulocytes.
CC BTL.009 is useful for reducing platelet activation and blood coagulation
CC and for the prophylactic or therapeutic treatment of patients undergoing
CC angioplasty. The present sequence is trypsin inhibitor peptide related to
CC the invention
XX
XX Sequence 54 AA;
SQ
Query Match 55.0%; Score 166; DB 4; Length 54;
Best Local Similarity 51.0%; Pred. No. 2.6e-13;
Matches 26; Conservative 8; Mismatches 17; Indels 0; Gaps 0;
Qy 1 CSMPOEAGPCLASIPHHWYKTKICSEFIYGGCGNNNFQTEAICLVTC 51
| : | | | | | | | | | | : | | | | | | | | | | |
Db 3 CQLPQARGPCAKALLRYFNSTSNACEPFYIYGGCGNNNFQTEMCRLIC 53
RESULT 39
AAB48380
ID AAB48380 standard; protein; 86 AA.
XX
XX AAB48380;
AC
XX
XX 20-APR-2001 (first entry)
DT
XX
XX I. ricinus salivary gland polypeptide.
DE
XX
XX Salivary gland; arthropod; tick; therapeutic; anticoagulant; vaccine;
KW medicinal agent; hematology; transplantation; rheumatology; Lyme disease;
KW tick encephalitis virus disease; antibacterial; antirheumatic; antiviral.
XX
XX Ixodes ricinus.
OS
XX
XX WO200077198-A2.
PN
XX
XX 21-DEC-2000.
PD
XX
XX
```

```
PF 06-JUN-2000; 2000WO-BE000061.
XX
PR 09-JUN-1999; 99CB-00013425.
XX
PA (HENO-) HENOGEN SA.
XX
PI Godfroid E, Bollen A, Lebouille G;
XX
DR WPI; 2001-080687/09.
DR N-PSDB; AAC64925.
XX
PT Characterization of genes induced in tick salivary glands during slow
PT feeding phase of blood meal by cloning genes by forming subtractive
PT library containing selectively induced mRNA during tick feeding phase.
XX
PS Claim 19; Page 42-43; 77pp; English.
XX
CC The invention relates to producing a library of cDNAs which are induced
CC in the salivary gland of Ixodes ricinus arthropod tick. The method
CC involves selectively cloning mRNAs induced during the tick feeding phase
CC to obtain a corresponding cDNA library and cloning full-length cDNAs
CC corresponding to at least one incomplete cDNA sequence identified in the
CC library obtained. The method is useful for identifying genes induced
CC during feeding. A therapeutic agent having anticoagulant or
CC immunomodulatory properties comprising a salivary gland polypeptide can
CC be used alone or in combination with an anti-tick vaccine to prevent the
CC transmission of pathogens carried by the ticks. The polypeptides encoded
CC by the isolated cDNAs are useful in the manufacture of medicinal agents
CC for use in hematology, transplantation, rheumatology and for general
CC treatment. The salivary gland polypeptides, or its epitope bearing
CC fragments, analogs, outer membrane vesicles or cells (attenuated or
CC otherwise) are useful for inducing an immunological response in a mammal
CC adequate to produce antibody and/or T cell immune response to protect the
CC animal from bacteria and viruses which could be transmitted during the
CC blood meal of I. ricinus and other related species. The vectors
CC comprising the cDNAs are also useful for inducing immunological response
CC in a mammal by expressing the polypeptides in vivo in order induce an
CC antibody response to protect the animal from diseases such as Lyme
CC disease, tick encephalitis virus disease etc. The polynucleotides and
CC polypeptides may be employed as research reagents and materials for
CC discovery of treatments and diagnostics to animal and human disease. The
CC present sequence represents a tick salivary gland polypeptide similar to
CC a human tissue factor pathway inhibitor PI-2
XX
SQ Sequence 86 AA;

Query Match 55.0%; Score 166; DB 4; Length 86;
Best Local Similarity 49.0%; Pred. NO. 4.2e-13;
Matches 25; Conservative 10; Mismatches 16; Indels 0; Gaps 0;

OY 1 CSMPOEAGPCLASIPHWYNNKTKICSEFIYGGCGGNNNNFQTEAICLVTC 51
DB 31 CKLPPDGPGRAPISYFDRTKTKCEPMYGGCGGNNNNFENITTCQEC 81

RESULT 40
AAW25929
ID AAW25929 standard; peptide; 51 AA.
XX
AC AAW25929;
XX
DT 11-NOV-1997 (first entry)
XX
DE Anti-trypsin inhibitor UTI Kunitz domain 1.
XX
KW Trypsin inhibitor; Kunitz domain; protease; active site; elastase;
KW neutrophil; disease; modification; site directed mutagenesis.
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Disulfide-bond 1. .51
FT Disulfide-bond 10. .34

Query Match 53.3%; Score 161; DB 2; Length 51;
Best Local Similarity 51.0%; Pred. NO. 1e-12;
Matches 26; Conservative 6; Mismatches 19; Indels 0; Gaps 0;

OY 1 CSMPOEAGPCLASIPHWYNNKTKICSEFIYGGCGGNNNNFQTEAICLVTC 51
DB 1 COLGYSAGPACIAFFPRYPYNGTSMACQTFVYGGCGGNNGNFFVTEKCLQTC 51

RESULT 41
AAW25931
ID AAW25931 standard; peptide; 55 AA.
XX
AC AAW25931;
XX
DT 11-NOV-1997 (first entry)
XX
DE RPDP-Kunitz domain 1.
XX
KW Trypsin inhibitor; Kunitz domain; protease; active site; elastase;
KW neutrophil; disease; modification; site directed mutagenesis.
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Disulfide-bond 5. .55
FT Disulfide-bond 14. .38
FT Modified-site 24
FT Disulfide-bond 30. .51
FT Disulfide-bond 30. .51
XX
PN JP09124700-A.
XX
PD 13-MAY-1997.
XX
PF 07-NOV-1995; 95JP-00288527.
XX
PR 07-NOV-1995; 95JP-00288527.
XX
PA (GREC ) GREEN CROSS CORP.
XX
DR WPI; 1997-316576/29.
DR N-PSDB; AAT79077.
XX
PT New protease inhibitor - useful for treating diseases involving elastase.
XX
PS Claim 1; Page 2; 37pp; Japanese.
XX
CC This is the amino acid sequence of the anti-trypsin inhibitor UTI Kunitz
CC domain 1. The encoding nucleotide sequence was used to construct a novel
CC protease inhibitor by replacing the active site of the Kunitz domain 1
CC (see AAT79080, AAT79081 and AAT79083). The modified protease inhibitors
CC are targeted to the protease elastase, especially from neutrophils and
CC can be used to treat diseases associated with elastase. Modifications of
CC the active site were done by site directed mutagenesis
XX
SQ Sequence 51 AA;

Query Match 53.3%; Score 161; DB 2; Length 51;
Best Local Similarity 51.0%; Pred. NO. 1e-12;
Matches 26; Conservative 6; Mismatches 19; Indels 0; Gaps 0;

OY 1 CSMPOEAGPCLASIPHWYNNKTKICSEFIYGGCGGNNNNFQTEAICLVTC 51
DB 1 COLGYSAGPACIAFFPRYPYNGTSMACQTFVYGGCGGNNGNFFVTEKCLQTC 51

RESULT 41
AAW25931
ID AAW25931 standard; peptide; 55 AA.
XX
AC AAW25931;
XX
DT 11-NOV-1997 (first entry)
XX
DE RPDP-Kunitz domain 1.
XX
KW Trypsin inhibitor; Kunitz domain; protease; active site; elastase;
KW neutrophil; disease; modification; site directed mutagenesis.
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Disulfide-bond 5. .55
FT Disulfide-bond 14. .38
FT Modified-site 24
FT Disulfide-bond 30. .51
FT Disulfide-bond 30. .51
XX
PN JP09124700-A.
XX
PD 13-MAY-1997.
XX
PF 07-NOV-1995; 95JP-00288527.
XX
PR 07-NOV-1995; 95JP-00288527.
XX
PA (GREC ) GREEN CROSS CORP.
XX
DR WPI; 1997-316576/29.
DR
```

DR N-PSDB; AAT79079.

XX New protease inhibitor - useful for treating diseases involving elastase.

XX Claim 2; Page 2; 37pp; Japanese.

XX This is the amino acid sequence of a construct comprising the anti-
trypsin inhibitor UTI Kunitz domain 1 (AAT79077) linked at the N-terminus
to the peptide Arg-Pro-Asp-Phe. The recombinant sequence is used in the
construction of a novel protease inhibitor where the active site residues
of the Kunitz domain 1 (see AAT79080, AAT79081 and AAT79083) are
substituted. The modified protease inhibitors are targeted to the
protease elastase, especially from neutrophils and can be used to treat
diseases associated with elastase. Modifications of the active site were
done by site directed mutagenesis

XX Sequence 55 AA;

Query Match 53.3%; Score 161; DB 2; Length 55;
Best Local Similarity 51.0%; Pred. No. 1.1e-12;
Matches 26; Conservative 6; Mismatches 19; Indels 0; Gaps 0;

Oy 1 CSMPQEAGPCLASIPHWYNNKTKICSEFIYGGCGQNNNNFQTEAICLVTC 51
| : ||||| : : : : : ||||| : : : : : ||||| : : : : : |||||
Db 5 CQLGYSAGPCIAFFPRFYNGTSMACQTFVYGGCGNGNMFVTEKECLQTC 55

RESULT 42

ID AAR27402 standard; peptide; 58 AA.

XX AAR27402;

XX 07-OCT-2004 (revised)

XX 25-MAR-2003 (revised)

XX 20-MAY-1998 (first entry)

XX Human neutrophil elastase inhibitor MUTQE.

XX Kunitz Domain serine protease inhibitor; mutant;

XX Bovine pancreatic trypsin inhibitor.

XX Synthetic.

XX Key Location/Qualifiers

XX Region 1..4

XX /note= "mutated from ITI-D1 (KEDS) -> (RPDF)"

XX Region 15..19

XX /note= "mutated from ITI-D1 (MGMTS) -> (VAMFP)"

XX Region 34

XX /note= "mutated from ITI-D1 (Q) -> (V)"

XX WO9215605-A2.

XX 17-SEP-1992.

XX 28-FEB-1992; 92WO-US001501.

XX 01-MAR-1991; 91US-00664989.

XX 17-JUN-1991; 91US-00715834.

XX (PROT-) PROTEIN ENG CORP.

XX Ley AC, Ladner RC, Guterman SK, Roberts BL, Markland W, Kent RB;

XX WPI; 1992-331666/40.

XX New peptide inhibitors of elastase or cathepsin G - are e.g. mutants of
Kunitz Domain serine protease inhibitors, useful for treating and
preventing conditions caused by excessive neutrophil elastase or
cathepsin G.

XX Example; Page 103; 126pp; English.

PS

XX The sequence is that of a mutant of inter-alpha trypsin inhibitor-D1 (ITI
-D1) MUTQE which is an inhibitor with very strong (kd< 10-11) specific
binding activity for human neutrophil elastase (hNE). It can be used for
the treatment or prophylaxis of a condition caused by excessive hNE
activity, e.g. inflammation, emphysema, cystic fibrosis, adult
respiratory distress syndrome or rheumatoid arthritis. It may also be
used to purify hNE. See also AAR27373-R27403 and AAR27443. (Updated on 25
-MAR-2003 to correct PN field.)

XX Revised record issued on 07-OCT-2004 : Correction to FT field

XX Sequence 58 AA;

Query Match 53.3%; Score 161; DB 2; Length 58;
Best Local Similarity 51.0%; Pred. No. 1.2e-12;
Matches 26; Conservative 6; Mismatches 19; Indels 0; Gaps 0;

Oy 1 CSMPQEAGPCLASIPHWYNNKTKICSEFIYGGCGQNNNNFQTEAICLVTC 51
| : ||||| : : : : : ||||| : : : : : ||||| : : : : : |||||
Db 5 CQLGYSAGPCVAMPFRFYNGTSMACETFYGGCGNGNMFVTEKDCLOTC 55

RESULT 43

ID AAR99160 standard; protein; 58 AA.

XX AAR99160;

XX 12-FEB-1997 (first entry)

XX Genetically engineered aprotinin-like Kunitz domain (MUTQE).

XX Aprotinin; Kunitz domain; human neutrophil elastase; hNE;

XX connective tissue; alpha 1 protease inhibitor; API; neutrophil;

XX alpha antitrypsin; respiratory disorder; cystic fibrosis;

XX smokers emphysema.

XX Synthetic.

XX WO9620278-A2.

XX 04-JUL-1996.

XX 15-DEC-1995; 95WO-US016349.

XX 16-DEC-1994; 94US-00358160.

XX (PROT-) PROTEIN ENG CORP.

XX Ley AC, Ladner RC, Guterman SK, Roberts BL, Markland W, Kent RB;

XX WPI; 1996-321851/32.

XX New engineered inhibitors of human neutrophil elastase - contg. aprotinin
-like Kunitz domain for treating, e.g. cystic fibrosis or other
respiratory disorders.

XX Claim 1; Page 48; 105pp; English.

XX Genetically engineered human derived Kunitz domains can be used to
inhibit human neutrophil elastase, an enzyme involved in the elimination
of pathogens and the restructuring of connective tissue. In cases of
reduction of the circulating alpha-1-protease inhibitor (API or alpha
antitrypsin), or the inactivation of API by oxidation (smokers
emphysema), extensive destruction of the lung tissue may result from
uncontrolled elastolytic activity of human neutrophil elastase. Other
respiratory disorders such as cystic fibrosis are thought to be caused by
human neutrophil elastase release by neutrophils. The genetically
engineered human derived Kunitz domains can be used to treat such
respiratory disorders. See AAR99146-R99211

XX Sequence 58 AA;

XX

Query Match 53.3%; Score 161; DB 2; Length 58;
Best Local Similarity 51.0%; Pred. No. 1.2e-12;
Matches 26; Conservative 6; Mismatches 19; Indels 0; Gaps 0;

XX AAR99158;
AC 12-FEB-1997 (first entry)
XX Genetically engineered aprotinin-like Kunitz domain (BITI-E7-141).
DE CSMQDAGPCLASIPHWYNNKTKICSEFIYGGCGGNNNFQTEAICLVTC 51
KW : ||||| : : || : - : ||||| ||||| ||||| |||||
DB 5 CQLGSAGPCVAMFPFRFYNGTSMACQTFVYGCGMGNGNFFVTERKDCLQC 55

RESULT 44
AAR99159 standard; protein; 58 AA.
ID ID AAR99159 standard; protein; 58 AA.
XX AC AAR99159;
XX DT 12-FEB-1997 (first entry)
XX DE Genetically engineered aprotinin-like Kunitz domain (MUT26A).
XX APotinin; Kunitz domain; human neutrophil elastase; hNE;
KW connective tissue; alpha 1 protease inhibitor; API; neutrophil;
KW alpha antitrypsin; respiratory disorder; cystic fibrosis;
KW smokers emphysema.
XX Synthetic.
OS OS WO9620278-A2.
PN PN 04-JUL-1996.
XX XX 15-DEC-1995; 95WO-US016349.
PF PF 16-DEC-1994; 94US-00358160.
XX PR (PROT-) PROTEIN ENG CORP.
XX PA Ley AC, Ladner RC, Guterman SK, Roberts BL, Markland W, Kent RB;
PI WPI; 1996-321851/32.
XX DR New engineered inhibitors of human neutrophil elastase - contg. aprotinin
XX PT -like Kunitz domain for treating, e.g. cystic fibrosis or other
PT respiratory disorders.
XX Claim 1; Page 48; 105pp; English.
PS Genetically engineered human derived Kunitz domains can be used to
XX inhibit human neutrophil elastase, an enzyme involved in the elimination
CC of pathogens and the restructuring of connective tissue. In cases of
CC reduction of the circulating alpha-1-protease inhibitor (API or alpha
CC antitrypsin), or the inactivation of API by oxidation (smokers
CC emphysema), extensive destruction of the lung tissue may result from
CC uncontrolled elastolytic activity of human neutrophil elastase. Other
CC respiratory disorders such as cystic fibrosis are thought to be caused by
CC human neutrophil elastase release by neutrophils. The genetically
CC engineered human derived Kunitz domains can be used to treat such
CC respiratory disorders. See AAR99146-R99211
XX Sequence 58 AA;
SQ Query Match 53.3%; Score 161; DB 2; Length 58;
Best Local Similarity 51.0%; Pred. No. 1.2e-12;
Matches 26; Conservative 6; Mismatches 19; Indels 0; Gaps 0;

Qy 1 CSMQDAGPCLASIPHWYNNKTKICSEFIYGGCGGNNNFQTEAICLVTC 51
Db 5 CQLGSAGPCVAMFPFRFYNGTSMACQTFVYGCGMGNGNFFVTERKDCLQC 55

RESULT 45
AAR99158 standard; protein; 58 AA.
ID ID AAR99158 standard; protein; 58 AA.
XX AC AAR99158;
XX DT 11-MAR-2004 (first entry)
XX DE Kallikrein inhibitor related amino acid sequence SEQ ID NO:44.
KW ischaemia; vasotropic; kallikrein inhibitor; blood loss;
KW systemic inflammatory response.
XX Homo sapiens.
XX WO2003103475-A2.

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XX PD 18-DEC-2003.
XX PF 06-JUN-2003; 2003WO-US017665.
XX PR 07-JUN-2002; 2002US-0387239P.
XX PR 28-AUG-2002; 2002US-0407003P.
XX PA (DYAX-) DYAX CORP.
XX PI Ladner RC, Ley AC, Hirani S, Williams A;
XX DR WPI; 2004-062190/06.
XX PT Preventing or reducing ischemia in patient involves administering to
XX PT patient composition comprising a kallikrein inhibitory polypeptide.
XX PS Disclosure; SEQ ID NO 44; 46pp; English.
XX CC The present invention describes a method (M1) for preventing or reducing
XX CC ischaemia in a patient. M1 involves administering to the patient a
XX CC composition comprising a polypeptide (I) having an amino acid sequence of
XX CC ADF71926 and inhibiting kallikrein. (I) has vasotropic activity, and can
XX CC be used as a kallikrein inhibitor. (M1) is useful for preventing or
XX CC reducing ischaemia in a patient such as perioperative blood loss due to a
XX CC surgical procedure which is cardiothoracic surgery (e.g. cardiopulmonary
XX CC bypass or coronary artery bypass grafting) performed on the patient. (M1)
XX CC is also useful for preventing or reducing the onset of systemic
XX CC inflammatory response associated with a surgical procedure in a patient
XX CC which involves administering (I) to a patient. The present sequence is
XX CC used in the exemplification of the present invention.
XX SQ Sequence 58 AA;

Query Match 53.3%; Score 161; DB 8; Length 58;
Best Local Similarity 51.0%; Pred. No. 1.2e-12;
Matches 26; Conservative 6; Mismatches 19; Indels 0; Gaps 0;

Qy 1 CSMPQAGPCLASIPHWYNNKTKICSEFIYGGCGQNNNFQTEAICLVTC 51
Db 5 COLGYSAGPCVAMPFRPYFYNGASMACQTFYGGCMGNGNFFVTEKDLQTC 55

RESULT 47
ADF71963
ID ADF71963 standard; protein; 58 AA.
XX AC ADF71963;
XX DT 11-MAR-2004 (first entry)
XX DE Kallikrein inhibitor related amino acid sequence SEQ ID NO:43.
XX KW ischaemia; vasotropic; kallikrein inhibitor; blood loss;
XX KW systemic inflammatory response.
XX OS Homo sapiens.
XX PN W02003103475-A2.
XX PD 18-DEC-2003.
XX PF 06-JUN-2003; 2003WO-US017665.
XX PR 07-JUN-2002; 2002US-0387239P.
XX PR 28-AUG-2002; 2002US-0407003P.
XX PA (DYAX-) DYAX CORP.
XX PI Ladner RC, Ley AC, Hirani S, Williams A;
XX DR WPI; 2004-062190/06.
XX PT Preventing or reducing ischemia in patient involves administering to
XX PT patient composition comprising a kallikrein inhibitory polypeptide.
XX PS Disclosure; SEQ ID NO 42; 46pp; English.
XX CC The present invention describes a method (M1) for preventing or reducing
XX CC ischaemia in a patient. M1 involves administering to the patient a
XX CC composition comprising a polypeptide (I) having an amino acid sequence of
XX CC ADF71926 and inhibiting kallikrein. (I) has vasotropic activity, and can
XX CC be used as a kallikrein inhibitor. (M1) is useful for preventing or
XX CC reducing ischaemia in a patient such as perioperative blood loss due to a
XX CC surgical procedure which is cardiothoracic surgery (e.g. cardiopulmonary
XX CC bypass or coronary artery bypass grafting) performed on the patient. (M1)
XX CC is also useful for preventing or reducing the onset of systemic
XX CC inflammatory response associated with a surgical procedure in a patient
XX CC which involves administering (I) to a patient. The present sequence is
XX CC used in the exemplification of the present invention.
XX SQ Sequence 58 AA;

Query Match 53.3%; Score 161; DB 8; Length 58;
Best Local Similarity 51.0%; Pred. No. 1.2e-12;
Matches 26; Conservative 6; Mismatches 19; Indels 0; Gaps 0;

Qy 1 CSMPQAGPCLASIPHWYNNKTKICSEFIYGGCGQNNNFQTEAICLVTC 51
Db 5 COLGYSAGPCVAMPFRPYFYNGASMACQTFYGGCMGNGNFFVTEKDLQTC 55

RESULT 48
ADF71962
ID ADF71962 standard; protein; 58 AA.
XX AC ADF71962;
XX DT 11-MAR-2004 (first entry)
XX DE Kallikrein inhibitor related amino acid sequence SEQ ID NO:42.
XX KW ischaemia; vasotropic; kallikrein inhibitor; blood loss;
XX KW systemic inflammatory response.
XX OS Homo sapiens.
XX PN W02003103475-A2.
XX PD 18-DEC-2003.
XX PF 06-JUN-2003; 2003WO-US017665.
XX PR 07-JUN-2002; 2002US-0387239P.
XX PR 28-AUG-2002; 2002US-0407003P.
XX PA (DYAX-) DYAX CORP.
XX PI Ladner RC, Ley AC, Hirani S, Williams A;
XX DR WPI; 2004-062190/06.
XX PT Preventing or reducing ischemia in patient involves administering to
XX PT patient composition comprising a kallikrein inhibitory polypeptide.
XX PS Disclosure; SEQ ID NO 42; 46pp; English.
XX CC The present invention describes a method (M1) for preventing or reducing
XX CC ischaemia in a patient. M1 involves administering to the patient a
XX CC composition comprising a polypeptide (I) having an amino acid sequence of
XX CC ADF71926 and inhibiting kallikrein. (I) has vasotropic activity, and can
XX CC be used as a kallikrein inhibitor. (M1) is useful for preventing or
XX CC reducing ischaemia in a patient such as perioperative blood loss due to a
XX CC surgical procedure which is cardiothoracic surgery (e.g. cardiopulmonary
XX CC bypass or coronary artery bypass grafting) performed on the patient. (M1)
XX CC is also useful for preventing or reducing the onset of systemic
```

CC inflammatory response associated with a surgical procedure in a patient
CC which involves administering (I) to a patient. The present sequence is
CC used in the exemplification of the present invention.

XX Sequence 58 AA;

SQ Query Match 53.3%; Score 161; DB 8; Length 58;
Best Local Similarity 51.0%; Pred. No. 1.2e-12;
Matches 26; Conservative 6; Mismatches 19; Indels 0; Gaps 0;

QY 1 CSMPOEAGPCLASIPHWYKTKCSFHYGGCGNNNFOTEALCLVTC 51
Db 5 COLGYSAGPCVAMPFRFYNGTSMACQTFVYGGCGNGNFFVTEKCLQTC 55

RESULT 49
AAW25933
ID AAW25933 standard; protein; 124 AA.

XX AAW25933;

XX 11-NOV-1997 (first entry)

XX New protease inhibitor Epl-d21-RPDF-52-55.

XX Trypsin inhibitor; Kunitz domain; protease; active site; elastase;
KW neutrophil; disease; modification; site directed mutagenesis.

XX Synthetic.

XX Key Location/Qualifiers
FH Domain 5..56
FT /note= "Kunitz domain 1"
FT Disulfide-bond 5..55
FT Disulfide-bond 14..38
FT Misc-difference 15..19

FT /note= "mutated region; amino acids substituted for wild
FT type amino acid sequence MGMTS; this includes the active
FT site residue of domain 1 (aa 36 of the wild type sequence
FT AAW25928)"

FT Disulfide-bond 30..51
FT Misc-difference 31

FT /note= "mutated amino acid; replaces amino acid Glu in
FT wild type sequence"

FT Misc-difference 34
FT /note= "mutated amino acid; replaces amino acid Gln in
FT wild type sequence"

FT Domain 57..126
FT /note= "Kunitz domain 2"

FT Disulfide-bond 61..111
FT Disulfide-bond 70..94

FT Active-site 71
FT /note= "active site residue"

FT Disulfide-bond 86..107

XX JP09124700-A.

XX 13-MAY-1997.

XX 07-NOV-1995; 95JP-00288527.

XX 07-NOV-1995; 95JP-00288527.

XX (GREC) GREEN CROSS CORP.

XX WPI; 1997-316576/29.

XX N-PSDB; AAT79081.

XX New protease inhibitor - useful for treating diseases involving elastase.

XX Claim 6; Page 3; 37pp; Japanese.

XX This is the amino acid sequence of a novel protease inhibitor based on

CC the sequence of the anti-trypsin inhibitor UTI. The protein comprises
CC Kunitz domains 1 and 2 of UTI, but lacks amino acids 1-21. Of the
CC remaining amino acids, residues 1-4 (22-26 of the native sequence) are
CC replaced by the peptide Arg-Pro-Asp-Phe. The construct also has the
CC sequence encoding the active site residue and the adjacent amino acids
CC (amino acids 36-40 of the wild type sequence) and amino acids 52 and 55
CC substituted. The modified protease inhibitors are targeted to the
CC protease elastase, especially from neutrophils and can be used to treat
CC diseases associated with elastase. Modifications of the active site were
CC done by site directed mutagenesis

XX Sequence 124 AA;

SQ Query Match 53.3%; Score 161; DB 2; Length 124;
Best Local Similarity 51.0%; Pred. No. 2.7e-12;
Matches 26; Conservative 6; Mismatches 19; Indels 0; Gaps 0;

QY 1 CSMPOEAGPCLASIPHWYKTKCSFHYGGCGNNNFOTEALCLVTC 51

Db 5 COLGYSAGPCVAMPFRFYNGTSMACQTFVYGGCGNGNFFVTEKCLQTC 55

RESULT 50
AAW25932
ID AAW25932 standard; protein; 124 AA.

XX AAW25932;

XX 11-NOV-1997 (first entry)

XX New protease inhibitor Epl-d21-RPDF-52-55.

XX Trypsin inhibitor; Kunitz domain; protease; active site; elastase;
KW neutrophil; disease; modification; site directed mutagenesis.

XX Synthetic.

XX Key Location/Qualifiers
FH Domain 5..56
FT /note= "Kunitz domain 1"

FT Disulfide-bond 5..55
FT Disulfide-bond 14..38
FT Misc-difference 15..19

FT /note= "mutated region; amino acids substituted for wild
FT type amino acid sequence MGMTS; this includes the active
FT site residue of domain 1 (aa 36 of the wild type sequence
FT AAW25928)"

FT Disulfide-bond 30..51
FT Misc-difference 31

FT /note= "mutated amino acid; replaces amino acid Glu in
FT wild type sequence"

FT Misc-difference 34
FT /note= "mutated amino acid; replaces amino acid Gln in
FT wild type sequence"

FT Domain 57..126
FT /note= "Kunitz domain 2"

FT Disulfide-bond 61..111
FT Disulfide-bond 70..94

FT Active-site 71
FT /note= "active site residue"

FT Disulfide-bond 86..107

XX JP09124700-A.

XX 13-MAY-1997.

XX 07-NOV-1995; 95JP-00288527.

XX 07-NOV-1995; 95JP-00288527.

XX (GREC) GREEN CROSS CORP.

XX WPI; 1997-316576/29.

XX N-PSDB; AAT79081.

XX New protease inhibitor - useful for treating diseases involving elastase.

XX Claim 6; Page 3; 37pp; Japanese.

XX This is the amino acid sequence of a novel protease inhibitor based on

DR N-PSDB; AAT79080.
XX
PT New protease inhibitor - useful for treating diseases involving elastase.
XX
PS Claim 5; Page 3; 37pp; Japanese.
XX
CC This is the amino acid sequence of a novel protease inhibitor based on
CC the sequence of the anti-trypsin inhibitor UTI. The protein comprises
CC Kunitz domains 1 and 2 of UTI, but lacks amino acids 1-21. Of the
CC remaining amino acids, residues 1-4 (22-26 of the native sequence) are
CC replaced by the peptide Arg-Pro-Asp-Phe. The construct also has the
CC sequence encoding the active site residue and the adjacent amino acids
CC (amino acids 36-40 of the wild type sequence) and amino acids 52 and 55
CC substituted. The modified protease inhibitors are targeted to the
CC protease elastase, especially from neutrophils and can be used to treat
CC diseases associated with elastase. Modifications of the active site were
CC done by site directed mutagenesis
XX
SQ Sequence 124 AA;
Query Match 53.3%; Score 161; DB 2; Length 124;
Best Local Similarity 51.0%; Pred. No. 2.7e-12;
Matches 26; Conservative 6; Mismatches 19; Indels 0; Gaps 0;
Qy 1 CSMPQEAGPCLASIPHWYNNKTKICSEFIYGGCGGNNNFQTEAICLVTC 51
Db : ||||| :
5 COLGYSAGPCIAFPFRYPYNGTSMACQTFVYGGCGNGNFFVTEKECLQTC 55
Search completed: September 21, 2005, 16:36:49
Job time : 32.8938 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 21, 2005, 16:27:13 ; Search time 9.32743 Seconds
(without alignments)
408.162 Million cell updates/sec

Title: US-10-807-204-1_COPY_77_127
Perfect score: 302
Sequence: 1 CSMPOEAGPCLASIPHWYNN.....GCGCGNNNNFQTEAICLVTC 51

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 50 summaries

Database : Issued Patents AA:*

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2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*

3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*

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5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*

6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	219	72.5	54	US-09-358-569D-8	Sequence 8, Appli
2	219	72.5	55	US-09-358-569D-1	Sequence 1, Appli
3	219	72.5	58	US-09-369-494-8	Sequence 8, Appli
4	219	72.5	58	US-09-569-670-8	Sequence 8, Appli
5	219	72.5	64	US-09-358-569D-10	Sequence 10, Appli
6	219	72.5	133	US-09-152-060-75	Sequence 75, Appli
7	170	56.3	43	US-09-358-569D-13	Sequence 13, Appli
8	170	56.3	66	US-08-358-160-113	Sequence 113, App
9	170	56.3	79	5466783-7	Patent No. 5466783
10	170	56.3	79	5466783-7	Patent No. 5466783
11	167	55.3	58	US-08-358-160-71	Sequence 71, Appli
12	166	55.0	67	US-09-358-569D-9	Sequence 9, Appli
13	166	55.0	64	US-08-358-160-123	Sequence 123, App
14	166	55.0	86	US-09-910-430-8	Sequence 8, Appli
15	161	53.3	58	US-08-358-160-17	Sequence 17, Appli
16	161	53.3	58	US-08-358-160-18	Sequence 18, Appli
17	160	53.0	77	5466783-4	Patent No. 5466783
18	160	53.0	77	5466783-4	Patent No. 5466783
19	157	52.0	61	US-08-829-876-211	Sequence 211, App
20	157	52.0	61	US-08-829-876-214	Sequence 214, App
21	157	52.0	61	US-09-234-874A-211	Sequence 211, App
22	157	52.0	61	US-09-234-874A-214	Sequence 214, App
23	157	52.0	61	US-09-234-873A-211	Sequence 211, App
24	157	52.0	61	US-09-234-873A-214	Sequence 214, App
25	156	51.7	58	US-07-664-989B-48	Sequence 48, Appli
26	156	51.7	58	US-07-664-989B-51	Sequence 51, Appli
27	156	51.7	58	US-08-358-160-1	Sequence 1, Appli

ALIGNMENTS

RESULT 1
US-09-358-569D-8
; Sequence 8, Application US/09358569D
; Patent No. 6294648
; GENERAL INFORMATION:
; APPLICANT: Delaria, Kathy
; APPLICANT: Rocznia, Steve
; APPLICANT: Davies, Christopher
; TITLE OF INVENTION: Protein Having Proteinase Inhibitor Activity
; FILE REFERENCE: MSB-7259
; CURRENT APPLICATION NUMBER: US/09/358,569D
; CURRENT FILING DATE: 1999-07-20
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 8
; LENGTH: 54
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:derived from
; OTHER INFORMATION: EST sequence database

US-09-358-569D-8
Query Match 72.5%; Score 219; DB 3; Length 54;
Best Local Similarity 68.6%; Pred. No. 3.1e-21;
Matches 35; Conservative 5; Mismatches 11; Indels 0; Gaps 0;

QY 1 CSMPOEAGPCLASIPHWYNNKTKTCSBFYGGCGGNNNNFQTEAICLVTC 51
DB 3 CEMPKEGPECLAYFLHWYDKDNTCSMFVYGGCGGNNNNFQSKANCLNTC 53

RESULT 2
US-09-358-569D-1
; Sequence 1, Application US/09358569D
; Patent No. 6294648
; GENERAL INFORMATION:
; APPLICANT: Delaria, Kathy
; APPLICANT: Rocznia, Steve
; APPLICANT: Davies, Christopher
; TITLE OF INVENTION: Protein Having Proteinase Inhibitor Activity
; FILE REFERENCE: MSB-7259
; CURRENT APPLICATION NUMBER: US/09/358,569D
; CURRENT FILING DATE: 1999-07-20
; NUMBER OF SEQ ID NOS: 15

28 156 51.7 58 1 US-08-358-160-26 Sequence 26, Appli
29 156 51.7 58 1 US-08-463-455A-56 Sequence 56, Appli
30 156 51.7 58 1 US-08-463-432B-56 Sequence 56, Appli
31 156 51.7 61 2 US-08-829-876-180 Sequence 180, App
32 156 51.7 61 2 US-08-829-876-218 Sequence 218, App
33 156 51.7 61 3 US-09-234-874A-180 Sequence 180, App
34 156 51.7 61 3 US-09-234-874A-218 Sequence 218, App
35 156 51.7 61 4 US-08-234-873A-180 Sequence 180, App
36 156 51.7 61 4 US-08-234-873A-218 Sequence 218, App
37 156 51.7 62 1 US-08-358-160-27 Sequence 27, Appli
38 155 51.3 58 1 US-07-664-989B-49 Sequence 49, Appli
39 155 51.3 58 1 US-08-358-160-9 Sequence 9, Appli
40 155 51.3 58 1 US-08-358-160-10 Sequence 10, Appli
41 155 51.3 58 1 US-08-358-160-11 Sequence 11, Appli
42 155 51.3 58 1 US-08-358-160-15 Sequence 15, Appli
43 155 51.3 58 1 US-08-358-160-16 Sequence 16, Appli
44 155 51.3 58 1 US-08-358-160-24 Sequence 24, Appli
45 155 51.3 61 2 US-08-829-876-129 Sequence 129, App
46 155 51.3 61 2 US-08-829-876-139 Sequence 139, App
47 155 51.3 61 2 US-08-829-876-208 Sequence 208, App
48 155 51.3 61 2 US-08-829-876-217 Sequence 217, App
49 155 51.3 61 2 US-08-829-876-222 Sequence 222, App
50 155 51.3 61 3 US-09-234-874A-129 Sequence 129, App

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; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 55
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:derived from
; OTHER INFORMATION: EST sequence database
US-09-358-569D-1

Query Match          72.5%; Score 219; DB 3; Length 55;
Best Local Similarity 68.6%; Pred. No. 3.2e-21;
Matches 35; Conservative 5; Mismatches 11; Indels 0; Gaps 0;

Qy 1 CSMPOEAGPCLASIPHHWYKTKICSEFIYGGCGGNNNNFQTEAICLVTC 51
Db 5 CEMPKEGTGCLAYFLHWWYDKDKNTCSMFVYGGCGGNNNNFQSKANCLNTC 55

RESULT 3
US-09-369-494-8
; Sequence 8, Application US/09369494
; Patent No. 6180607
; GENERAL INFORMATION:
; APPLICANT: Davies, Christopher
; APPLICANT: Chen, Dadong
; APPLICANT: Rocznia, Steve
; TITLE OF INVENTION: Protein Having Proteinase Inhibitor Activity
; FILE REFERENCE: MSB-7260
; CURRENT APPLICATION NUMBER: US/09/369,494
; CURRENT FILING DATE: 1999-08-05
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 8
; LENGTH: 58
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:fragment from
; OTHER INFORMATION: computer database
US-09-369-494-8

Query Match          72.5%; Score 219; DB 3; Length 58;
Best Local Similarity 68.6%; Pred. No. 3.4e-21;
Matches 35; Conservative 5; Mismatches 11; Indels 0; Gaps 0;

Qy 1 CSMPOEAGPCLASIPHHWYKTKICSEFIYGGCGGNNNNFQTEAICLVTC 51
Db 5 CEMPKEGTGCLAYFLHWWYDKDKNTCSMFVYGGCGGNNNNFQSKANCLNTC 55

RESULT 4
US-09-569-670-8
; Sequence 8, Application US/09569670
; Patent No. 6689582
; GENERAL INFORMATION:
; APPLICANT: Davies, Christopher
; APPLICANT: Chen, Dadong
; APPLICANT: Rocznia, Steve
; TITLE OF INVENTION: Protein Having Proteinase Inhibitor Activity
; FILE REFERENCE: MSB-7260
; CURRENT APPLICATION NUMBER: US/09/569,670
; CURRENT FILING DATE: 2000-05-12
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 8
; LENGTH: 58
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:fragment from
; OTHER INFORMATION: computer database
US-09-569-670-8
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Query Match          72.5%; Score 219; DB 4; Length 58;
Best Local Similarity 68.6%; Pred. No. 3.4e-21;
Matches 35; Conservative 5; Mismatches 11; Indels 0; Gaps 0;

Qy 1 CSMPOEAGPCLASIPHHWYKTKICSEFIYGGCGGNNNNFQTEAICLVTC 51
Db 5 CEMPKEGTGCLAYFLHWWYDKDKNTCSMFVYGGCGGNNNNFQSKANCLNTC 55

RESULT 5
US-09-358-569D-10
; Sequence 10, Application US/09358569D
; Patent No. 6294648
; GENERAL INFORMATION:
; APPLICANT: Delaria, Kathy
; APPLICANT: Rocznia, Steve
; APPLICANT: Davies, Christopher
; TITLE OF INVENTION: Protein Having Proteinase Inhibitor Activity
; FILE REFERENCE: MSB-7259
; CURRENT APPLICATION NUMBER: US/09/358,569D
; CURRENT FILING DATE: 1999-07-20
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 10
; LENGTH: 64
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Extension of
; OTHER INFORMATION: Seq Id 1
US-09-358-569D-10

Query Match          72.5%; Score 219; DB 3; Length 64;
Best Local Similarity 68.6%; Pred. No. 3.7e-21;
Matches 35; Conservative 5; Mismatches 11; Indels 0; Gaps 0;

Qy 1 CSMPOEAGPCLASIPHHWYKTKICSEFIYGGCGGNNNNFQTEAICLVTC 51
Db 7 CEMPKEGTGCLAYFLHWWYDKDKNTCSMFVYGGCGGNNNNFQSKANCLNTC 57

RESULT 6
US-09-152-060-75
; Sequence 75, Application US/09152060
; Patent No. 6448230
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 28 Human Secreted Proteins
; FILE REFERENCE: P2003P1.US
; CURRENT APPLICATION NUMBER: US/09/152,060
; CURRENT FILING DATE: 1998-09-11
; EARLIER APPLICATION NUMBER: PCT/US98/04858
; EARLIER FILING DATE: 1998-03-12
; EARLIER APPLICATION NUMBER: 60/040,762
; EARLIER FILING DATE: 1997-03-14
; EARLIER APPLICATION NUMBER: 60/040,710
; EARLIER FILING DATE: 1997-03-14
; EARLIER APPLICATION NUMBER: 60/050,934
; EARLIER FILING DATE: 1997-05-30
; EARLIER APPLICATION NUMBER: 60/048,100
; EARLIER FILING DATE: 1997-05-30
; EARLIER APPLICATION NUMBER: 60/048,357
; EARLIER FILING DATE: 1997-05-30
; EARLIER APPLICATION NUMBER: 60/048,189
; EARLIER FILING DATE: 1997-05-30
; EARLIER APPLICATION NUMBER: 60/057,765
; EARLIER FILING DATE: 1997-09-05
; EARLIER APPLICATION NUMBER: 60/048,970
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/068,368
; EARLIER FILING DATE: 1997-12-19
; NUMBER OF SEQ ID NOS: 118
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; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 75
; LENGTH: 133
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-152-060-75

Query Match          72.5%; Score 219; DB 4; Length 133;
Best Local Similarity 68.6%; Pred. No. 8.2e-21;
Matches 35; Conservative 5; Mismatches 11; Indels 0; Gaps 0;

QY 1 CSMPOEAGPCLASIPHWYNNKTKICSEFIYGGCGGNNNNFOTEALCLVTC 51
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 77 CEMPKEGTCLAYFLHWYDKDNTCSMFYVGGCGGNNNNFQSKANCLNTC 127

RESULT 7
US-09-358-569D-13
; Sequence 13, Application US/09358569D
; Patent No. 6294648
; GENERAL INFORMATION:
; APPLICANT: Delaria, Kathy
; APPLICANT: Rocznia, Steve
; APPLICANT: Davies, Christopher
; TITLE OF INVENTION: Protein Having Proteinase Inhibitor Activity
; FILE REFERENCE: MSB-7259
; CURRENT APPLICATION NUMBER: US/09/358,569D
; CURRENT FILING DATE: 1999-07-20
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 13
; LENGTH: 43
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Artificial
; OTHER INFORMATION: sequence derived from EST database
US-09-358-569D-13

Query Match          56.3%; Score 170; DB 3; Length 43;
Best Local Similarity 68.3%; Pred. No. 5.3e-15;
Matches 28; Conservative 4; Mismatches 9; Indels 0; Gaps 0;

QY 11 LASIPHWYNNKTKICSEFIYGGCGGNNNNFOTEALCLVTC 51
    |||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 LAYFLHWYDKDNTCSMFYVGGCGGNNNNFQSKANCLNTC 41

RESULT 8
US-08-358-160-113
; Sequence 113, Application US/08358160
; Patent No. 5663143
; GENERAL INFORMATION:
; APPLICANT: LEY, Arthur C.
; APPLICANT: LADNER, Robert C.
; APPLICANT: GUTERMAN, Sonia K.
; APPLICANT: ROBERTS, Bruce L.
; APPLICANT: MARKLAND, William
; APPLICANT: KENT, Rachel B.
; TITLE OF INVENTION: ENGINEERED HUMAN-DERIVED KUNITZ
; TITLE OF INVENTION: DOMAINS THAT INHIBIT HUMAN NEUTROPHIL ELASTASE
; NUMBER OF SEQUENCES: 234
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEWMARK
; STREET: 419 Seventh Street, N.W. Suite 300
; CITY: Washington
; STATE: District of Columbia
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
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; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/358,160
; FILING DATE: 16-DEC-1994
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/133,031
; FILING DATE: 13-OCT-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/009,319
; FILING DATE: 26-JAN-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/664,989
; FILING DATE: 01-MAR-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/487,063
; FILING DATE: 02-MAR-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/240,160
; FILING DATE: 02-SEP-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Cooper, Iver P.
; REGISTRATION NUMBER: 28,005
; REFERENCE/DOCKET NUMBER: LEY=1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; TELEX: 248633
; INFORMATION FOR SEQ ID NO: 113:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 66 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-358-160-113

Query Match          56.3%; Score 170; DB 1; Length 66;
Best Local Similarity 51.0%; Pred. No. 8.4e-15;
Matches 26; Conservative 10; Mismatches 15; Indels 0; Gaps 0;

QY 1 CSMPOEAGPCLASIPHWYNNKTKICSEFIYGGCGGNNNNFOTEALCLVTC 51
    |||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 8 CRLPPEQGPKGRIPRYFYNPASRMCESEFIYGGCKGNKNFKYKAEQVRAC 58

RESULT 9
5466783-7
; Patent No. 5466783
; APPLICANT: Wun, Tze-Chen, Kretzmer, Kuniko K.; Broze,
; George J. Jr.
; TITLE OF INVENTION: HUMAN TISSUE FACTOR INHIBITOR
; NUMBER OF SEQUENCES: 26
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/93,285
; FILING DATE: 15-JUL-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 566,280
; FILING DATE: 13-AUG-1990
; APPLICATION NUMBER: 123,753
; FILING DATE: 23-NOV-1987
; APPLICATION NUMBER: 77,366
; FILING DATE: 23-JUL-1987
; SEQ ID NO: 7
; LENGTH: 79
5466783-7

Query Match          56.3%; Score 170; DB 6; Length 79;
Best Local Similarity 51.0%; Pred. No. 1e-14;
Matches 26; Conservative 10; Mismatches 15; Indels 0; Gaps 0;

QY 1 CSMPOEAGPCLASIPHWYNNKTKICSEFIYGGCGGNNNNFOTEALCLVTC 51
    |||:|||||:|||||:|||||:|||||:|||||:|||||:
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```

Db      8 CRLPPEQGCKGRIPRYFNPAASRCESFIYGGCKGNKNFKTKAECVRAC 58

RESULT 10
5466783-7
; Patent No. 5466783
; APPLICANT: Wun, Tze-Chuin, Kretzmer, Kuniko K.; Broze, George J., Jr.
; TITLE OF INVENTION: HUMAN TISSUE FACTOR INHIBITOR
; NUMBER OF SEQUENCES: 26
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/93,285
; FILING DATE: 15-JUL-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 566,280
; FILING DATE: 13-AUG-1990
; APPLICATION NUMBER: 123,753
; FILING DATE: 23-NOV-1987
; APPLICATION NUMBER: 77,366
; FILING DATE: 23-JUL-1987
; SEQ ID NO: 7:
; LENGTH: 79
5466783-7

Query Match          56.3%; Score 170; DB 6; Length 79;
Best Local Similarity 51.0%; Pred. No. 1e-14;
Matches 26; Conservative 10; Mismatches 15; Indels 0; Gaps 0;

Qy      1 CSMPOEAGPCLASIPHWYNKTKICSEFYGGCGNNNFQTEAICLVTC 51
| : | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| : | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      8 CRLPPEQGCKGRIPRYFNPAASRCESFIYGGCKGNKNFKTKAECVRAC 58

RESULT 11
US-08-358-160-71
; Sequence 71, Application US/08358160
; Patent No. 5663143
; GENERAL INFORMATION:
; APPLICANT: LEY, Arthur C.
; APPLICANT: LADNER, Robert C.
; APPLICANT: GUTERMAN, Sonia K.
; APPLICANT: ROBERTS, Bruce L.
; APPLICANT: MARKLAND, William
; APPLICANT: KENT, Rachel B.
; TITLE OF INVENTION: ENGINEERED HUMAN-DERIVED KUNITZ
; NUMBER OF SEQUENCES: 234
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W. Suite 300
; CITY: Washington
; STATE: District of Columbia
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/358,160
; FILING DATE: 16-DEC-1994
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/133,031
; FILING DATE: 13-OCT-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/009,319
; FILING DATE: 26-JAN-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/664,989
; FILING DATE: 01-MAR-1991
; PRIOR APPLICATION DATA:

```

```
; APPLICANT: KENT, Rachel B.
; TITLE OF INVENTION: ENGINEERED HUMAN-DERIVED KUNITZ
; NUMBER OF SEQUENCES: 234
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W. Suite 300
; CITY: Washington
; STATE: District of Columbia
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/358,160
; FILING DATE: 16-DEC-1994
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/133,031
; FILING DATE: 13-OCT-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/009,319
; FILING DATE: 26-JAN-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/664,989
; FILING DATE: 01-MAR-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/487,063
; FILING DATE: 02-MAR-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/240,160
; FILING DATE: 02-SEP-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Cooper, Iver P.
; REGISTRATION NUMBER: 28,005
; REFERENCE/DOCKET NUMBER: LEY=1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; TELEX: 248633
; INFORMATION FOR SEQ ID NO: 123:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 67 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-358-160-123

Query Match 55.0%; Score 166; DB 1; Length 67;
Best Local Similarity 51.0%; Pred. No. 2.8e-14;
Matches 26; Conservative 8; Mismatches 17; Indels 0; Gaps 0;

QY 1 CSMQEGAGCLASIPHWYNNKTKICSEFIYGGCGGNNNFQTEAICLVTC 51
DB 8 CQLPQARGPCKAALLRYFNSTSNACEPFTYGGCGGNNNFETEMCLRIC 58

RESULT 14
US-09-910-430-8
; Sequence 8, Application US/09910430
; Patent No. 6794166
; GENERAL INFORMATION:
; APPLICANT: Godfroi, Edmond
; APPLICANT: Bollen, Alex
; APPLICANT: Lebouille, Gerard
; TITLE OF INVENTION: IDENTIFICATION AND MOLECULAR CHARACTERIZATION OF
; TITLE OF INVENTION: PROTEINS, EXPRESSED IN THE IXODES RICINUS SALIVARY
; TITLE OF INVENTION: GLANDS
; FILE REFERENCE: VANM229.001CP1
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; CURRENT APPLICATION NUMBER: US/09/910,430
; CURRENT FILING DATE: 2001-07-19
; PRIOR APPLICATION NUMBER: PCT/BE00/00061
; FILING DATE: 2000-06-06
; PRIOR APPLICATION NUMBER: GB 9913425.6
; PRIOR FILING DATE: 1999-06-09
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 8
; LENGTH: 86
; TYPE: PRT
; ORGANISM: Ixodes ricinus
; US-09-910-430-8

Query Match 55.0%; Score 166; DB 4; Length 86;
Best Local Similarity 49.0%; Pred. No. 3.7e-14;
Matches 25; Conservative 10; Mismatches 16; Indels 0; Gaps 0;

QY 1 CSMQEGAGCLASIPHWYNNKTKICSEFIYGGCGGNNNFQTEAICLVTC 51
DB 31 CKLPDDGFCRARIPSYFYDRKTKCKEFMYGGCGGNNNFENITTCQEEC 81

RESULT 15
US-08-358-160-17
; Sequence 17, Application US/08358160
; Patent No. 5663143
; GENERAL INFORMATION:
; APPLICANT: LEY, Arthur C.
; APPLICANT: LADNER, Robert C.
; APPLICANT: GUTERMAN, Sonia K.
; APPLICANT: ROBERTS, Bruce L.
; APPLICANT: MARKLAND, William
; APPLICANT: KENT, Rachel B.
; TITLE OF INVENTION: ENGINEERED HUMAN-DERIVED KUNITZ
; TITLE OF INVENTION: DOMAINS THAT INHIBIT HUMAN NEUTROPHIL ELASTASE
; NUMBER OF SEQUENCES: 234
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W. Suite 300
; CITY: Washington
; STATE: District of Columbia
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/358,160
; FILING DATE: 16-DEC-1994
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/133,031
; FILING DATE: 13-OCT-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/009,319
; FILING DATE: 26-JAN-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/664,989
; FILING DATE: 01-MAR-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/487,063
; FILING DATE: 02-MAR-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/240,160
; FILING DATE: 02-SEP-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Cooper, Iver P.
; REGISTRATION NUMBER: 28,005
; REFERENCE/DOCKET NUMBER: LEY=1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; TELEX: 248633
; INFORMATION FOR SEQ ID NO: 123:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 67 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-358-160-123
```

```
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; TELEX: 248633
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 58 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-358-160-17

Query Match 53.3%; Score 161; DB 1; Length 58;
Best Local Similarity 51.0%; Pred. No. 1.1e-13;
Matches 26; Conservative 6; Mismatches 19; Indels 0; Gaps 0;

Qy 1 CSMQEQAGPCLASIPHHWYNNKTKICSEFIYGGCGGNNNFQTEAICLVTC 51
| : ||||| : : || : : ||||| : : ||||| : : ||||| : : |||||
Db 5 CQLGYSAGPCVAMPFRYPFYNGTSMACETFYVGGCMGNGNMFVTEKDCIQTC 55

RESULT 16
US-08-358-160-18
; Patent No. 5663143
; Sequence 18, Application US/08358160
; GENERAL INFORMATION:
; APPLICANT: LEY, Arthur C.
; APPLICANT: LADNER, Robert C.
; APPLICANT: GUTERMAN, Sonia K.
; APPLICANT: ROBERTS, Bruce L.
; APPLICANT: MARKLAND, William
; APPLICANT: KENT, Rachel B.
; TITLE OF INVENTION: ENGINEERED HUMAN-DERIVED KUNITZ
; TITLE OF INVENTION: DOMAINS THAT INHIBIT HUMAN NEUTROPHIL ELASTASE
; NUMBER OF SEQUENCES: 234
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W. Suite 300
; CITY: Washington
; STATE: District of Columbia
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/358,160
; FILING DATE: 16-DEC-1994
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/133,031
; FILING DATE: 13-OCT-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/009,319
; FILING DATE: 26-JAN-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/664,989
; FILING DATE: 01-MAR-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/487,063
; FILING DATE: 02-MAR-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/240,160
; FILING DATE: 02-SEP-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Cooper, Iver P.
; REGISTRATION NUMBER: 28,005
; REFERENCE/DOCKET NUMBER: LEY=1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528

; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; TELEX: 248633
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 58 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-358-160-18

Query Match 53.3%; Score 161; DB 1; Length 58;
Best Local Similarity 51.0%; Pred. No. 1.1e-13;
Matches 26; Conservative 6; Mismatches 19; Indels 0; Gaps 0;

Qy 1 CSMQEQAGPCLASIPHHWYNNKTKICSEFIYGGCGGNNNFQTEAICLVTC 51
| : ||||| : : || : : ||||| : : ||||| : : ||||| : : |||||
Db 5 CQLGYSAGPCVAMPFRYPFYNGASMACOTFYVGGCMGNGNMFVTEKDCIQTC 55

RESULT 17
5466783-4
; Patent No. 5466783
; APPLICANT: Wun, Tze-Chain; Kretzmer, Kuniko K.; Broze,
; George J. Jr.
; TITLE OF INVENTION: HUMAN TISSUE FACTOR INHIBITOR
; NUMBER OF SEQUENCES: 26
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/93,285
; FILING DATE: 15-JUL-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 566,280
; FILING DATE: 13-AUG-1990
; APPLICATION NUMBER: 123,753
; FILING DATE: 23-NOV-1987
; APPLICATION NUMBER: 77,366
; FILING DATE: 23-JUL-1987
; SEQ ID NO: 4
; LENGTH: 77
5466783-4

Query Match 53.0%; Score 160; DB 6; Length 77;
Best Local Similarity 47.1%; Pred. No. 1.9e-13;
Matches 24; Conservative 10; Mismatches 17; Indels 0; Gaps 0;

Qy 1 CSMQEQAGPCLASIPHHWYNNKTKICSEFIYGGCGGNNNFQTEAICLVTC 51
| : ||||| : : || : : ||||| : : ||||| : : ||||| : : |||||
Db 8 CQLFQARGPCVKAALRYFYBSTSNACEPFTYVGGCGGNNNFETTEMCLRIC 58

RESULT 18
5466783-4
; Patent No. 5466783
; APPLICANT: Wun, Tze-Chain; Kretzmer, Kuniko K.; Broze,
; George J. Jr.
; TITLE OF INVENTION: HUMAN TISSUE FACTOR INHIBITOR
; NUMBER OF SEQUENCES: 26
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/93,285
; FILING DATE: 15-JUL-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 566,280
; FILING DATE: 13-AUG-1990
; APPLICATION NUMBER: 123,753
; FILING DATE: 23-NOV-1987
; APPLICATION NUMBER: 77,366
; FILING DATE: 23-JUL-1987
; SEQ ID NO: 4
; LENGTH: 77
5466783-4

Query Match 53.0%; Score 160; DB 6; Length 77;
Best Local Similarity 47.1%; Pred. No. 1.9e-13;
Matches 24; Conservative 10; Mismatches 17; Indels 0; Gaps 0;
```

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; TITLE OF INVENTION:  PROTEASE INHIBITOR PEPTIDES
; NUMBER OF SEQUENCES:  228
; CORRESPONDENCE ADDRESS:
; ADDRESSEE:  Foley & Lardner
; STREET:  3000 K Street, N.W., Suite 500
; CITY:  Washington
; STATE:  D.C.
; COUNTRY:  USA
; ZIP:  20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE:  Floppy disk
; COMPUTER:  IBM PC compatible
; OPERATING SYSTEM:  PC-DOS/MS-DOS
; SOFTWARE:  Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER:  US/08/829,876
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:  US 08/436,555
; FILING DATE:  08-MAY-1995
; ATTORNEY/AGENT INFORMATION:
; NAME:  Peltto, Don J.
; REGISTRATION NUMBER:  33,754
; REFERENCE/DOCKET NUMBER:  56324/106/SCNO
; TELECOMMUNICATION INFORMATION:
; TELEPHONE:  (202)672-5300
; TELEFAX:  (202)672-5399
; TELEX:  904136
; INFORMATION FOR SEQ ID NO:  214:
; SEQUENCE CHARACTERISTICS:
; LENGTH:  61 amino acids
; TYPE:  amino acid
; STRANDEDNESS:  single
; TOPOLOGY:  linear
; MOLECULE TYPE:  protein
; US-08-829-876-214

Query Match      52.0%; Score 157; DB 2; Length 61;
Best Local Similarity 49.0%; Pred. No. 3.7e-13;
Matches 25; Conservative 6; Mismatches 20; Indels 0;

QY  1  CSMPOAGPCLASIPHWYNNKTKICSEFYGGCGGNNNNFQTEAICLVTC 51
Db  7  CSEQAETGPCRALIPRWYFDVTEGKCAPFFYGGCGGNNNNFQTEYCMAVC 57

RESULT 21
US-09-234-874A-211
; Sequence 211, Application US/09234874A
; Patent No. 6376648
; GENERAL INFORMATION:
; APPLICANT:  White, Tyler R.
; Damm, Deborah
; Lesikar, David D.
; McFadden, Kathleen
; Garrick, Brett L.
; TITLE OF INVENTION:  PROTEASE INHIBITOR PEPTIDES
; NUMBER OF SEQUENCES:  228
; CORRESPONDENCE ADDRESS:
; ADDRESSEE:  Foley & Lardner
; STREET:  3000 K Street, N.W., Suite 500
; CITY:  Washington
; STATE:  D.C.
; COUNTRY:  USA
; ZIP:  20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE:  Floppy disk
; COMPUTER:  IBM PC compatible
; OPERATING SYSTEM:  PC-DOS/MS-DOS
; SOFTWARE:  Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER:  US/09/234,874A

; TITLE OF INVENTION:  PROTEASE INHIBITOR PEPTIDES
; NUMBER OF SEQUENCES:  228
; CORRESPONDENCE ADDRESS:
; ADDRESSEE:  Foley & Lardner
; STREET:  3000 K Street, N.W., Suite 500
; CITY:  Washington
; STATE:  D.C.
; COUNTRY:  USA
; ZIP:  20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE:  Floppy disk
; COMPUTER:  IBM PC compatible
; OPERATING SYSTEM:  PC-DOS/MS-DOS
; SOFTWARE:  Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER:  US/09/234,874A

```

```

; FILING DATE: 11-Jun-2001
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/436,555
; FILING DATE: 08-MAY-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Bent, Stephen
; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 056324/0106
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 672-5300
; TELEFAX: (202) 672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 211:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 61 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 211:
US-09-234-874A-211

Query Match 52.0%; Score 157; DB 3; Length 61;
Best Local Similarity 49.0%; Pred. No. 3.7e-13;
Matches 25; Conservative 6; Mismatches 20; Indels 0; Gaps 0;

QY 1 CSMPOEAGPCLASPHWYNNKTKICSEFIYGGCGGNNNFOTEAICLVTC 51
Db 7 CSEQETGPCTRAALQHWYFDVTEGKCAPFFYGGCGGNRNNFTTEYCMVC 57

RESULT 22
US-09-234-874A-214
; Sequence 214, Application US/09234874A
; Patent No. 6376648
; GENERAL INFORMATION:
; APPLICANT: White, Tyler R.
; Damm, Deborah
; Lesikar, David D.
; McPadden, Kathleen
; Garrick, Brett L.
; TITLE OF INVENTION: PROTEASE INHIBITOR PEPTIDES
; NUMBER OF SEQUENCES: 228
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/234,874A
; FILING DATE: 11-Jun-2001
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/436,555
; FILING DATE: 08-MAY-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Bent, Stephen
; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 056324/0106
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 672-5300
; TELEFAX: (202) 672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 214:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 61 amino acids
; TYPE: amino acid

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RESULT 24
US-09-234-873A-214
; Sequence 214, Application US/09234873A
; Patent No. 6613890
; GENERAL INFORMATION:
; APPLICANT: White, Tyler R.
; Damm, Deborah
; Lesikar, David D.
; McFadden, Kathleen
; Garrick, Brett L.
; TITLE OF INVENTION: PROTEASE INHIBITOR PEPTIDES
; NUMBER OF SEQUENCES: 228
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/234,873A
; FILING DATE: 21-Jan-1999
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/829,876
; FILING DATE: 02-APR-1997
; APPLICATION NUMBER: 08/436,555
; FILING DATE: 08-MAY-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Bent, Stephen
; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 056324/0116
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 672-5300
; TELEFAX: (202) 672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 214:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 61 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 214:
US-09-234-873A-214
Query Match 52.0%; Score 157; DB 4; Length 61;
Best Local Similarity 49.0%; Pred. No. 3.7e-13;
Matches 25; Conservative 6; Mismatches 20; Indels 0; Gaps 0;
QY 1 CSMQAGPCLASIPHHWYKTKICSEFIYGGCGGNNNNFQTEAICLVTC 51
Db 7 CSEQATGTCRALIPRWYFDVTGKCAPFFYGGCGRNNNFTTEYCMVAVC 57
RESULT 25
US-07-664-989B-48
; Sequence 48, Application US/07664989B
; Patent No. 5223409
; GENERAL INFORMATION:
; APPLICANT: Ladner, Robert Charles
; APPLICANT: Guterman, Sonia Kosow
; APPLICANT: Roberts, Bruce Lindsey
; APPLICANT: Markland, William
; APPLICANT: Ley, Arthur Charles
; TITLE OF INVENTION: Directed Evolution of No. 5223409e1
; TITLE OF INVENTION: Binding Proteins

; NUMBER OF SEQUENCES: 121
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Browdy and Neimark
; STREET: 419 Seventh Street, N.W.
; CITY: Washington,
; STATE: DC
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WORDPERFECT 4.2
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/664,989B
; FILING DATE: 19910301
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US89/03731
; FILING DATE: 01-SEP-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/487,063
; FILING DATE: 02-MAR-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/240,160
; FILING DATE: 02-SEP-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Cooper, Iver P.
; REGISTRATION NUMBER: 28005
; REFERENCE/DOCKET NUMBER: LADNER 7
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; INFORMATION FOR SEQ ID NO: 48:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 58 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-07-664-989B-48
Query Match 51.7%; Score 156; DB 1; Length 58;
Best Local Similarity 47.1%; Pred. No. 4.7e-13;
Matches 24; Conservative 8; Mismatches 19; Indels 0; Gaps 0;
QY 1 CSMQAGPCLASIPHHWYKTKICSEFIYGGCGGNNNNFQTEAICLVTC 51
Db 5 CLEPPYTGCVAMFFRYFNKAGLCQTFYGGCGNGNNGNFKASAECDMRTC 55
RESULT 26
US-07-664-989B-51
; Sequence 51, Application US/07664989B
; Patent No. 5223409
; GENERAL INFORMATION:
; APPLICANT: Ladner, Robert Charles
; APPLICANT: Guterman, Sonia Kosow
; APPLICANT: Roberts, Bruce Lindsey
; APPLICANT: Markland, William
; APPLICANT: Ley, Arthur Charles
; APPLICANT: Kent, Rachel Baribault
; TITLE OF INVENTION: Directed Evolution of No. 5223409e1
; TITLE OF INVENTION: Binding Proteins
; NUMBER OF SEQUENCES: 121
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Browdy and Neimark
; STREET: 419 Seventh Street, N.W.
; CITY: Suite 300
; CITY: Washington,
; STATE: DC
; COUNTRY: USA
; ZIP: 20004

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; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WORDPERFECT 4.2
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/664,989B
; FILING DATE: 19910301
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US89/03731
; FILING DATE: 01-SEP-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/487,063
; FILING DATE: 02-MAR-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/240,160
; FILING DATE: 02-SEP-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Cooper, Iver P.
; REGISTRATION NUMBER: 28005
; REFERENCE/DOCKET NUMBER: LADNER 7
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; INFORMATION FOR SEQ ID NO: 51:
; LENGTH: 58 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-07-664-989B-51

Query Match 51.7%; Score 156; DB 1; Length 58;
Best Local Similarity 47.1%; Pred. No. 4.7e-13;
Matches 24; Conservative 8; Mismatches 19; Indels 0; Gaps 0;

Qy 1 CSMPEAGPCIASIPHHWYKTKICSEFIYGGCGNNNFQTEAICLVTC 51
Db 5 CLEPPYTGPCIAFPFRYFNKAGLCQTFVYGGCGNGNFKSAEDCMRTC 55

RESULT 27
US-08-358-160-1
; Sequence 1, Application US/08358160
; Patent No. 5663143
; GENERAL INFORMATION:
; APPLICANT: LEY, Arthur C.
; APPLICANT: LADNER, Robert C.
; APPLICANT: GUTERMAN, Sonia K.
; APPLICANT: ROBERTS, Bruce L.
; APPLICANT: MARKLAND, William
; APPLICANT: KENT, Rachel B.
; TITLE OF INVENTION: ENGINEERED HUMAN-DERIVED KUNITZ
; TITLE OF INVENTION: DOMAINS THAT INHIBIT HUMAN NEUTROPHIL ELASTASE
; NUMBER OF SEQUENCES: 234
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W. Suite 300
; CITY: Washington
; STATE: District of Columbia
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/358,160
; FILING DATE: 16-DEC-1994
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
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; APPLICATION NUMBER: US 08/133,031
; FILING DATE: 13-OCT-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/009,319
; FILING DATE: 26-JAN-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/664,989
; FILING DATE: 01-MAR-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/487,063
; FILING DATE: 02-MAR-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/240,160
; FILING DATE: 02-SEP-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Cooper, Iver P.
; REGISTRATION NUMBER: 28,005
; REFERENCE/DOCKET NUMBER: LEY=1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; TELEX: 248633
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 58 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-358-160-1

Query Match 51.7%; Score 156; DB 1; Length 58;
Best Local Similarity 47.1%; Pred. No. 4.7e-13;
Matches 24; Conservative 8; Mismatches 19; Indels 0; Gaps 0;

Qy 1 CSMPEAGPCIASIPHHWYKTKICSEFIYGGCGNNNFQTEAICLVTC 51
Db 5 CLEPPYTGPCVAMFPFRYFNKAGLCQTFVYGGCGNGNFKSAEDCMRTC 55

RESULT 28
US-08-358-160-26
; Sequence 26, Application US/08358160
; Patent No. 5663143
; GENERAL INFORMATION:
; APPLICANT: LEY, Arthur C.
; APPLICANT: LADNER, Robert C.
; APPLICANT: GUTERMAN, Sonia K.
; APPLICANT: ROBERTS, Bruce L.
; APPLICANT: MARKLAND, William
; APPLICANT: KENT, Rachel B.
; TITLE OF INVENTION: ENGINEERED HUMAN-DERIVED KUNITZ
; TITLE OF INVENTION: DOMAINS THAT INHIBIT HUMAN NEUTROPHIL ELASTASE
; NUMBER OF SEQUENCES: 234
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W. Suite 300
; CITY: Washington
; STATE: District of Columbia
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/358,160
; FILING DATE: 16-DEC-1994
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/133,031
; FILING DATE: 13-OCT-1993
```

PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/009,319
 FILING DATE: 26-JAN-1993
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/664,989
 FILING DATE: 01-MAR-1991
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/487,063
 FILING DATE: 02-MAR-1990
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/240,160
 FILING DATE: 02-SEP-1988
 ATTORNEY/AGENT INFORMATION:
 NAME: Cooper, Iver P.
 REGISTRATION NUMBER: 28,005
 REFERENCE/DOCKET NUMBER: LEV=1
 TELEPHONE: 202-628-5197
 TELEFAX: 202-737-3528
 TELEX: 248633
 INFORMATION FOR SEQ ID NO: 26:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 58 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-358-160-26

Query Match 51.7%; Score 156; DB 1; Length 58;
 Best Local Similarity 47.1%; Pred. No. 4.7e-13;
 Matches 24; Conservative 8; Mismatches 19; Indels 0; Gaps 0;

QY 1 CSMQAEAGCLASIPHWYNNKTKICSEFIYGGCGNNNNFOTEALCLVTC 51
 DB 5 CLEPPYTGPCIAFFPRFYNAKGLCQTFVYGGCGMGNFKSABDCMTC 55

RESULT 29
 US-08-463-155A-56
 Sequence 56, Application US/08463155A
 Patent No. 5780265
 GENERAL INFORMATION:
 APPLICANT: Dennis, Mark S.
 APPLICANT: Lazarus, Robert A.
 TITLE OF INVENTION: KUNITZ TYPE PLASMA KALLIKREIN INHIBITORS
 NUMBER OF SEQUENCES: 72
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Genentech, Inc.
 STREET: 460 Point San Bruno Blvd
 CITY: South San Francisco
 STATE: California
 COUNTRY: USA
 ZIP: 94080
 COMPUTER READABLE FORM:
 MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: WinPatIn (Genentech)
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/463,155A
 FILING DATE: 05-Jun-1995
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: Kubinec, Jeffrey S.
 REGISTRATION NUMBER: 36,575
 REFERENCE/DOCKET NUMBER: P0944
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 415/225-8228
 TELEFAX: 415/952-9881
 TELEX: 910/371-7168
 INFORMATION FOR SEQ ID NO: 56:
 SEQUENCE CHARACTERISTICS:

LENGTH: 58 amino acids
 TYPE: Amino Acid
 TOPOLOGY: Linear
 US-08-463-155A-56
 Query Match 51.7%; Score 156; DB 1; Length 58;
 Best Local Similarity 51.0%; Pred. No. 4.7e-13;
 Matches 26; Conservative 5; Mismatches 20; Indels 0; Gaps 0;
 QY 1 CSMQAEAGCLASIPHWYNNKTKICSEFIYGGCGNNNNFOTEALCLVTC 51
 DB 5 CSEQAEDGPCRAAIPRWYFDVTEGKCAPFIYGGCGNNRNNFDTTEYCAAVC 55

RESULT 30
 US-08-463-432B-56
 Sequence 56, Application US/08463432B
 Patent No. 5786328
 GENERAL INFORMATION:
 APPLICANT: Dennis, Mark S.
 APPLICANT: Lazarus, Robert A.
 TITLE OF INVENTION: KUNITZ TYPE PLASMA KALLIKREIN INHIBITORS
 NUMBER OF SEQUENCES: 72
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Genentech, Inc.
 STREET: 460 Point San Bruno Blvd
 CITY: South San Francisco
 STATE: California
 COUNTRY: USA
 ZIP: 94080
 COMPUTER READABLE FORM:
 MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: WinPatIn (Genentech)
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/463,432B
 FILING DATE: 05-Jun-1995
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: Kubinec, Jeffrey S.
 REGISTRATION NUMBER: 36,575
 REFERENCE/DOCKET NUMBER: P0944-2
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 415/225-8228
 TELEFAX: 415/952-9881
 TELEX: 910/371-7168
 INFORMATION FOR SEQ ID NO: 56:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 58 amino acids
 TYPE: Amino Acid
 TOPOLOGY: Linear
 US-08-463-432B-56

Query Match 51.7%; Score 156; DB 1; Length 58;
 Best Local Similarity 51.0%; Pred. No. 4.7e-13;
 Matches 26; Conservative 5; Mismatches 20; Indels 0; Gaps 0;

QY 1 CSMQAEAGCLASIPHWYNNKTKICSEFIYGGCGNNNNFOTEALCLVTC 51
 DB 5 CSEQAEDGPCRAAIPRWYFDVTEGKCAPFIYGGCGNNRNNFDTTEYCAAVC 55

RESULT 31
 US-08-829-876-180
 Sequence 180, Application US/08829876
 Patent No. 5962266
 GENERAL INFORMATION:
 APPLICANT: White, Tyler R.
 APPLICANT: Damm, Deborah
 APPLICANT: Lesikar, David D.
 APPLICANT: McFadden, Kathleen
 APPLICANT: Garrick, Brett L.

```
;
; TITLE OF INVENTION: PROTEASE INHIBITOR PEPTIDES
;
; NUMBER OF SEQUENCES: 228
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
;
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/829,876
; FILING DATE:
; CLASSIFICATION:
;
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/436,555
; FILING DATE: 08-MAY-1995
;
; ATTORNEY/AGENT INFORMATION:
; NAME: Peltto, Don J.
; REGISTRATION NUMBER: 33,754
; REFERENCE/DOCKET NUMBER: 56324/106/SCNO
;
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
;
; INFORMATION FOR SEQ ID NO: 180:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 61 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
;
; US-08-829-876-180
;
; Query Match 51.7%; Score 156; DB 2; Length 61;
; Best Local Similarity 49.0%; Pred. NO. 5e-13;
; Matches 25; Conservative 5; Mismatches 21; Indels 0; Gaps 0;
;
; Qy 1 CSMQEQAGPCLASIPHWYNNKTKICSEFIYGGCGNNNNFOTEAICLVTC 51
; Db 7 CSEQAETGCRAGIPRWYFDVTEGKCAPFFYGGCGNNRNFDTBEYCMAVC 57
;
; RESULT 32
; US-08-829-876-218
; Sequence 218, Application US/08829876
; Patent No. 5962266
;
; GENERAL INFORMATION:
; APPLICANT: White, Tyler R.
; APPLICANT: Damm, Deborah
; APPLICANT: Lesikar, David D.
; APPLICANT: McFadden, Kathleen
; APPLICANT: Garrick, Brett L.
; APPLICANT: McFadden, Kathleen
; APPLICANT: Garrick, Brett L.
;
; TITLE OF INVENTION: PROTEASE INHIBITOR PEPTIDES
; NUMBER OF SEQUENCES: 228
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
;
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/829,876
; FILING DATE:
; CLASSIFICATION:
;
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/436,555
; FILING DATE: 08-MAY-1995
;
; ATTORNEY/AGENT INFORMATION:
; NAME: Bent, Stephen
; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 056324/0106
;
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
;
; INFORMATION FOR SEQ ID NO: 180:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 61 amino acids
; TYPE: amino acid
;
; US/08/829,876
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;
; FILING DATE:
; CLASSIFICATION:
;
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/436,555
; FILING DATE: 08-MAY-1995
;
; ATTORNEY/AGENT INFORMATION:
; NAME: Peltto, Don J.
; REGISTRATION NUMBER: 33,754
; REFERENCE/DOCKET NUMBER: 56324/106/SCNO
;
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
;
; INFORMATION FOR SEQ ID NO: 218:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 61 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
;
; US-08-829-876-218
;
; Query Match 51.7%; Score 156; DB 2; Length 61;
; Best Local Similarity 49.0%; Pred. No. 5e-13;
; Matches 25; Conservative 7; Mismatches 19; Indels 0; Gaps 0;
;
; Qy 1 CSMQEQAGPCLASIPHWYNNKTKICSEFIYGGCGNNNNFOTEAICLVTC 51
; Db 7 CSEQAESGPCRAAIYHWYFDVTEGKCAPFFYGGCGNNRNFDTBEYCMAVC 57
;
; RESULT 33
; US-09-234-874A-180
; Sequence 180, Application US/09234874A
; Patent No. 6376648
;
; GENERAL INFORMATION:
; APPLICANT: White, Tyler R.
; APPLICANT: Damm, Deborah
; APPLICANT: Lesikar, David D.
; APPLICANT: McFadden, Kathleen
; APPLICANT: Garrick, Brett L.
;
; TITLE OF INVENTION: PROTEASE INHIBITOR PEPTIDES
; NUMBER OF SEQUENCES: 228
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
;
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/234,874A
; FILING DATE: 11-Jun-2001
;
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/436,555
; FILING DATE: 08-MAY-1995
;
; ATTORNEY/AGENT INFORMATION:
; NAME: Bent, Stephen
; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 056324/0106
;
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
;
; INFORMATION FOR SEQ ID NO: 180:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 61 amino acids
; TYPE: amino acid
;
; US/08/829,876
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US-09-234-874A-180
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 180:
US-09-234-874A-180
Query Match 51.7%; Score 156; DB 3; Length 61;
Best Local Similarity 49.0%; Pred. No. 5e-13;
Matches 25; Conservative 5; Mismatches 21; Indels 0; Gaps 0;
QY 1 CSMPOEAGPCLASIPHHWYNNKTKICSEFIYGGCGGNNNNFOTEALCLVTC 51
DB 7 CSEQAETGCRAGIPRWYFDVTEGKCAPFFYGGCGGNNRNNFDTBYCMAVC 57
RESULT 34
US-09-234-874A-218
; Sequence 218, Application US/09234874A
; Patent No. 6376648
; GENERAL INFORMATION:
; APPLICANT: White, Tyler R.
; Damm, Deborah
; Lesikar, David D.
; McFadden, Kathleen
; Garrick, Brett L.
; TITLE OF INVENTION: PROTEASE INHIBITOR PEPTIDES
; NUMBER OF SEQUENCES: 228
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/234,874A
; FILING DATE: 21-Jan-1999
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/829,876
; FILING DATE: 02-APR-1997
; APPLICATION NUMBER: 08/436,555
; FILING DATE: 08-MAY-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Bent, Stephen
; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 056324/0116
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 218:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 61 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 218:
US-09-234-874A-218
Query Match 51.7%; Score 156; DB 3; Length 61;
Best Local Similarity 49.0%; Pred. No. 5e-13;
Matches 25; Conservative 7; Mismatches 19; Indels 0; Gaps 0;
QY 1 CSMPOEAGPCLASIPHHWYNNKTKICSEFIYGGCGGNNNNFOTEALCLVTC 51
DB 7 CSEQAEGPCRAAIYHWYFDVTEGKCAPFFYGGCGGNNRNNFDTBYCMAVC 57
RESULT 35

US-09-234-873A-180
; Sequence 180, Application US/09234873A
; Patent No. 6613890
; GENERAL INFORMATION:
; APPLICANT: White, Tyler R.
; Damm, Deborah
; Lesikar, David D.
; McFadden, Kathleen
; Garrick, Brett L.
; TITLE OF INVENTION: PROTEASE INHIBITOR PEPTIDES
; NUMBER OF SEQUENCES: 228
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/234,873A
; FILING DATE: 21-Jan-1999
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/829,876
; FILING DATE: 02-APR-1997
; APPLICATION NUMBER: 08/436,555
; FILING DATE: 08-MAY-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Bent, Stephen
; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 056324/0116
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 180:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 61 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 180:
US-09-234-873A-180
Query Match 51.7%; Score 156; DB 4; Length 61;
Best Local Similarity 49.0%; Pred. No. 5e-13;
Matches 25; Conservative 5; Mismatches 21; Indels 0; Gaps 0;
QY 1 CSMPOEAGPCLASIPHHWYNNKTKICSEFIYGGCGGNNNNFOTEALCLVTC 51
DB 7 CSEQAETGCRAGIPRWYFDVTEGKCAPFFYGGCGGNNRNNFDTBYCMAVC 57
RESULT 36
US-09-234-873A-218
; Sequence 218, Application US/09234873A
; Patent No. 6613890
; GENERAL INFORMATION:
; APPLICANT: White, Tyler R.
; Damm, Deborah
; Lesikar, David D.
; McFadden, Kathleen
; Garrick, Brett L.
; TITLE OF INVENTION: PROTEASE INHIBITOR PEPTIDES
; NUMBER OF SEQUENCES: 228
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500

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? CLASSIFICATION: 514
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER: US 08/133,031
? FILING DATE: 13-OCT-1993
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER: US 08/009,319
? FILING DATE: 26-JAN-1993
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER: US 07/664,989
? FILING DATE: 01-MAR-1991
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER: US 07/487,063
? FILING DATE: 02-MAR-1990
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER: US 07/240,160
? FILING DATE: 02-SEP-1988
? ATTORNEY/AGENT INFORMATION:
? NAME: Cooper, Iver P.
? REGISTRATION NUMBER: 28,005
? REFERENCE/DOCKET NUMBER: LEY=1
? TELECOMMUNICATION INFORMATION:
? TELEPHONE: 202-628-5197
? TELEFAX: 202-737-3528
? TELEX: 248633
? INFORMATION FOR SEQ ID NO: 27:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 62 amino acids
? TYPE: amino acid
? STRANDEDNESS: single
? TOPOLOGY: linear
? MOLECULE TYPE: protein
? US-08-358-160-27

Query Match 51.7%; Score 156; DB 1; Length 62;
Best Local Similarity 47.1%; Pred. No. 5,1e-13;
Matches 24; Conservative 8; Mismatches 19; Indels 0;

Qy 1 CSMPEAGCLASIPHWYNTKTKCSFYGGCGNNNFOTEALCVTC 51
Db 9 CLEPPVTGCIAPFFRYFNAGKGLCQTFVYGGCGNGNFKSADCMRTC 59

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US-07-664-989B-49
; Sequence 49, Application US/07664989B
; Patent No. 5223409
; GENERAL INFORMATION:
; APPLICANT: Ladner, Robert Charles
; APPLICANT: Guterman, Sonia Kosow
; APPLICANT: Roberts, Bruce Lindsay
; APPLICANT: Markland, William
; APPLICANT: Ley, Arthur Charles
; APPLICANT: Kent, Rachel Baribault
; TITLE OF INVENTION: Directed Evolution of No. 5223409el
; TITLE OF INVENTION: Binding Proteins
; NUMBER OF SEQUENCES: 121
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Brodwy and Neimark
; STREET: 419 Seventh Street, N.W.
; STREET: Suite 300
; CITY: Washington,
; STATE: DC
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WORDPERFECT 4.2
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/664,989B
; FILING DATE: 19910301
; CLASSIFICATION: 530

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Patent No. 5663143

GENERAL INFORMATION:

APPLICANT: LEY, Arthur C.

APPLICANT: LADNER, Robert C.

APPLICANT: GUTERMAN, Sonia K.

APPLICANT: ROBERTS, Bruce L.

APPLICANT: MARKLAND, William

APPLICANT: KENT, Rachel B.

TITLE OF INVENTION: ENGINEERED HUMAN-DERIVED KUNITZ

TITLE OF INVENTION: DOMAINS THAT INHIBIT HUMAN NEUTROPHIL ELASTASE

NUMBER OF SEQUENCES: 234

CORRESPONDENCE ADDRESS:

ADDRESSEE: BROWDY AND NEIMARK

STREET: 419 Seventh Street, N.W. Suite 300

CITY: Washington

STATE: District of Columbia

COUNTRY: USA

ZIP: 20004

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/358,160

FILING DATE: 16-DEC-1994

CLASSIFICATION: 514

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/133,031

FILING DATE: 13-OCT-1993

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/009,319

FILING DATE: 26-JAN-1993

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/664,989

FILING DATE: 01-MAR-1991

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/487,063

FILING DATE: 02-MAR-1990

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; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/240,160
; FILING DATE: 02-SEP-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Cooper, Iver P.
; REGISTRATION NUMBER: 28,005
; REFERENCE/DOCKET NUMBER: LEY=1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; TELEX: 248633
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 58 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-358-160-10

Query Match 51.3%; Score 155; DB 1; Length 58;
Best Local Similarity 51.0%; Pred. No. 6.4e-13;
Matches 26; Conservative 5; Mismatches 20; Indels 0; Gaps 0;

Qy 1 CSMQEAQPCLASIPHHWYKTKICSEFIYGGCGNNNFQTEAICLVTC 51
   : |||||: |||||: |||||: |||||: |||||: |||||: |||||: |||||:
Db 5 CQLGYSAGPCVAMPFRYFYNGTSMACETFOYGGCMGNGNNFVTEKDCQTC 55

RESULT 41
US-08-358-160-11
; Sequence 11, Application US/08358160
; Patent No. 5663143
; GENERAL INFORMATION:
; APPLICANT: LEY, Arthur C.
; APPLICANT: LADNER, Robert C.
; APPLICANT: GUTERMAN, Sonia K.
; APPLICANT: ROBERTS, Bruce L.
; APPLICANT: MARKLAND, William
; APPLICANT: KENT, Rachel B.
; TITLE OF INVENTION: ENGINEERED HUMAN-DERIVED KUNITZ
; NUMBER OF SEQUENCES: 234
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W. Suite 300
; CITY: Washington
; STATE: District of Columbia
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/358,160
; FILING DATE: 16-DEC-1994
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/133,031
; FILING DATE: 13-OCT-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/009,319
; FILING DATE: 26-JAN-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/664,989
; FILING DATE: 01-MAR-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/487,063
; FILING DATE: 02-MAR-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/240,160
; ATTORNEY/AGENT INFORMATION:

; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/240,160
; FILING DATE: 02-SEP-1988
; ATTORNEY/AGENT INFORMATION:
```


NAME: Cooper, Iver P.
REGISTRATION NUMBER: 28,005
REFERENCE/DOCKET NUMBER: LEY=1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
TELEX: 248633
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 58 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-358-160-15

Query Match 51.3%; Score 155; DB 1; Length 58;
Best Local Similarity 51.0%; Pred. No. 6.4e-13;
Matches 26; Conservative 5; Mismatches 20; Indels 0; Gaps 0;

QY 1 CSMQEAGPCLASIPHHWYKTKICSEFIYGGCGNNNNFQTEAICLVTC 51
Db 5 COLGYSAGPCVAMPFRFYNGTSMACETFOYGGCGNGNMFVTEKDCLOTC 55

RESULT 43

US-08-358-160-16
Sequence 16, Application US/08358160
Patent No. 5663143
GENERAL INFORMATION:
APPLICANT: LEY, Arthur C.
APPLICANT: LADNER, Robert C.
APPLICANT: GUTERMAN, Sonia K.
APPLICANT: ROBERTS, Bruce L.
APPLICANT: MARKLAND, William
APPLICANT: KENT, Rachel B.
TITLE OF INVENTION: ENGINEERED HUMAN-DERIVED KUNITZ
TITLE OF INVENTION: DOMAINS THAT INHIBIT HUMAN NEUTROPHIL ELASTASE
NUMBER OF SEQUENCES: 234
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEIMARK
STREET: 419 Seventh Street, N.W. Suite 300
CITY: Washington
STATE: District of Columbia
COUNTRY: USA
ZIP: 20004

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/358,160
FILING DATE: 16-DEC-1994
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/133,031
FILING DATE: 13-OCT-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/009,319
FILING DATE: 26-JAN-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/664,989
FILING DATE: 01-MAR-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/487,063
FILING DATE: 02-MAR-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/240,160
FILING DATE: 02-SEP-1988
ATTORNEY/AGENT INFORMATION:
NAME: Cooper, Iver P.
REGISTRATION NUMBER: 28,005

REFERENCE/DOCKET NUMBER: LEY=1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
TELEX: 248633
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 58 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-358-160-16

Query Match 51.3%; Score 155; DB 1; Length 58;
Best Local Similarity 51.0%; Pred. No. 6.4e-13;
Matches 26; Conservative 5; Mismatches 20; Indels 0; Gaps 0;

QY 1 CSMQEAGPCLASIPHHWYKTKICSEFIYGGCGNNNNFQTEAICLVTC 51
Db 5 COLGYSAGPCVAMPFRFYNGTSMACETFOYGGCGNGNMFVTEKDCLOTC 55

RESULT 44

US-08-358-160-24
Sequence 24, Application US/08358160
Patent No. 5663143
GENERAL INFORMATION:
APPLICANT: LEY, Arthur C.
APPLICANT: LADNER, Robert C.
APPLICANT: GUTERMAN, Sonia K.
APPLICANT: ROBERTS, Bruce L.
APPLICANT: MARKLAND, William
APPLICANT: KENT, Rachel B.
TITLE OF INVENTION: ENGINEERED HUMAN-DERIVED KUNITZ
TITLE OF INVENTION: DOMAINS THAT INHIBIT HUMAN NEUTROPHIL ELASTASE
NUMBER OF SEQUENCES: 234
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEIMARK
STREET: 419 Seventh Street, N.W. Suite 300
CITY: Washington
STATE: District of Columbia
COUNTRY: USA
ZIP: 20004

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/358,160
FILING DATE: 16-DEC-1994
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/133,031
FILING DATE: 13-OCT-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/009,319
FILING DATE: 26-JAN-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/664,989
FILING DATE: 01-MAR-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/487,063
FILING DATE: 02-MAR-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/240,160
FILING DATE: 02-SEP-1988
ATTORNEY/AGENT INFORMATION:
NAME: Cooper, Iver P.
REGISTRATION NUMBER: 28,005
REFERENCE/DOCKET NUMBER: LEY=1
TELECOMMUNICATION INFORMATION:

TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
TELEX: 248633
INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
LENGTH: 58 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-829-876-129

Query Match 51.3%; Score 155; DB 1; Length 58;
Best Local Similarity 47.1%; Pred. No. 6.4e-13;
Matches 24; Conservative 8; Mismatches 19; Indels 0; Gaps 0;

Qy 1 CSMQAEAGPCLASIPHHWYNNKTKICSEFIYGGCGNNNFQTEAICLVTC 51
Db 5 CLEPPYTGPCVAIPRPYFNKAGLCQTFFYGGCGNGNFKSABDCWRTC 55

RESULT 45

US-08-829-876-129
Sequence 129, Application US/08829876
Patent No. 5962266

GENERAL INFORMATION:
APPLICANT: White, Tyler R.

APPLICANT: Damm, Deborah
APPLICANT: Lesikar, David D.
APPLICANT: McFadden, Kathleen
APPLICANT: Garrick, Brett L.

TITLE OF INVENTION: PROTEASE INHIBITOR PEPTIDES

NUMBER OF SEQUENCES: 228

CORRESPONDENCE ADDRESS:

ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
STATE: D.C.
COUNTRY: USA

ZIP: 20007-5109

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/829,876

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/436,555

FILING DATE: 08-MAY-1995

ATTORNEY/AGENT INFORMATION:

NAME: Pelto, Don J.

REGISTRATION NUMBER: 33,754

REFERENCE/DOCKET NUMBER: 56324/106/SCNO

TELECOMMUNICATION INFORMATION:

TELEPHONE: (202)672-5300

TELEFAX: (202)672-5399

TELEX: 904136

INFORMATION FOR SEQ ID NO: 129:

SEQUENCE CHARACTERISTICS:

LENGTH: 61 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-829-876-129

Query Match 51.3%; Score 155; DB 2; Length 61;
Best Local Similarity 49.0%; Pred. No. 6.7e-13;
Matches 25; Conservative 5; Mismatches 21; Indels 0; Gaps 0;

Qy 1 CSMQAEAGPCLASIPHHWYNNKTKICSEFIYGGCGNNNFQTEAICLVTC 51
Db 7 CSEQAETGPCRAMIPRWYFDVTGKCAFFYGGCGNNNFDTBEYCMAVC 57

RESULT 46

US-08-829-876-139

Sequence 139, Application US/08829876

Patent No. 5962266

GENERAL INFORMATION:

APPLICANT: White, Tyler R.

APPLICANT: Damm, Deborah

APPLICANT: Lesikar, David D.

APPLICANT: McFadden, Kathleen

APPLICANT: Garrick, Brett L.

TITLE OF INVENTION: PROTEASE INHIBITOR PEPTIDES

NUMBER OF SEQUENCES: 228

CORRESPONDENCE ADDRESS:

ADDRESSEE: Foley & Lardner

STREET: 3000 K Street, N.W., Suite 500

CITY: Washington

STATE: D.C.

COUNTRY: USA

ZIP: 20007-5109

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/829,876

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/436,555

FILING DATE: 08-MAY-1995

ATTORNEY/AGENT INFORMATION:

NAME: Pelto, Don J.

REGISTRATION NUMBER: 33,754

REFERENCE/DOCKET NUMBER: 56324/106/SCNO

TELECOMMUNICATION INFORMATION:

TELEPHONE: (202)672-5300

TELEFAX: (202)672-5399

TELEX: 904136

INFORMATION FOR SEQ ID NO: 139:

SEQUENCE CHARACTERISTICS:

LENGTH: 61 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-829-876-139

Query Match 51.3%; Score 155; DB 2; Length 61;

Best Local Similarity 49.0%; Pred. No. 6.7e-13;

Matches 25; Conservative 5; Mismatches 21; Indels 0; Gaps 0;

Qy 1 CSMQAEAGPCLASIPHHWYNNKTKICSEFIYGGCGNNNFQTEAICLVTC 51
Db 7 CSEQAETGPCRAMISHWYFDVTGKCAFFYGGCGNNNFDTBEYCMAVC 57

RESULT 47

US-08-829-876-208

Sequence 208, Application US/08829876

Patent No. 5962266

GENERAL INFORMATION:

APPLICANT: White, Tyler R.

APPLICANT: Damm, Deborah

APPLICANT: Lesikar, David D.

APPLICANT: McFadden, Kathleen

APPLICANT: Garrick, Brett L.

TITLE OF INVENTION: PROTEASE INHIBITOR PEPTIDES

STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-829-876-222

Query Match 51.3%; Score 155; DB 2; Length 61;
Best Local Similarity 49.0%; Pred. No. 6.7e-13;
Matches 25; Conservative 5; Mismatches 21; Indels 0; Gaps 0;

Qy 1 CSMQEGAGPCLASIPHHWYKTKICSEFIYGGCGGNNNNFQTEAICLVTC 51
Db 7 CSEQAETGPCRSIRHWYFDVTEGKCAPPFFYGGCGGNRNNFDTSEYCNVAVC 57

RESULT 50

US-09-234-874A-129
Sequence 129, Application US/09234874A
Patent No. 6376648

GENERAL INFORMATION:
APPLICANT: White, Tyler R.
Damm, Deborah
Lesikar, David D.
McFadden, Kathleen
Garrick, Brett L.

TITLE OF INVENTION: PROTEASE INHIBITOR PEPTIDES
NUMBER OF SEQUENCES: 228
CORRESPONDENCE ADDRESS:

ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
STATE: D.C.
COUNTRY: USA

ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/234,874A
FILING DATE: 11-Jun-2001

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/436,555
FILING DATE: 08-MAY-1995

ATTORNEY/AGENT INFORMATION:
NAME: Bent, Stephen
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 056324/0106
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
TELEX: 904136

INFORMATION FOR SEQ ID NO: 129:

SEQUENCE CHARACTERISTICS:

LENGTH: 61 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 129:

US-09-234-874A-129

Query Match 51.3%; Score 155; DB 3; Length 61;
Best Local Similarity 49.0%; Pred. No. 6.7e-13;
Matches 25; Conservative 5; Mismatches 21; Indels 0; Gaps 0;

Qy 1 CSMQEGAGPCLASIPHHWYKTKICSEFIYGGCGGNNNNFQTEAICLVTC 51
Db 7 CSEQAETGPCRAMIPRWYFDVTEGKCAPPFFYGGCGGNRNNFDTSEYCNVAVC 57

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OM protein - protein search, using sw model

Run on: September 21, 2005, 16:33:14 ; Search time 31.8938 Seconds
(without alignments)
650.835 Million cell updates/sec

Title: US-10-807-204-1_COPY_77_127

Perfect score: 302

Sequence: 1 CSMPOEAGFCLASIPHWYN.....GCGQGNNNNFQTEAICLVTC 51

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1826521 seqs, 407012169 residues

Total number of hits satisfying chosen parameters: 1826521

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 50 summaries

Database : Published Applications AA:*

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11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep.*
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16: /cgn2_6/ptodata/2/pubpaa/US10D_PUBCOMB.pep.*
17: /cgn2_6/ptodata/2/pubpaa/US10E_PUBCOMB.pep.*
18: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep.*
19: /cgn2_6/ptodata/2/pubpaa/US11A_PUBCOMB.pep.*
20: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep.*
21: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*
22: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	302	100.0	106	16 US-10-807-204-2	Sequence 2, Appli
2	302	100.0	131	16 US-10-807-204-1	Sequence 1, Appli
3	302	100.0	131	16 US-10-807-204-12	Sequence 12, Appli
4	292	96.7	131	16 US-10-807-204-15	Sequence 15, Appli
5	224	74.2	136	16 US-10-807-204-16	Sequence 16, Appli
6	219	72.5	51	15 US-10-058-993-118	Sequence 118, Appli
7	219	72.5	58	16 US-10-361-997-5	Sequence 5, Appli
8	219	72.5	58	17 US-10-931-153-21	Sequence 21, Appli
9	219	72.5	102	9 US-09-852-659A-120	Sequence 120, App
10	219	72.5	102	15 US-10-058-993-121	Sequence 121, App
11	219	72.5	117	9 US-09-852-659A-119	Sequence 119, App

12	219	72.5	117	15	US-10-058-993-120	Sequence 120, App
13	219	72.5	133	9	US-09-853-161-75	Sequence 75, Appli
14	219	72.5	133	9	US-09-852-659A-75	Sequence 75, Appli
15	219	72.5	133	9	US-09-852-797-75	Sequence 75, Appli
16	219	72.5	133	15	US-10-058-993-75	Sequence 75, Appli
17	219	72.5	133	16	US-10-807-204-13	Sequence 13, Appli
18	188	62.3	134	16	US-10-807-204-14	Sequence 14, Appli
19	169	56.0	571	14	US-10-369-736-3	Sequence 3, Appli
20	169	56.0	571	14	US-10-369-736-49	Sequence 49, Appli
21	169	56.0	571	14	US-10-369-738-3	Sequence 3, Appli
22	169	56.0	571	14	US-10-369-738-49	Sequence 49, Appli
23	169	56.0	571	19	US-11-028-058-3	Sequence 3, Appli
24	169	56.0	571	19	US-11-028-058-49	Sequence 49, Appli
25	168	55.6	64	10	US-09-856-095-160	Sequence 160, App
26	168	55.6	64	14	US-10-038-722-103	Sequence 103, App
27	168	55.6	64	15	US-10-115-134-17	Sequence 17, Appli
28	167	55.3	58	14	US-10-038-722-5	Sequence 5, Appli
29	166	55.0	67	10	US-09-896-095-147	Sequence 147, App
30	166	55.0	67	14	US-10-038-722-90	Sequence 90, Appli
31	166	55.0	67	15	US-10-115-134-4	Sequence 4, Appli
32	166	55.0	86	9	US-09-910-430-8	Sequence 8, Appli
33	166	55.0	86	14	US-10-165-605A-8	Sequence 8, Appli
34	161	53.3	58	14	US-10-038-722-17	Sequence 17, Appli
35	161	53.3	58	14	US-10-038-722-18	Sequence 18, Appli
36	161	53.3	58	14	US-10-038-722-19	Sequence 19, Appli
37	161	53.3	58	15	US-10-115-134-88	Sequence 88, Appli
38	161	53.3	58	15	US-10-115-134-89	Sequence 89, Appli
39	161	53.3	58	15	US-10-115-134-90	Sequence 90, Appli
40	161	53.3	58	15	US-10-456-986A-42	Sequence 42, Appli
41	161	53.3	58	15	US-10-456-986A-43	Sequence 43, Appli
42	161	53.3	58	15	US-10-456-986A-44	Sequence 44, Appli
43	161	53.3	58	18	US-10-953-902A-42	Sequence 42, Appli
44	161	53.3	58	18	US-10-953-902A-43	Sequence 43, Appli
45	161	53.3	58	18	US-10-953-902A-44	Sequence 44, Appli
46	160	53.0	503	14	US-10-007-280A-233	Sequence 233, App
47	160	53.0	576	9	US-09-794-589-2	Sequence 2, Appli
48	160	53.0	576	14	US-10-315-380-2	Sequence 2, Appli
49	160	53.0	576	14	US-10-369-736-7	Sequence 7, Appli
50	160	53.0	576	14	US-10-369-738-7	Sequence 7, Appli

ALIGNMENTS

RESULT 1
US-10-807-204-2
; Sequence 2, Application US/10807204
; Publication No. US2004022912A1
; GENERAL INFORMATION:
; APPLICANT: Bougueleret, Lydie
; APPLICANT: Bairoch, Amos
; APPLICANT: Niknejad, Anne
; TITLE OF INVENTION: Engineered Human Kunitz-Type Protease
; TITLE OF INVENTION: Inhibitor
; FILE REFERENCE: 54720-8015.US00
; CURRENT APPLICATION NUMBER: US/10/807,204
; PRIOR FILING DATE: 2004-03-22
; PRIOR APPLICATION NUMBER: PCT/EP03/01629
; PRIOR FILING DATE: 2003-02-18
; PRIOR APPLICATION NUMBER: US 60/358,683
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 106
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (1)...(106)
; OTHER INFORMATION: mature form
; FEATURE:
; NAME/KEY: DOMAIN

; LOCATION: (52)...(102)
; OTHER INFORMATION: Kunitz domain predicted by pfscan
; FEATURE:
; NAME/KEY: DISULFID
; LOCATION: (8)...(36)
; OTHER INFORMATION: predicted disulfide bond
; FEATURE:
; NAME/KEY: DISULFID
; LOCATION: (15)...(40)
; OTHER INFORMATION: predicted disulfide bond
; FEATURE:
; NAME/KEY: DISULFID
; LOCATION: (23)...(35)
; OTHER INFORMATION: predicted disulfide bond
; FEATURE:
; NAME/KEY: DISULFID
; LOCATION: (29)...(44)
; OTHER INFORMATION: predicted disulfide bond
; FEATURE:
; NAME/KEY: DISULFID
; LOCATION: (52)...(102)
; OTHER INFORMATION: predicted disulfide bond
; FEATURE:
; NAME/KEY: DISULFID
; LOCATION: (61)...(85)
; OTHER INFORMATION: predicted disulfide bond
; FEATURE:
; NAME/KEY: DISULFID
; LOCATION: (77)...(98)
; OTHER INFORMATION: predicted disulfide bond
US-10-807-204-2

Query Match 100.0%; Score 302; DB 16; Length 106;
Best Local Similarity 100.0%; Pred. No. 3.1e-29;
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CSMPQAGPCLASIPHWYNNKTKICSEFIYGGCGNNNNFQTEAICLVTC 51
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Db 52 CSMPQAGPCLASIPHWYNNKTKICSEFIYGGCGNNNNFQTEAICLVTC 102
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RESULT 2
US-10-807-204-1
; Sequence 1, Application US/10807204
; Publication No. US20040229312A1
; GENERAL INFORMATION:
; APPLICANT: Bougueleret, Lydie
; APPLICANT: Bairoch, Amos
; APPLICANT: Niknejad, Anne
; TITLE OF INVENTION: Engineered Human Kunitz-Type Protease
; TITLE OF INVENTION: Inhibitor
; FILE REFERENCE: 54720-8015.US00
; CURRENT APPLICATION NUMBER: US/10/807,204
; CURRENT FILING DATE: 2004-03-22
; PRIOR APPLICATION NUMBER: PCT/EP03/01629
; PRIOR FILING DATE: 2003-02-18
; PRIOR APPLICATION NUMBER: US 60/358,683
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 131
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (1)...(131)
; OTHER INFORMATION: eppin-like precursor
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: (1)...(25)
; OTHER INFORMATION: predicted by SignalP 2.0
; FEATURE:

; NAME/KEY: PEPTIDE
; LOCATION: (26)...(131)
; OTHER INFORMATION: mature peptide
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (77)...(127)
; OTHER INFORMATION: Kunitz domain predicted by pfscan
; FEATURE:
; NAME/KEY: DISULFID
; LOCATION: (33)...(61)
; OTHER INFORMATION: predicted disulfide bond
; FEATURE:
; NAME/KEY: DISULFID
; LOCATION: (40)...(65)
; OTHER INFORMATION: predicted disulfide bond
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; NAME/KEY: DISULFID
; LOCATION: (48)...(60)
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; NAME/KEY: DISULFID
; LOCATION: (54)...(69)
; OTHER INFORMATION: predicted disulfide bond
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; LOCATION: (77)...(127)
; OTHER INFORMATION: predicted disulfide bond
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; LOCATION: (86)...(110)
; OTHER INFORMATION: predicted disulfide bond
; FEATURE:
; NAME/KEY: DISULFID
; LOCATION: (102)...(123)
; OTHER INFORMATION: predicted disulfide bond
US-10-807-204-1

Query Match 100.0%; Score 302; DB 16; Length 131;
Best Local Similarity 100.0%; Pred. No. 3.8e-29;
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CSMPQAGPCLASIPHWYNNKTKICSEFIYGGCGNNNNFQTEAICLVTC 51
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Db 77 CSMPQAGPCLASIPHWYNNKTKICSEFIYGGCGNNNNFQTEAICLVTC 127
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RESULT 3
US-10-807-204-12
; Sequence 12, Application US/10807204
; Publication No. US20040229312A1
; GENERAL INFORMATION:
; APPLICANT: Bougueleret, Lydie
; APPLICANT: Bairoch, Amos
; APPLICANT: Niknejad, Anne
; TITLE OF INVENTION: Engineered Human Kunitz-Type Protease
; TITLE OF INVENTION: Inhibitor
; FILE REFERENCE: 54720-8015.US00
; CURRENT APPLICATION NUMBER: US/10/807,204
; CURRENT FILING DATE: 2004-03-22
; PRIOR APPLICATION NUMBER: PCT/EP03/01629
; PRIOR FILING DATE: 2003-02-18
; PRIOR APPLICATION NUMBER: US 60/358,683
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12
; LENGTH: 131
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-807-204-12

Query Match 100.0%; Score 302; DB 16; Length 131;
Best Local Similarity 100.0%; Pred. No. 3.8e-29;

Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CSMQAEAGPCLASIPHHWYNNKTKICSEFIYGGCGQNNNNFQTEAICLVTC 51
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DB 77 CSMQAEAGPCLASIPHHWYNNKTKICSEFIYGGCGQNNNNFQTEAICLVTC 127
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RESULT 4

US-10-807-204-15
; Sequence 15, Application US/10807204
; Publication No. US20040229312A1
; GENERAL INFORMATION:
; APPLICANT: Bougueleret, Lydie
; APPLICANT: Bairoch, Anos
; APPLICANT: Niknejad, Anne
; TITLE OF INVENTION: Engineered Human Kunitz-Type Protease
; TITLE OF INVENTION: Inhibitor
; FILE REFERENCE: 54720-8015.US00
; CURRENT APPLICATION NUMBER: US/10/807,204
; CURRENT FILING DATE: 2004-03-22
; PRIOR APPLICATION NUMBER: PCT/EP03/01629
; PRIOR FILING DATE: 2003-02-18
; PRIOR APPLICATION NUMBER: US 60/358,683
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15
; LENGTH: 131
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-807-204-15

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Best Local Similarity 98.0%; Pred. No. 6.5e-28;
Matches 50; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CSMQAEAGPCLASIPHHWYNNKTKICSEFIYGGCGQNNNNFQTEAICLVTC 51
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DB 77 CSMQAEAGPCLASIPHHWYNNKTKICSEFIYGGCGQNNNNFQTEAICLVTC 127
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RESULT 5

US-10-807-204-16
; Sequence 16, Application US/10807204
; Publication No. US20040229312A1
; GENERAL INFORMATION:
; APPLICANT: Bougueleret, Lydie
; APPLICANT: Bairoch, Anos
; APPLICANT: Niknejad, Anne
; TITLE OF INVENTION: Engineered Human Kunitz-Type Protease
; TITLE OF INVENTION: Inhibitor
; FILE REFERENCE: 54720-8015.US00
; CURRENT APPLICATION NUMBER: US/10/807,204
; CURRENT FILING DATE: 2004-03-22
; PRIOR APPLICATION NUMBER: PCT/EP03/01629
; PRIOR FILING DATE: 2003-02-18
; PRIOR APPLICATION NUMBER: US 60/358,683
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 16
; LENGTH: 136
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-807-204-16

Query Match 74.2%; Score 224; DB 16; Length 136;
Best Local Similarity 66.7%; Pred. No. 1.5e-19;
Matches 34; Conservative 8; Mismatches 9; Indels 0; Gaps 0;

QY 1 CSMQAEAGPCLASIPHHWYNNKTKICSEFIYGGCGQNNNNFQTEAICLVTC 51
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DB 77 CSLPQDPGCLAYLPWWYNNQETDLCTEFYGGCGQNNPNNFPSEGICTVVC 127
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RESULT 6

US-10-058-993-118
; Sequence 118, Application US/10058993
; Publication No. US20030225009A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 28 Human Secreted Proteins
; FILE REFERENCE: P2003P5
; CURRENT APPLICATION NUMBER: US/10/058,993
; CURRENT FILING DATE: 2002-01-30
; PRIOR APPLICATION NUMBER: 09/852,659
; PRIOR FILING DATE: 2001-05-11
; PRIOR APPLICATION NUMBER: 09/852,797
; PRIOR FILING DATE: 2001-05-11
; PRIOR APPLICATION NUMBER: 09/853,161
; PRIOR FILING DATE: 2001-05-11
; PRIOR APPLICATION NUMBER: 60/265,583
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: 09/152,060
; PRIOR FILING DATE: 1998-09-11
; PRIOR APPLICATION NUMBER: PCT/US98/04858
; PRIOR FILING DATE: 1998-03-12
; PRIOR APPLICATION NUMBER: 60/068,368
; PRIOR FILING DATE: 1997-12-19
; PRIOR APPLICATION NUMBER: 60/057,765
; PRIOR FILING DATE: 1997-09-05
; PRIOR APPLICATION NUMBER: 60/048,970
; PRIOR FILING DATE: 1997-06-05
; PRIOR APPLICATION NUMBER: 60/050,934
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/048,100
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/048,189
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/048,357
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/040,710
; PRIOR FILING DATE: 1997-03-14
; PRIOR APPLICATION NUMBER: 60/040,762
; PRIOR FILING DATE: 1997-03-14
; NUMBER OF SEQ ID NOS: 122
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 118
; LENGTH: 51
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-058-993-118

Query Match 72.5%; Score 219; DB 15; Length 51;
Best Local Similarity 68.6%; Pred. No. 2.5e-19;
Matches 35; Conservative 5; Mismatches 11; Indels 0; Gaps 0;

QY 1 CSMQAEAGPCLASIPHHWYNNKTKICSEFIYGGCGQNNNNFQTEAICLVTC 51
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DB 1 CEMPKEGTGCLAYFLHWYDKDNTCSMFVYGGCGQNNNNFQSKANCLNTC 51
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RESULT 7

US-10-361-997-5
; Sequence 5, Application US/10361997
; Publication No. US20040171794A1
; GENERAL INFORMATION:
; APPLICANT: Ladner, Robert Charles
; APPLICANT: Ley, Arthur C.
; TITLE OF INVENTION: KUNITZ DOMAIN PEPTIDES
; FILE REFERENCE: 3421.1015-000
; CURRENT APPLICATION NUMBER: US/10/361,997
; CURRENT FILING DATE: 2003-02-07
; PRIOR APPLICATION NUMBER: US 60/355,547
; PRIOR FILING DATE: 2002-02-07
; NUMBER OF SEQ ID NOS: 84

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; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 58
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-361-997-5

Query Match          72.5%; Score 219; DB 16; Length 58;
Best Local Similarity 68.6%; Pred. No. 2.8e-19;
Matches 35; Conservative 5; Mismatches 11; Indels 0; Gaps 0;

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Db 5 CEMPKEIGPCLAYFLHWWYDKKNTCSMFVYGGCGGNNNNFQSKANCLNTC 55

RESULT 8
US-10-931-153-21
; Sequence 21, Application US/10931153
; Publication No. US20050089515A1
; GENERAL INFORMATION:
; APPLICANT: Ley, Arthur C.
; APPLICANT: Sato, Aaron K.
; APPLICANT: Ladner, Robert C.
; APPLICANT: Stochl, Mark
; TITLE OF INVENTION: POLY-PEGYLATED PROTEASE INHIBITORS
; FILE REFERENCE: 10280-119001
; CURRENT APPLICATION NUMBER: US/10/931,153
; CURRENT FILING DATE: 2004-08-30
; PRIOR APPLICATION NUMBER: US 60/498,845
; PRIOR FILING DATE: 2003-08-29
; PRIOR APPLICATION NUMBER: US 60/598,967
; PRIOR FILING DATE: 2004-08-04
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 21
; LENGTH: 58
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-931-153-21

Query Match          72.5%; Score 219; DB 17; Length 58;
Best Local Similarity 68.6%; Pred. No. 2.8e-19;
Matches 35; Conservative 5; Mismatches 11; Indels 0; Gaps 0;

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Db 5 CEMPKEIGPCLAYFLHWWYDKKNTCSMFVYGGCGGNNNNFQSKANCLNTC 55

RESULT 9
US-09-852-659A-120
; Sequence 120, Application US/09852659A
; Patent No. US2002007287A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 28 Human Secreted Proteins
; FILE REFERENCE: P2003P4
; CURRENT APPLICATION NUMBER: US/09/852,659A
; CURRENT FILING DATE: 2001-05-11
; PRIOR APPLICATION NUMBER: 60/265,583
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: 09/152,060
; PRIOR FILING DATE: 1998-09-11
; PRIOR APPLICATION NUMBER: PCT/US98/04858
; PRIOR FILING DATE: 1998-03-12
; PRIOR APPLICATION NUMBER: 60/040,762
; PRIOR FILING DATE: 1997-03-14
; PRIOR APPLICATION NUMBER: 60/040,710
; PRIOR FILING DATE: 1997-03-14
; PRIOR APPLICATION NUMBER: 60/050,934
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/048,100
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/048,189
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/048,357
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/040,710
; PRIOR FILING DATE: 1997-03-14
; PRIOR APPLICATION NUMBER: 60/040,762
; PRIOR FILING DATE: 1997-03-14
; NUMBER OF SEQ ID NOS: 122
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 121
; LENGTH: 102
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-852-659A-120

Query Match          72.5%; Score 219; DB 9; Length 102;
Best Local Similarity 68.6%; Pred. No. 4.8e-19;
Matches 35; Conservative 5; Mismatches 11; Indels 0; Gaps 0;

Qy 1 CSMPOEAGPCLASIPHHWYNNKTKICSEFIYGGCGGNNNNFQTEAICLVTC 51
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Db 46 CEMPKEIGPCLAYFLHWWYDKKNTCSMFVYGGCGGNNNNFQSKANCLNTC 96

RESULT 10
US-10-058-993-121
; Sequence 121, Application US/10058993
; Publication No. US20030225009A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 28 Human Secreted Proteins
; FILE REFERENCE: P2003P5
; CURRENT APPLICATION NUMBER: US/10/058,993
; CURRENT FILING DATE: 2002-01-30
; PRIOR APPLICATION NUMBER: 09/852,659
; PRIOR FILING DATE: 2001-05-11
; PRIOR APPLICATION NUMBER: 09/852,797
; PRIOR FILING DATE: 2001-05-11
; PRIOR APPLICATION NUMBER: 09/853,161
; PRIOR FILING DATE: 2001-05-11
; PRIOR APPLICATION NUMBER: 60/265,583
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: 09/152,060
; PRIOR FILING DATE: 1998-09-11
; PRIOR APPLICATION NUMBER: PCT/US98/04858
; PRIOR FILING DATE: 1998-03-12
; PRIOR APPLICATION NUMBER: 60/068,368
; PRIOR FILING DATE: 1997-12-19
; PRIOR APPLICATION NUMBER: 60/057,765
; PRIOR FILING DATE: 1997-09-05
; PRIOR APPLICATION NUMBER: 60/048,970
; PRIOR FILING DATE: 1997-06-05
; PRIOR APPLICATION NUMBER: 60/050,934
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/048,100
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/048,189
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/048,357
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/040,710
; PRIOR FILING DATE: 1997-03-14
; PRIOR APPLICATION NUMBER: 60/040,762
; PRIOR FILING DATE: 1997-03-14
; NUMBER OF SEQ ID NOS: 122
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 121
; LENGTH: 102
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-852-659A-120
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; ORGANISM: Homo sapiens
US-10-058-993-121

Query Match          72.5%; Score 219; DB 15; Length 102;
Best Local Similarity 68.6%; Pred. No. 4.8e-19;
Matches 35; Conservative 5; Mismatches 11; Indels 0; Gaps 0;

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Db 46 CEMPKEGTGCLAYFLHWYDKDNTCSMFVYGGCGGNNNNFQSKANCLNTC 96

RESULT 11
US-09-852-659A-119
; Sequence 119, Application US/09852659A
; Patent No. US20020077287A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 28 Human Secreted Proteins
; FILE REFERENCE: PZ003P4
; CURRENT APPLICATION NUMBER: US/09/852,659A
; CURRENT FILING DATE: 2001-05-11
; PRIOR APPLICATION NUMBER: 60/265,583
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: 09/152,060
; PRIOR FILING DATE: 1998-09-11
; PRIOR APPLICATION NUMBER: PCT/US98/04858
; PRIOR FILING DATE: 1998-03-12
; PRIOR APPLICATION NUMBER: 60/048,100
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/048,357
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/048,189
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/040,710
; PRIOR FILING DATE: 1997-03-14
; PRIOR APPLICATION NUMBER: 60/050,934
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/048,100
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/048,762
; PRIOR FILING DATE: 1997-03-12
; PRIOR APPLICATION NUMBER: 60/048,970
; PRIOR FILING DATE: 1997-03-14
; PRIOR APPLICATION NUMBER: 60/040,710
; PRIOR FILING DATE: 1997-03-14
; PRIOR APPLICATION NUMBER: 60/040,762
; PRIOR FILING DATE: 1997-03-14
; NUMBER OF SEQ ID NOS: 121
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 119
; LENGTH: 117
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-852-659A-119

Query Match          72.5%; Score 219; DB 9; Length 117;
Best Local Similarity 68.6%; Pred. No. 5.5e-19;
Matches 35; Conservative 5; Mismatches 11; Indels 0; Gaps 0;

QY 1 CSMPOEAGPCLASIPHHWYNNKTKICSEFIYGGCGGNNNNFQTEAICLVTC 51
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 61 CEMPKEGTGCLAYFLHWYDKDNTCSMFVYGGCGGNNNNFQSKANCLNTC 111

RESULT 12
US-10-058-993-120
; Sequence 120, Application US/10058993
; Publication No. US20030225009A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 28 Human Secreted Proteins
; FILE REFERENCE: PZ003P5
; CURRENT APPLICATION NUMBER: US/10/058,993
; CURRENT FILING DATE: 2002-01-30
```

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; PRIOR APPLICATION NUMBER: 09/852,659
; PRIOR FILING DATE: 2001-05-11
; PRIOR APPLICATION NUMBER: 09/852,797
; PRIOR FILING DATE: 2001-05-11
; PRIOR APPLICATION NUMBER: 09/853,161
; PRIOR FILING DATE: 2001-05-11
; PRIOR APPLICATION NUMBER: 60/265,583
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: 09/152,060
; PRIOR FILING DATE: 1998-09-11
; PRIOR APPLICATION NUMBER: PCT/US98/04858
; PRIOR FILING DATE: 1998-03-12
; PRIOR APPLICATION NUMBER: 60/068,368
; PRIOR FILING DATE: 1997-12-19
; PRIOR APPLICATION NUMBER: 60/057,765
; PRIOR FILING DATE: 1997-09-05
; PRIOR APPLICATION NUMBER: 60/048,970
; PRIOR FILING DATE: 1997-06-05
; PRIOR APPLICATION NUMBER: 60/050,934
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/048,100
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/048,189
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/048,357
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/040,710
; PRIOR FILING DATE: 1997-03-14
; PRIOR APPLICATION NUMBER: 60/040,762
; PRIOR FILING DATE: 1997-03-14
; NUMBER OF SEQ ID NOS: 122
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 120
; LENGTH: 117
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-058-993-120

Query Match          72.5%; Score 219; DB 15; Length 117;
Best Local Similarity 68.6%; Pred. No. 5.5e-19;
Matches 35; Conservative 5; Mismatches 11; Indels 0; Gaps 0;

QY 1 CSMPOEAGPCLASIPHHWYNNKTKICSEFIYGGCGGNNNNFQTEAICLVTC 51
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 61 CEMPKEGTGCLAYFLHWYDKDNTCSMFVYGGCGGNNNNFQSKANCLNTC 111

RESULT 13
US-09-853-161-75
; Sequence 75, Application US/09853161
; Patent No. US20020076756A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 28 Human Secreted Proteins
; FILE REFERENCE: PZ003P3
; CURRENT APPLICATION NUMBER: US/09/853,161
; CURRENT FILING DATE: 2001-05-11
; PRIOR APPLICATION NUMBER: 60/265,583
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: 09/152,060
; PRIOR FILING DATE: 1998-09-11
; PRIOR APPLICATION NUMBER: PCT/US98/04858
; PRIOR FILING DATE: 1998-03-12
; PRIOR APPLICATION NUMBER: 60/040,762
; PRIOR FILING DATE: 1997-03-14
; PRIOR APPLICATION NUMBER: 60/040,710
; PRIOR FILING DATE: 1997-03-14
; PRIOR APPLICATION NUMBER: 60/050,934
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/048,100
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/048,357
; PRIOR FILING DATE: 1997-05-30
```

1 PRIOR APPLICATION NUMBER: 60/048,189
2 PRIOR FILING DATE: 1997-05-30
3 PRIOR APPLICATION NUMBER: 60/057,765
4 PRIOR FILING DATE: 1997-09-05
5 PRIOR APPLICATION NUMBER: 60/048,970
6 PRIOR FILING DATE: 1997-06-06
7 PRIOR APPLICATION NUMBER: 60/068,368
8 PRIOR FILING DATE: 1997-12-19
9 NUMBER OF SEQ ID NOS: 118
10 SOFTWARE: PatentIn Ver. 2.0
11 SEQ ID NO 75
12 LENGTH: 133
13 TYPE: PRT
14 ORGANISM: Homo sapiens
15 US-09-853-161-75

Query Match 72.5%; Score 219; DB 9; Length 133;
Best Local Similarity 68.6%; Pred. No. 6.2e-19;
Matches 35; Conservative 5; Mismatches 11; Indels 0; Gaps 0;

Qy 1 CSMPOEAGPCLASIPHHWYKDKTCSMFYVGGCGNNNFQSKANCLNTC 51
Db 77 CEMPKEIGPCLAYFLHWWYKDKTCSMFYVGGCGNNNFQSKANCLNTC 127

RESULT 14
US-09-852-659A-75
1 Sequence 75, Application US/09852659A
2 Patent No. US2002007287A1
3 GENERAL INFORMATION:
4 APPLICANT: Rosen et al.
5 TITLE OF INVENTION: 28 Human Secreted Proteins
6 FILE REFERENCE: P2003P4
7 CURRENT APPLICATION NUMBER: US/09/852,659A
8 CURRENT FILING DATE: 2001-05-11
9 PRIOR APPLICATION NUMBER: 60/265,583
10 PRIOR FILING DATE: 2001-02-02
11 PRIOR APPLICATION NUMBER: 09/152,060
12 PRIOR FILING DATE: 1998-09-11
13 PRIOR APPLICATION NUMBER: PCT/US98/04858
14 PRIOR FILING DATE: 1998-03-12
15 PRIOR APPLICATION NUMBER: 60/040,762
16 PRIOR FILING DATE: 1997-03-14
17 PRIOR APPLICATION NUMBER: 60/040,710
18 PRIOR FILING DATE: 1997-03-14
19 PRIOR APPLICATION NUMBER: 60/050,934
20 PRIOR FILING DATE: 1997-05-30
21 PRIOR APPLICATION NUMBER: 60/048,100
22 PRIOR FILING DATE: 1997-05-30
23 PRIOR APPLICATION NUMBER: 60/048,357
24 PRIOR FILING DATE: 1997-05-30
25 PRIOR APPLICATION NUMBER: 60/048,189
26 PRIOR FILING DATE: 1997-05-30
27 PRIOR APPLICATION NUMBER: 60/057,765
28 PRIOR FILING DATE: 1997-09-05
29 PRIOR APPLICATION NUMBER: 60/048,970
30 PRIOR FILING DATE: 1997-06-06
31 PRIOR APPLICATION NUMBER: 60/068,368
32 NUMBER OF SEQ ID NOS: 121
33 SOFTWARE: PatentIn Ver. 2.0
34 SEQ ID NO 75
35 LENGTH: 133
36 TYPE: PRT
37 ORGANISM: Homo sapiens
38 US-09-852-659A-75

Query Match 72.5%; Score 219; DB 9; Length 133;
Best Local Similarity 68.6%; Pred. No. 6.2e-19;
Matches 35; Conservative 5; Mismatches 11; Indels 0; Gaps 0;

Qy 1 CSMPOEAGPCLASIPHHWYKDKTCSMFYVGGCGNNNFQTEAICLVTC 51
Db 77 CEMPKEIGPCLAYFLHWWYKDKTCSMFYVGGCGNNNFQSKANCLNTC 127

Db 77 CEMPKEIGPCLAYFLHWWYKDKTCSMFYVGGCGNNNFQSKANCLNTC 127

RESULT 15
US-09-852-797-75
1 Sequence 75, Application US/09852797
2 Patent No. US20020172994A1
3 GENERAL INFORMATION:
4 APPLICANT: Rosen et al.
5 TITLE OF INVENTION: 28 Human Secreted Proteins
6 FILE REFERENCE: P2003P2
7 CURRENT APPLICATION NUMBER: US/09/852,797
8 CURRENT FILING DATE: 2001-05-11
9 PRIOR APPLICATION NUMBER: 60/265,583
10 PRIOR FILING DATE: 2001-02-02
11 PRIOR APPLICATION NUMBER: 09/152,060
12 PRIOR FILING DATE: 1998-09-11
13 PRIOR APPLICATION NUMBER: PCT/US98/04858
14 PRIOR FILING DATE: 1998-03-12
15 PRIOR APPLICATION NUMBER: 60/040,762
16 PRIOR FILING DATE: 1997-03-14
17 PRIOR APPLICATION NUMBER: 60/040,710
18 PRIOR FILING DATE: 1997-03-14
19 PRIOR APPLICATION NUMBER: 60/050,934
20 PRIOR FILING DATE: 1997-05-30
21 PRIOR APPLICATION NUMBER: 60/048,100
22 PRIOR FILING DATE: 1997-05-30
23 PRIOR APPLICATION NUMBER: 60/048,357
24 PRIOR FILING DATE: 1997-05-30
25 PRIOR APPLICATION NUMBER: 60/048,189
26 PRIOR FILING DATE: 1997-05-30
27 PRIOR APPLICATION NUMBER: 60/057,765
28 PRIOR FILING DATE: 1997-09-05
29 PRIOR APPLICATION NUMBER: 60/048,970
30 PRIOR FILING DATE: 1997-06-06
31 PRIOR APPLICATION NUMBER: 60/068,368
32 NUMBER OF SEQ ID NOS: 118
33 SOFTWARE: PatentIn Ver. 2.0
34 SEQ ID NO 75
35 LENGTH: 133
36 TYPE: PRT
37 ORGANISM: Homo sapiens
38 US-09-852-797-75

Query Match 72.5%; Score 219; DB 9; Length 133;
Best Local Similarity 68.6%; Pred. No. 6.2e-19;
Matches 35; Conservative 5; Mismatches 11; Indels 0; Gaps 0;

Qy 1 CSMPOEAGPCLASIPHHWYKDKTCSMFYVGGCGNNNFQTEAICLVTC 51
Db 77 CEMPKEIGPCLAYFLHWWYKDKTCSMFYVGGCGNNNFQSKANCLNTC 127

RESULT 16
US-10-058-993-75
1 Sequence 75, Application US/10058993
2 Publication No. US20030225009A1
3 GENERAL INFORMATION:
4 APPLICANT: Rosen et al.
5 TITLE OF INVENTION: 28 Human Secreted Proteins
6 FILE REFERENCE: P2003P5
7 CURRENT APPLICATION NUMBER: US/10/058,993
8 CURRENT FILING DATE: 2002-01-30
9 PRIOR APPLICATION NUMBER: 09/852,659
10 PRIOR FILING DATE: 2001-05-11
11 PRIOR APPLICATION NUMBER: 09/852,797
12 PRIOR FILING DATE: 2001-05-11
13 PRIOR APPLICATION NUMBER: 09/853,161
14 PRIOR FILING DATE: 2001-05-11
15 PRIOR APPLICATION NUMBER: 60/265,583
16 PRIOR FILING DATE: 2001-02-02
17 PRIOR APPLICATION NUMBER: 09/152,060

; PRIOR FILING DATE: 1998-09-11
; PRIOR APPLICATION NUMBER: PCT/US98/04858
; PRIOR FILING DATE: 1998-03-12
; PRIOR APPLICATION NUMBER: 60/068,368
; PRIOR FILING DATE: 1997-12-19
; PRIOR APPLICATION NUMBER: 60/057,765
; PRIOR FILING DATE: 1997-09-05
; PRIOR APPLICATION NUMBER: 60/048,970
; PRIOR FILING DATE: 1997-06-05
; PRIOR APPLICATION NUMBER: 60/050,934
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/048,100
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/048,189
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/048,357
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/040,710
; PRIOR FILING DATE: 1997-03-14
; PRIOR APPLICATION NUMBER: 60/040,762
; PRIOR FILING DATE: 1997-03-14
; NUMBER OF SEQ ID NOS: 122
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 75
; LENGTH: 133
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-058-993-75

Query Match 72.5%; Score 219; DB 15; Length 133;
Best Local Similarity 68.6%; Pred. No. 6.2e-19;
Matches 35; Conservative 5; Mismatches 11; Indels 0; Gaps 0;

QY 1 CSMPOEAGPCLASIPHHWYNNKTKICSEFYGGCGGNNNNFQTEAICLVTC 51
DB 77 CEMPKEGPCLAYFLHWYDKDKNTCSMFVYGGCGGNNNNFQSKANCLNTC 127

RESULT 17
US-10-807-204-13
; Sequence 13, Application US/10807204
; Publication No. US20040229312A1
; GENERAL INFORMATION:
; APPLICANT: Bougueleret, Lydie
; APPLICANT: Bairoch, Amos
; APPLICANT: Niknejad, Anne
; TITLE OF INVENTION: Engineered Human Kunitz-Type Protease
; TITLE OF INVENTION: Inhibitor
; FILE REFERENCE: 54720-8015.US00
; CURRENT APPLICATION NUMBER: US/10/807,204
; CURRENT FILING DATE: 2004-03-22
; PRIOR APPLICATION NUMBER: PCT/EP03/01629
; PRIOR FILING DATE: 2003-02-18
; PRIOR APPLICATION NUMBER: US 60/358,683
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13
; LENGTH: 133
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-807-204-13

Query Match 72.5%; Score 219; DB 16; Length 133;
Best Local Similarity 68.6%; Pred. No. 6.2e-19;
Matches 35; Conservative 5; Mismatches 11; Indels 0; Gaps 0;

QY 1 CSMPOEAGPCLASIPHHWYNNKTKICSEFYGGCGGNNNNFQTEAICLVTC 51
DB 77 CEMPKEGPCLAYFLHWYDKDKNTCSMFVYGGCGGNNNNFQSKANCLNTC 127

RESULT 18

US-10-807-204-14
; Sequence 14, Application US/10807204
; Publication No. US20040229312A1
; GENERAL INFORMATION:
; APPLICANT: Bougueleret, Lydie
; APPLICANT: Bairoch, Amos
; APPLICANT: Niknejad, Anne
; TITLE OF INVENTION: Engineered Human Kunitz-Type Protease
; TITLE OF INVENTION: Inhibitor
; FILE REFERENCE: 54720-8015.US00
; CURRENT APPLICATION NUMBER: US/10/807,204
; CURRENT FILING DATE: 2004-03-22
; PRIOR APPLICATION NUMBER: PCT/EP03/01629
; PRIOR FILING DATE: 2003-02-18
; PRIOR APPLICATION NUMBER: US 60/358,683
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14
; LENGTH: 134
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-807-204-14

Query Match 62.3%; Score 188; DB 16; Length 134;
Best Local Similarity 54.9%; Pred. No. 4e-15;
Matches 28; Conservative 10; Mismatches 13; Indels 0; Gaps 0;

QY 1 CSMPOEAGPCLASIPHHWYNNKTKICSEFYGGCGGNNNNFQTEAICLVTC 51
DB 77 CSLPKDSGVCYAFYFRWFWNKENSCTQVFIYGGCGGNNNNFQSQICQNAC 127

RESULT 19
US-10-369-736-3
; Sequence 3, Application US/10369736
; Publication No. US20030162714A1
; GENERAL INFORMATION:
; APPLICANT: HILL, JENNIFER J.
; APPLICANT: WOLFMAN, NEIL M.
; TITLE OF INVENTION: FOLLISTATIN DOMAIN CONTAINING PROTEINS
; FILE REFERENCE: 08702.0015-00
; CURRENT APPLICATION NUMBER: US/10/369,736
; CURRENT FILING DATE: 2003-02-21
; PRIOR APPLICATION NUMBER: 60/357,846
; PRIOR FILING DATE: 2002-02-21
; PRIOR APPLICATION NUMBER: 60/434,645
; PRIOR FILING DATE: 2002-12-20
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 571
; TYPE: PRT
; ORGANISM: Mus sp.
US-10-369-736-3

Query Match 56.0%; Score 169; DB 14; Length 571;
Best Local Similarity 49.0%; Pred. No. 3.6e-12;
Matches 25; Conservative 9; Mismatches 17; Indels 0; Gaps 0;

QY 1 CSMPOEAGPCLASIPHHWYNNKTKICSEFYGGCGGNNNNFQTEAICLVTC 51
DB 381 CSLPALQGPCKAYVPRWAYNSQTGLCQSFVYGGCGGNNNNFESREACEESC 431

RESULT 20
US-10-369-736-49
; Sequence 49, Application US/10369736
; Publication No. US20030162714A1
; GENERAL INFORMATION:
; APPLICANT: HILL, JENNIFER J.
; APPLICANT: WOLFMAN, NEIL M.
; TITLE OF INVENTION: FOLLISTATIN DOMAIN CONTAINING PROTEINS

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; FILE REFERENCE: 08702.0015-00
; CURRENT APPLICATION NUMBER: US/10/369,736
; CURRENT FILING DATE: 2003-02-21
; PRIOR APPLICATION NUMBER: 60/357,846
; PRIOR FILING DATE: 2002-02-21
; PRIOR APPLICATION NUMBER: 60/434,645
; PRIOR FILING DATE: 2002-12-20
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 49
; LENGTH: 571
; TYPE: PRT
; ORGANISM: Mus sp.
US-10-369-736-49

Query Match          56.0%; Score 169; DB 14; Length 571;
Best Local Similarity 49.0%; Pred. No. 3.6e-12;
Matches 25; Conservative 9; Mismatches 17; Indels 0; Gaps 0;

Qy 1 CSMPOEAGPCLASIPHHWYNNKTKICSEFYGGCGGNNNFQTEAICLVTC 51
Db 381 CSLPALQGPCKAYVPRWAYNSQTGLCQSFVYGGCGGNNNFESREACEESC 431

RESULT 21
US-10-369-738-3
; Sequence 3, Application US/10369738
; Publication No. US20030180306A1
; GENERAL INFORMATION:
; APPLICANT: HILL, JENNIFER J.
; APPLICANT: WOLFMAN, NEIL M.
; TITLE OF INVENTION: FOLLISTATIN DOMAIN CONTAINING PROTEINS
; FILE REFERENCE: 08702.0014-00
; CURRENT APPLICATION NUMBER: US/10/369,738
; CURRENT FILING DATE: 2003-02-21
; PRIOR APPLICATION NUMBER: 60/357,846
; PRIOR FILING DATE: 2002-02-21
; PRIOR APPLICATION NUMBER: 60/434,645
; PRIOR FILING DATE: 2002-12-20
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 571
; TYPE: PRT
; ORGANISM: Mus sp.
US-10-369-738-3

Query Match          56.0%; Score 169; DB 14; Length 571;
Best Local Similarity 49.0%; Pred. No. 3.6e-12;
Matches 25; Conservative 9; Mismatches 17; Indels 0; Gaps 0;

Qy 1 CSMPOEAGPCLASIPHHWYNNKTKICSEFYGGCGGNNNFQTEAICLVTC 51
Db 381 CSLPALQGPCKAYVPRWAYNSQTGLCQSFVYGGCGGNNNFESREACEESC 431

RESULT 22
US-10-369-738-49
; Sequence 49, Application US/10369738
; Publication No. US20030180306A1
; GENERAL INFORMATION:
; APPLICANT: HILL, JENNIFER J.
; APPLICANT: WOLFMAN, NEIL M.
; TITLE OF INVENTION: FOLLISTATIN DOMAIN CONTAINING PROTEINS
; FILE REFERENCE: 08702.0014-00
; CURRENT APPLICATION NUMBER: US/10/369,738
; CURRENT FILING DATE: 2003-02-21
; PRIOR APPLICATION NUMBER: 60/357,846
; PRIOR FILING DATE: 2002-02-21
; PRIOR APPLICATION NUMBER: 60/434,645
; PRIOR FILING DATE: 2002-12-20
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: PatentIn Ver. 2.1
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; SEQ ID NO 49
; LENGTH: 571
; TYPE: PRT
; ORGANISM: Mus sp.
US-10-369-738-49

Query Match          56.0%; Score 169; DB 14; Length 571;
Best Local Similarity 49.0%; Pred. No. 3.6e-12;
Matches 25; Conservative 9; Mismatches 17; Indels 0; Gaps 0;

Qy 1 CSMPOEAGPCLASIPHHWYNNKTKICSEFYGGCGGNNNFQTEAICLVTC 51
Db 381 CSLPALQGPCKAYVPRWAYNSQTGLCQSFVYGGCGGNNNFESREACEESC 431

RESULT 23
US-11-028-058-3
; Sequence 3, Application US/11028058
; Publication No. US20050106154A1
; GENERAL INFORMATION:
; APPLICANT: HILL, JENNIFER J.
; APPLICANT: WOLFMAN, NEIL M.
; TITLE OF INVENTION: FOLLISTATIN DOMAIN CONTAINING PROTEINS
; FILE REFERENCE: 08702.0015-00
; CURRENT APPLICATION NUMBER: US/11/028,058
; CURRENT FILING DATE: 2005-01-04
; PRIOR APPLICATION NUMBER: US/10/369,736
; PRIOR FILING DATE: 2003-02-21
; PRIOR APPLICATION NUMBER: 60/357,846
; PRIOR FILING DATE: 2002-02-21
; PRIOR APPLICATION NUMBER: 60/434,645
; PRIOR FILING DATE: 2002-12-20
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 571
; TYPE: PRT
; ORGANISM: Mus sp.
US-11-028-058-3

Query Match          56.0%; Score 169; DB 19; Length 571;
Best Local Similarity 49.0%; Pred. No. 3.6e-12;
Matches 25; Conservative 9; Mismatches 17; Indels 0; Gaps 0;

Qy 1 CSMPOEAGPCLASIPHHWYNNKTKICSEFYGGCGGNNNFQTEAICLVTC 51
Db 381 CSLPALQGPCKAYVPRWAYNSQTGLCQSFVYGGCGGNNNFESREACEESC 431

RESULT 24
US-11-028-058-49
; Sequence 49, Application US/11028058
; Publication No. US20050106154A1
; GENERAL INFORMATION:
; APPLICANT: HILL, JENNIFER J.
; APPLICANT: WOLFMAN, NEIL M.
; TITLE OF INVENTION: FOLLISTATIN DOMAIN CONTAINING PROTEINS
; FILE REFERENCE: 08702.0015-00
; CURRENT APPLICATION NUMBER: US/11/028,058
; CURRENT FILING DATE: 2005-01-04
; PRIOR APPLICATION NUMBER: US/10/369,736
; PRIOR FILING DATE: 2003-02-21
; PRIOR APPLICATION NUMBER: 60/357,846
; PRIOR FILING DATE: 2002-02-21
; PRIOR APPLICATION NUMBER: 60/434,645
; PRIOR FILING DATE: 2002-12-20
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 49
; LENGTH: 571
; TYPE: PRT
; ORGANISM: Mus sp.
US-11-028-058-49
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; LENGTH: 58
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Consensus Kunitz domain
US-10-038-722-5

Query Match      55.3%; Score 167; DB 14; Length 58;
Best Local Similarity 56.9%; Pred. No. 6.9e-13;
Matches 29; Conservative 5; Mismatches 17; Indels 0; Gaps 0;

Qy 1 CSMQAEAGPCLASIPHHWYKTKICSEFIYGGCGGNNNNFQTEAICLVTC 51
   | : | | | | | | | | | | : | : | | | | | | | | | | |
Db 5 CLLPAETGPCRAMIPRFYNNAKSGKCEPFIYGGCGGNNNNFKTEECRRTC 55

RESULT 29
US-09-896-095-147
; Sequence 147, Application US/09896095
; Publication No. US20030219886A1
; GENERAL INFORMATION:
; APPLICANT: LADNER, Charles C.
; APPLICANT: GUTERMAN, Sonia K.
; APPLICANT: ROBERTS, Bruce L.
; APPLICANT: MARKLAND, William
; APPLICANT: LEY, Arthur C.
; APPLICANT: KENT, Rachel B.
; TITLE OF INVENTION: DIRECTED EVOLUTION OF NOVEL BINDING PROTEINS
; FILE REFERENCE: LADNER=7L
; CURRENT APPLICATION NUMBER: US/09/896,095
; PRIOR FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: 08/415,922
; PRIOR FILING DATE: 1995-03-04
; PRIOR APPLICATION NUMBER: 08/009,319
; PRIOR FILING DATE: 1993-01-26
; PRIOR APPLICATION NUMBER: 07/664,989
; PRIOR FILING DATE: 1991-03-01
; PRIOR APPLICATION NUMBER: 08/993,776
; PRIOR FILING DATE: 1997-12-18
; NUMBER OF SEQ ID NOS: 274
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 147
; LENGTH: 67
; TYPE: PRT
; ORGANISM: Bos taurus
US-09-896-095-147

Query Match      55.0%; Score 166; DB 10; Length 67;
Best Local Similarity 51.0%; Pred. No. 1e-12;
Matches 26; Conservative 8; Mismatches 17; Indels 0; Gaps 0;

Qy 1 CSMQAEAGPCLASIPHHWYKTKICSEFIYGGCGGNNNNFQTEAICLVTC 51
   | : | | | | | | | | | | : | : | | | | | | | | | | |
Db 8 CQLPQARGPCKAALLRYFYNSTNACEPFIYGGCGGNNNNFETTEMCLRIC 58

RESULT 30
US-10-038-722-90
; Sequence 90, Application US/10038722
; Publication No. US20030175919A1
; GENERAL INFORMATION:
; APPLICANT: LEY, Arthur C.
; APPLICANT: GUTERMAN, Sonia K.
; APPLICANT: MARKLAND, William
; APPLICANT: KENT, Rachel B.
; APPLICANT: ROBERTS, Bruce L.
; APPLICANT: LADNER, Robert C.
; TITLE OF INVENTION: ITI-DI KUNITZ DOMAIN MUTANTS AS nHE INHIBITORS
; FILE REFERENCE: LEY=1B
; CURRENT APPLICATION NUMBER: US/10/038,722
; CURRENT FILING DATE: 2002-01-08
; PRIOR APPLICATION NUMBER: US 08/849,406
; PRIOR FILING DATE: 1999-07-21
```

```
; PRIOR APPLICATION NUMBER: PCT/US95/16349
; PRIOR FILING DATE: 1995-12-15
; PRIOR APPLICATION NUMBER: US 08/358,160
; PRIOR FILING DATE: 1994-12-16
; NUMBER OF SEQ ID NOS: 129
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 90
; LENGTH: 67
; TYPE: PRT
; ORGANISM: Bos taurus
US-10-038-722-90

Query Match      55.0%; Score 166; DB 14; Length 67;
Best Local Similarity 51.0%; Pred. No. 1e-12;
Matches 26; Conservative 8; Mismatches 17; Indels 0; Gaps 0;

Qy 1 CSMQAEAGPCLASIPHHWYKTKICSEFIYGGCGGNNNNFQTEAICLVTC 51
   | : | | | | | | | | | | : | : | | | | | | | | | | |
Db 8 CQLPQARGPCKAALLRYFYNSTNACEPFIYGGCGGNNNNFETTEMCLRIC 58

RESULT 31
US-10-115-134-4
; Sequence 4, Application US/10115134
; Publication No. US20030223977A1
; GENERAL INFORMATION:
; APPLICANT: LEY, Arthur Charles
; APPLICANT: GUTERMAN, Sonia Kosow
; APPLICANT: MARKLAND, William
; APPLICANT: KENT, Rachel Baribault
; APPLICANT: ROBERTS, Bruce Lindsey
; APPLICANT: LADNER, Robert Charles
; TITLE OF INVENTION: DOMAIN MUTANTS AS CATHEPSIN G INHIBITORS
; FILE REFERENCE: LEY=1C
; CURRENT APPLICATION NUMBER: US/10/115,134
; CURRENT FILING DATE: 2002-04-04
; PRIOR APPLICATION NUMBER: 08/849,406
; PRIOR FILING DATE: 2001-07-21
; NUMBER OF SEQ ID NOS: 92
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 4
; LENGTH: 67
; TYPE: PRT
; ORGANISM: Bos taurus
US-10-115-134-4

Query Match      55.0%; Score 166; DB 15; Length 67;
Best Local Similarity 51.0%; Pred. No. 1e-12;
Matches 26; Conservative 8; Mismatches 17; Indels 0; Gaps 0;

Qy 1 CSMQAEAGPCLASIPHHWYKTKICSEFIYGGCGGNNNNFQTEAICLVTC 51
   | : | | | | | | | | | | : | : | | | | | | | | | | |
Db 8 CQLPQARGPCKAALLRYFYNSTNACEPFIYGGCGGNNNNFETTEMCLRIC 58

RESULT 32
US-09-910-430-8
; Sequence 8, Application US/09910430
; Patent No. US20020127235A1
; GENERAL INFORMATION:
; APPLICANT: Godfroi, Edmond
; APPLICANT: Bollen, Alex
; APPLICANT: Leboulle, Gerard
; TITLE OF INVENTION: IDENTIFICATION AND MOLECULAR CHARACTERIZATION OF
; TITLE OF INVENTION: PROTEINS, EXPRESSED IN THE IXODES RICINUS SALIVARY
; TITLE OF INVENTION: GLANDS
; FILE REFERENCE: VANM229.001CPI
; CURRENT APPLICATION NUMBER: US/09/910,430
; CURRENT FILING DATE: 2001-07-19
; PRIOR APPLICATION NUMBER: PCT/BE00/00061
; PRIOR FILING DATE: 2000-06-06
; PRIOR APPLICATION NUMBER: GB 9913425.6
; PRIOR FILING DATE: 1999-06-09
```

```
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 8
; LENGTH: 86
; TYPE: PRT
; ORGANISM: Ixodes ricinus
US-09-910-430-8

Query Match      55.0%; Score 166; DB 9; Length 86;
Best Local Similarity 49.0%; Pred. No. 1.3e-12;
Matches 25; Conservative 10; Mismatches 16; Indels 0; Gaps 0;

QY 1 CSMPOEAGPCLASIPHHWYNNKTKICSEFIYGGCGGNNNNFQTEAICLVTC 51
Db 31 CKLPDGDGFCRARIPSYFDRKTKCKEPMYGCCEGNNENNENFNTTCQEEC 81

RESULT 33
US-10-165-605A-8
; Sequence 8, Application US/10165605A
; Publication No. US20030086937A1
; GENERAL INFORMATION:
; APPLICANT: Godfroid, Edmond
; APPLICANT: Bollen, Alex
; APPLICANT: Lebouille, Gerard
; TITLE OF INVENTION: IDENTIFICATION AND MOLECULAR CHARACTERIZATION OF
; TITLE OF INVENTION: PROTEINS, EXPRESSED IN THE IXODES RICINUS SALIVARY
; TITLE OF INVENTION: GLANDS
; FILE REFERENCE: VANN229.001CP2
; CURRENT APPLICATION NUMBER: US/10/165,605A
; CURRENT FILING DATE: 2002-06-07
; PRIOR APPLICATION NUMBER: 09/910,430
; PRIOR FILING DATE: 2001-07-19
; PRIOR APPLICATION NUMBER: PCT/BE00/00061
; PRIOR FILING DATE: 2000-06-06
; PRIOR APPLICATION NUMBER: GB9913425.6
; PRIOR FILING DATE: 1999-06-09
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 8
; LENGTH: 86
; TYPE: PRT
; ORGANISM: Ixodes ricinus
US-10-165-605A-8

Query Match      55.0%; Score 166; DB 14; Length 86;
Best Local Similarity 49.0%; Pred. No. 1.3e-12;
Matches 25; Conservative 10; Mismatches 16; Indels 0; Gaps 0;

QY 1 CSMPOEAGPCLASIPHHWYNNKTKICSEFIYGGCGGNNNNFQTEAICLVTC 51
Db 31 CKLPDGDGFCRARIPSYFDRKTKCKEPMYGCCEGNNENNENFNTTCQEEC 81

RESULT 34
US-10-038-722-17
; Sequence 17, Application US/10038722
; Publication No. US20030175919A1
; GENERAL INFORMATION:
; APPLICANT: LEY, Arthur C.
; APPLICANT: GUTERMAN, Sonia K.
; APPLICANT: MARKLAND, William
; APPLICANT: KENT, Rachel B.
; APPLICANT: ROBERTS, Bruce L.
; APPLICANT: LADNER, Robert C.
; TITLE OF INVENTION: ITI-D1 KUNITZ DOMAIN MUTANTS AS rHE INHIBITORS
; FILE REFERENCE: LEY=1B
; CURRENT APPLICATION NUMBER: US/10/038,722
; CURRENT FILING DATE: 2002-01-08
; PRIOR APPLICATION NUMBER: US 08/849,406
; PRIOR FILING DATE: 1999-07-21
; PRIOR APPLICATION NUMBER: PCT/US95/16349
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 18
; LENGTH: 58
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: MUTT26A
US-10-038-722-18

Query Match      53.3%; Score 161; DB 14; Length 58;
Best Local Similarity 51.0%; Pred. No. 3.7e-12;
Matches 26; Conservative 6; Mismatches 19; Indels 0; Gaps 0;

QY 1 CSMPOEAGPCLASIPHHWYNNKTKICSEFIYGGCGGNNNNFQTEAICLVTC 51
Db 5 COLGYSAGPCVAMPFRYFNGTSMACQTFVYGGCGNGNNGNFVTEKDCLOTC 55

RESULT 35
US-10-038-722-18
; Sequence 18, Application US/10038722
; Publication No. US20030175919A1
; GENERAL INFORMATION:
; APPLICANT: LEY, Arthur C.
; APPLICANT: GUTERMAN, Sonia K.
; APPLICANT: MARKLAND, William
; APPLICANT: KENT, Rachel B.
; APPLICANT: ROBERTS, Bruce L.
; APPLICANT: LADNER, Robert C.
; TITLE OF INVENTION: ITI-D1 KUNITZ DOMAIN MUTANTS AS rHE INHIBITORS
; FILE REFERENCE: LEY=1B
; CURRENT APPLICATION NUMBER: US/10/038,722
; CURRENT FILING DATE: 2002-01-08
; PRIOR APPLICATION NUMBER: US 08/849,406
; PRIOR FILING DATE: 1999-07-21
; PRIOR APPLICATION NUMBER: PCT/US95/16349
; PRIOR FILING DATE: 1995-12-15
; PRIOR APPLICATION NUMBER: US 08/358,160
; PRIOR FILING DATE: 1994-12-16
; NUMBER OF SEQ ID NOS: 129
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 18
; LENGTH: 58
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: MUTT26A
US-10-038-722-18

Query Match      53.3%; Score 161; DB 14; Length 58;
Best Local Similarity 51.0%; Pred. No. 3.7e-12;
Matches 26; Conservative 6; Mismatches 19; Indels 0; Gaps 0;

QY 1 CSMPOEAGPCLASIPHHWYNNKTKICSEFIYGGCGGNNNNFQTEAICLVTC 51
Db 5 COLGYSAGPCVAMPFRYFNGTSMACQTFVYGGCGNGNNGNFVTEKDCLOTC 55

RESULT 36
US-10-038-722-19
; Sequence 19, Application US/10038722
; Publication No. US20030175919A1
; GENERAL INFORMATION:
; APPLICANT: LEY, Arthur C.
; APPLICANT: GUTERMAN, Sonia K.
; APPLICANT: MARKLAND, William
; APPLICANT: KENT, Rachel B.
; APPLICANT: ROBERTS, Bruce L.
; APPLICANT: LADNER, Robert C.
; TITLE OF INVENTION: ITI-D1 KUNITZ DOMAIN MUTANTS AS rHE INHIBITORS
; FILE REFERENCE: LEY=1B
; CURRENT APPLICATION NUMBER: US/10/038,722
; CURRENT FILING DATE: 2002-01-08
; PRIOR APPLICATION NUMBER: US 08/849,406
; PRIOR FILING DATE: 1999-07-21
; PRIOR APPLICATION NUMBER: PCT/US95/16349
; PRIOR FILING DATE: 1995-12-15
```

```
; FILE REFERENCE: LEY=1B
; CURRENT APPLICATION NUMBER: US/10/038,722
; CURRENT FILING DATE: 2002-01-08
; PRIOR APPLICATION NUMBER: US 08/849,406
; PRIOR FILING DATE: 1999-07-21
; PRIOR APPLICATION NUMBER: PCT/US95/16349
; PRIOR FILING DATE: 1995-12-15
; PRIOR APPLICATION NUMBER: US 08/358,160
; PRIOR FILING DATE: 1994-12-16
; NUMBER OF SEQ ID NOS: 129
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 19
; LENGTH: 58
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: MUTQE
US-10-038-722-19

Query Match      53.3%; Score 161; DB 14; Length 58;
Best Local Similarity 51.0%; Pred. No. 3.7e-12;
Matches 26; Conservative 6; Mismatches 19; Indels 0; Gaps 0;

Qy 1 CSMPQEAGPCLASIPHHWYNNKTKICSEFYGGCGQNNNNFQTEAICLVTC 51
   | : ||||| : || : || : || : || : || : || : || : || : ||
Db 5 CQLGYSAGPCVAMPFRYPFYNGTSMACQTFVYGGCGNGNGNFFVTEKDCIQC 55

RESULT 37
US-10-115-134-88
; Sequence 88, Application US/10115134
; Publication No. US20030223977A1
; GENERAL INFORMATION:
; APPLICANT: LEY, Arthur Charles
; APPLICANT: GUTERMAN, Sonia Kosow
; APPLICANT: MARKLAND, William
; APPLICANT: KENT, Rachel Baribault
; APPLICANT: ROBERTS, Bruce Lindsey
; APPLICANT: LADNER, Robert Charles
; TITLE OF INVENTION: DOMAIN MUTANTS AS CATHEPSIN G INHIBITORS
; FILE REFERENCE: LEY=1C
; CURRENT APPLICATION NUMBER: US/10/115,134
; CURRENT FILING DATE: 2002-04-04
; PRIOR APPLICATION NUMBER: 08/849,406
; PRIOR FILING DATE: 2001-07-21
; NUMBER OF SEQ ID NOS: 92
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 88
; LENGTH: 58
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: BITI-E7-141
US-10-115-134-88

Query Match      53.3%; Score 161; DB 15; Length 58;
Best Local Similarity 51.0%; Pred. No. 3.7e-12;
Matches 26; Conservative 6; Mismatches 19; Indels 0; Gaps 0;

Qy 1 CSMPQEAGPCLASIPHHWYNNKTKICSEFYGGCGQNNNNFQTEAICLVTC 51
   | : ||||| : || : || : || : || : || : || : || : || : ||
Db 5 CQLGYSAGPCVAMPFRYPFYNGTSMACQTFVYGGCGNGNGNFFVTEKDCIQC 55

RESULT 38
US-10-115-134-89
; Sequence 89, Application US/10115134
; Publication No. US20030223977A1
; GENERAL INFORMATION:
; APPLICANT: LEY, Arthur Charles
; APPLICANT: GUTERMAN, Sonia Kosow
; APPLICANT: MARKLAND, William
; APPLICANT: KENT, Rachel Baribault
```

```
; APPLICANT: ROBERTS, Bruce Lindsay
; APPLICANT: LADNER, Robert Charles
; TITLE OF INVENTION: DOMAIN MUTANTS AS CATHEPSIN G INHIBITORS
; FILE REFERENCE: LEY=1C
; CURRENT APPLICATION NUMBER: US/10/115,134
; CURRENT FILING DATE: 2002-04-04
; PRIOR APPLICATION NUMBER: 08/849,406
; PRIOR FILING DATE: 2001-07-21
; NUMBER OF SEQ ID NOS: 92
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 89
; LENGTH: 58
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: MUTT26A
US-10-115-134-89

Query Match      53.3%; Score 161; DB 15; Length 58;
Best Local Similarity 51.0%; Pred. No. 3.7e-12;
Matches 26; Conservative 6; Mismatches 19; Indels 0; Gaps 0;

Qy 1 CSMPQEAGPCLASIPHHWYNNKTKICSEFYGGCGQNNNNFQTEAICLVTC 51
   | : ||||| : || : || : || : || : || : || : || : || : ||
Db 5 CQLGYSAGPCVAMPFRYPFYNGASMACQTFVYGGCGNGNGNFFVTEKDCIQC 55

RESULT 39
US-10-115-134-90
; Sequence 90, Application US/10115134
; Publication No. US20030223977A1
; GENERAL INFORMATION:
; APPLICANT: LEY, Arthur Charles
; APPLICANT: GUTERMAN, Sonia Kosow
; APPLICANT: MARKLAND, William
; APPLICANT: KENT, Rachel Baribault
; APPLICANT: ROBERTS, Bruce Lindsay
; APPLICANT: LADNER, Robert Charles
; TITLE OF INVENTION: DOMAIN MUTANTS AS CATHEPSIN G INHIBITORS
; FILE REFERENCE: LEY=1C
; CURRENT APPLICATION NUMBER: US/10/115,134
; CURRENT FILING DATE: 2002-04-04
; PRIOR APPLICATION NUMBER: 08/849,406
; PRIOR FILING DATE: 2001-07-21
; NUMBER OF SEQ ID NOS: 92
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 90
; LENGTH: 58
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: MUTQE
US-10-115-134-90

Query Match      53.3%; Score 161; DB 15; Length 58;
Best Local Similarity 51.0%; Pred. No. 3.7e-12;
Matches 26; Conservative 6; Mismatches 19; Indels 0; Gaps 0;

Qy 1 CSMPQEAGPCLASIPHHWYNNKTKICSEFYGGCGQNNNNFQTEAICLVTC 51
   | : ||||| : || : || : || : || : || : || : || : || : ||
Db 5 CQLGYSAGPCVAMPFRYPFYNGTSMACQTFVYGGCGNGNGNFFVTEKDCIQC 55

RESULT 40
US-10-456-986A-42
; Sequence 42, Application US/10456986A
; Publication No. US20040038893A1
; GENERAL INFORMATION:
; APPLICANT: Ladner, Robert C.
; APPLICANT: Ley, Arthur C.
; APPLICANT: Hirani, Shirish
; APPLICANT: Williams, Anthony
; TITLE OF INVENTION: Prevention and Reduction of Blood Loss
```



```

RESULT 42
US-10-456-986A-44
; Sequence 44, Application US/10456986A
; Publication No. US2004038893A1
; GENERAL INFORMATION:
; APPLICANT: Ladner, Robert C.
; APPLICANT: Lev, Arthur C.
; APPLICANT: Hirani, Shirish
; APPLICANT: Williams, Anthony
; TITLE OF INVENTION: Prevention and Reduction
; FILE REFERENCE: 3421.1001-002

```

RESULT 44
US-10-953-302A-43
; Sequence 43, Application US/10953902A
; Publication No. US20050164928A1
; GENERAL INFORMATION: Robert C.
; APPLICANT: Ladner, Robert C.
; APPLICANT: Ley, Arthur C.
; APPLICANT: Hiran, Shrish
; APPLICANT: Hiran, Shrish

```

: APPLICANT: Williams, Anthony
: APPLICANT: De Simoni, Maria Garzia
: APPLICANT: Bergamaschini, Luigi
: TITLE OF INVENTION: KALIKREIN-INHIBITOR THERAPIES
: FILE REFERENCE: 10280-120001
: CURRENT APPLICATION NUMBER: US/10/953,902A
: CURRENT FILING DATE: 2004-09-27
: PRIOR APPLICATION NUMBER: US 60/387,239
: PRIOR FILING DATE: 2002-06-07
: PRIOR APPLICATION NUMBER: US 60/407,003
: PRIOR FILING DATE: 2002-08-28
: PRIOR APPLICATION NUMBER: US 10/456,986
: PRIOR FILING DATE: 2003-06-06
: NUMBER OF SEQ ID NOS: 57
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 43
: LENGTH: 58
: TYPE: PRT
: ORGANISM: Artificial Sequence
: FEATURE:
: OTHER INFORMATION: Synthetically generated peptide
US-10-953-902A-43

```

Query Match 53.3%; Score 161; DB 18; Length 58;
Best Local Similarity 51.0%; Pred. No. 3.7e-12;
Matches 26; Conservative 6; Mismatches 19; Indels 0; Gaps 0;

Qy	1	C	S	M	P	Q	E	A	G	P	C	L	A	S	I	P	H	W	N	K	T	K	I	C	S	F	I	Y	G	C	G	C	G	N	N	N	F	O	T	E	A	I	C	L	V	T	C	51
		-	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:		
D_b	5	C	Q	L	G	S	A	G	P	C	V	A	M	F	R	I	F	Y	N	G	A	S	M	A	C	Q	T	F	V	Y	G	C	G	M	G	N	N	F	T	E	K	D	C	L	Q	T	C	55

RESULT 45

```

US-10-953-902A-44
; Sequence 44, Application US/10953902A
; Publication No. US20050164928A1
; GENERAL INFORMATION:
; APPLICANT: Ladner, Robert C.
; APPLICANT: Lev, Arthur C.
; APPLICANT: Hirani, Shirish
; APPLICANT: Williams, Anthony
; APPLICANT: De Simoni, Maria Garzia
; APPLICANT: Bergamaschini, Luigi
; TITLE OF INVENTION: KALTIKRIIN-INHIBITOR THERAPIES
; FILE REFERENCE: 10280-120001
; CURRENT APPLICATION NUMBER: US/10/953,902A
; CURRENT FILING DATE: 2004-09-27
; PRIOR APPLICATION NUMBER: US 60/387,239
; PRIOR FILING DATE: 2002-06-07
; PRIOR APPLICATION NUMBER: US 60/407,003
; PRIOR FILING DATE: 2002-08-28
; PRIOR APPLICATION NUMBER: US 10/456,986
; PRIOR FILING DATE: 2003-06-06
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 44
; LENGTH: 58
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetically generated peptide
US-10-953-902A-44

```

Query Match 53.3%; Score 161; DB 18; Length 58;
Best Local Similarity 51.0%; Pred. No. 3.7e-12;
Matches 26; Conservative 6; Mismatches 19; Indels 0; Gaps 0;

Qy	1	CSMPQ	EAGP	CLAS	IPHW	YNNK	TKIC	SF	YGGC	GN	NFQ	EAI	CL	VTC	51
		:	:	:	:	:	:	:	:	:	:	:	:	:	
Dp	5	COLGX	SAGP	CVAM	PPRY	FNGT	SMAC	ETFY	GGC	NGN	NFVE	KDCL	OTC	55	

RESULT 46

```

US-10-007-280A-233
; Sequence 233, Application US/10007280A
; Publication No. US20030059784A1
; GENERAL INFORMATION:
; APPLICANT: Sun, Yongming
; APPLICANT: Recipon, Herve
; APPLICANT: Salceda, Susana
; APPLICANT: Chenghua, Liu
; TITLE OF INVENTION: Compositions and I
; FILE REFERENCE: DEX-0257
; CURRENT APPLICATION NUMBER: US/10/007
; CURRENT FILING DATE: 2001-11-07
; PRIOR APPLICATION NUMBER: US 60/246,6
; PRIOR FILING DATE: 2000-11-08
; NUMBER OF SEQ ID NOS: 238
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 233
; LENGTH: 503
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-007-280A-233

```

Query Match	53.0%	Score 160;	DB 14;	Length 503;
Best Local Similarity	49.0%	Pred. No. 4e-11;		
Matches 25; Conservative	7;	Mismatches 19;	Indels 0;	Gaps 0;

QY 1 CSMPQBAGPCLASIPHWYNKTKICSEFIYGCCQGNNNNFQTEAICLVTC 51
||: ||| ||| ||| ||| : | : ||| : ||| : ||| :
Pb 317 CSLPALGCPCKAYPRWAYNSOTGCOSCFVYGCEGNNGNPFESREACEESC 367

RESULT 47

```

US-09-794-589-2
; Sequence 2, Application US/09794589
; Patent No. US20020004224A1
; GENERAL INFORMATION:
; APPLICANT: Sheppard, Paul O.
; TITLE OF INVENTION: KUNITZ DOMAIN POLYPEPTIDE ZKUN8
; FILE REFERENCE: 00-01
; CURRENT APPLICATION NUMBER: US/09/794,589
; CURRENT FILING DATE: 2001-02-27
; PRIOR APPLICATION NUMBER: US 60/186,069
; PRIOR FILING DATE: 2000-02-29
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 576
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-794-589-2

```

Query Match	53.0%	Score 160;	DB 9;	Length 576;
Best Local Similarity	49.0%	Pred. No. 4.6e-11;		
Matches 25; Conservative	7;	Mismatches 19;	Indels 0;	Gaps 0;

[illegible]

RESULT 48

```

US-10-315-380-2
; Sequence 2, Application US/10315380
; Publication No. US20030129577A1
; GENERAL INFORMATION:
; APPLICANT: Sheppard, Paul O.
; TITLE OF INVENTION: KUNITZ DOMAIN POLYPEPTIDE ZKUN8
; FILE REFERENCE: 00-01
; CURRENT APPLICATION NUMBER: US/10/315,380
; PRIOR FILING DATE: 2002-12-09
; PRIOR APPLICATION NUMBER: US/09/794,589
; PRIOR FILING DATE: 2001-02-27
; PRIOR APPLICATION NUMBER: US 60/186,069

```

Query Match 53.0%; Score 160; DB 14; Length 576;
Best Local Similarity 49.0%; Pred. No. 4.6e-11;
Matches 25; Conservative 7; Mismatches 19; Indels 0; Gaps 0;

Search completed: September 21, 2005, 16:45:52
Job time : 32.8938 secs

Query Match	53.0%;	Score 160;	DB 14;	Length 576;
Best Local Similarity	49.0%;	Pred. No. 4.6e-11;		
Matches 25:	Conservative	7: Mismatches	19: Indels	0: Gaps

QY 1 CSMPQEAGPCLASIPHHWYNKTKICSEFIYGCQGNNNFQTEALCVTC 51
||:||| || | || : ||:||||| ||:: |:
pb 186 CSlPALOGPCXAYAPRWYNSTGOCsfyGCGEGNGNfESRACeESC 436

RESULT 50
US-10-369-738-7
; Sequence 7, Application US/10369738
; Publication No. US20030180306A1
; GENERAL INFORMATION:
; APPLICANT: HILL, JENNIFER J.
; APPLICANT: WOLFMAN, NEIL M.
; TITLE OF INVENTION: FOLLISTATIN DOMAIN CONTAINING PROTEINS
; FILE REFERENCE: 08702.0014-00
; CURRENT APPLICATION NUMBER: US/10/369,738
; CURRENT FILING DATE: 2003-02-21
; PRIOR APPLICATION NUMBER: 60/357,846
; PRIOR FILING DATE: 2002-02-21
; PRIOR APPLICATION NUMBER: 60/434,645
; PRIOR FILING DATE: 2002-12-20
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
; LENGTH: 576
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-369-738-7

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OM protein - protein search, using sw model

Run on: September 21, 2005, 16:21:48 ; Search time 7.37168 Seconds
(without alignments)
665.663 Million cell updates/sec

Title: US-10-807-204-1_COPY_77_127

Perfect score: 302
Sequence: 1 CSMPOEAGPCLASIPHWYN.....GSCQGNNNFQTEAICLVTC 51

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 50 summaries

Database :

PIR_79: *
1: PIR1: *
2: PIR2: *
3: PIR3: *
4: PIR4: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	170	56.3	110	1 TITTCR	basic proteinase i
2	163	54.0	67	1 TIBOC	trypsin inhibitor,
3	160	53.0	252	2 JG0185	hepatocyte growth
4	158	52.3	62	2 A4180	taicotoxin serine
5	154	51.0	747	2 JH0773	Alzheimer's disease
6	153	50.7	58	1 TIRABK	isolnhibitor K (BP
7	153	50.7	62	2 S19127	proteinase inhibit
8	152	50.3	62	2 S07451	hypothetical prote
9	152	50.3	922	2 T23573	basic proteinase i
10	149	49.3	57	2 A59204	venom basic protei
11	148	49.0	65	1 TIVIVC	Alzheimer's diseas
12	147	48.7	76	2 S06678	Alzheimer's diseas
13	147	48.7	76	2 S03607	hypothetical Alzhe
14	147	48.7	484	4 A32761	Alzheimer's diseas
15	147	48.7	770	1 QRHUA4	amyloid precursor
16	146	48.3	111	2 S41082	beta-amyloid precu
17	146	48.3	751	2 A49974	amyloid beta (A4)
18	146	48.3	763	2 A49321	amyloid precursor-
19	146	48.3	765	2 S42880	proteinase inhibit
20	145	48.0	57	1 TIFRBP	uterine plasmin/tr
21	145	48.0	122	1 A55115	hypothetical prote
22	145	48.0	1599	2 T16210	chymotrypsin inhib
23	144	47.7	62	2 S01802	Alzheimer's diseas
24	144	47.7	76	2 S04855	Alzheimer's diseas
25	144	47.7	100	2 A32282	short epsilon-dend
26	143	47.4	57	2 B59399	venom basic protei
27	143	47.4	59	1 TIEPED	Long epsilon-dendr
28	143	47.4	59	2 A59399	chymotrypsin inhib
29	143	47.4	62	2 S01803	

30 143 47.4 302 1 TITTCR
31 143 47.4 352 2 HCHU
32 143 47.4 372 2 JC2556
33 142 47.0 61 1 TIVITR
34 142 47.0 337 1 TIPGBI
35 142 47.0 352 1 TIBOBI
36 141 46.7 1522 2 H88380
37 140 46.4 123 2 A29652
38 140 46.4 1558 2 C89114
39 140 46.4 2167 2 T34395
40 138 45.7 61 1 TIRCBP
41 138 45.7 125 1 TIRHBI
42 138 45.7 265 2 A53390
43 137 45.4 235 2 A54951
44 136 45.0 100 1 TIBO
45 136 45.0 805 2 T34212
46 135 44.7 1743 2 T26859
47 134 44.4 59 2 S00371
48 134 44.4 60 1 TIBOR
49 134 44.4 1474 2 D88550
50 134 44.4 2844 2 S28291

ALIGNMENTS

RESULT 1

TITTCR

basic proteinase inhibitor - loggerhead

C:Species: Caretta caretta (loggerhead)

C>Date: 31-May-1979 #sequence_revision 23-Oct-1981 #text_change 09-Jul-2004

C:Accession: A01224

R:Kato, I.; Tominaga, N.

Fed. Proc. 38, 832, 1979

A:Title: Trypsin-subtilisin inhibitor from red sea turtle eggwhite consists of two tand

A:Reference number: A01224

A:Accession: A01224

A:Molecule type: protein

A:Residues: 1-110 <KAT>

A:Cross-references: UNIPROT:P00993

C:Comment: This inhibitor, isolated from egg white, consists of two nonhomologous domain

C:Superfamily: loggerhead basic proteinase inhibitor; animal Kunitz-type proteinase inhi

C:Keywords: pyroglutamic acid; serine proteinase inhibitor

F:8-58/Domain: animal Kunitz-type proteinase inhibitor homology <BPI>

F:63-105/Domain: antileukoproteinase repeat homology <ALP>

F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

F:8-58,17-41,33-54,67-93,76-97,80-92,86-101/disulfide bonds: #status predicted

F:18/inhibitory site: Lys (trypsin) #status predicted

Query Match 56.3%; Score 170; DB 1; Length 110;

Best Local Similarity 51.0%; Pred. No. 2e-13;

Matches 26; Conservative 10; Mismatches 15; Indels 0; Gaps 0;

QY 1 CSMPOEAGPCLASIPHWYNKTKICSFYGGCGGNNNFQTEAICLVTC 51

DB 8 CRLPPEQGCGRIPRYFYNPASRMCSFIYGGCKGNKNFKYAEVCVRAC 58

RESULT 2

TIBOC

trypsin inhibitor, colostrum (BPI type) - bovine

C:Species: Bos primigenius taurus (cattle)

C>Date: 24-Apr-1984 #sequence_revision 31-Dec-1993 #text_change 09-Jul-2004

C:Accession: A01207

R:Čechova, D.; Jonakova, V.; Sorm, F.

Collect. Czech. Chem. Commun. 36, 3342-3357, 1971

A:Title: Primary structure of trypsin inhibitor from cow colostrum (component B2).

A:Reference number: A90928

A:Accession: A01207

A:Molecule type: protein

A:Residues: 1-26, B' 28-67 <CEC>

A:Cross-references: UNIPROT:P00976

A:Note: the residue identified as Asx is bound to carbohydrate; therefore, we have show

A:Molecule type: DNA
A:Residues: 1-770 <YOS1>
A:Cross-references: GB:M33112; NID:g178613; PIDN:AAB59502.1; PID:g178616
A:Accession: I39451
A>Status: nucleic acid sequence not shown; translation not shown; translated from GB/EMBL
A:Molecule type: DNA
A:Residues: 1-530, 'QWLMPVTPAFWEAKVGR' <YOS2>
A:Cross-references: GB:M34875; NID:g178608; PIDN:AAB59501.1; PID:g178615
R:Yoshikai, S.I.; Sasaki, H.; Doh-ura, K.; Furuya, H.; Sakaki, Y.
Gene 102, 291-292, 1991
A:Reference number: A59020; MUID:91340168; PMID:1908403
A:Contents: annotation; erratum
A>Note: revised physical map for reference I39451
R:Levy, E.; Carman, M.D.; Fernandez-Madrid, I.J.; Power, M.D.; Lieberburg, I.; van Duine
Science 248, 1124-1126, 1990
A:Title: Mutation of the Alzheimer's disease amyloid gene in hereditary cerebral hemorrh
A:Reference number: I39453; MUID:90260663; PMID:2111584
A:Accession: I39453
A>Status: translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 656-737 <LRV>
A:Cross-references: GB:M37896; NID:g178618; PIDN:AAA51727.1; PID:g178620
A>Note: a mutation with 693-Gln is presented
R:Murrell, J.; Farlow, M.; Ghetti, B.; Benson, M.D.
Science 254, 97-99, 1991
A:Title: A mutation in the amyloid precursor protein associated with hereditary Alzheimer
A:Reference number: I59562; MUID:92022553; PMID:1925564
A:Accession: I59562
A>Status: translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 689-716, 'F', 718-737 <MUR>
A:Cross-references: GB:S57665; NID:g236720; PIDN:AAB19991.1; PID:g236721
R:Kamino, K.; Orr, H.T.; Payami, H.; Wijsman, E.M.; Alonso, M.E.; Pulst, S.M.; Anderson,
arakis, S.E.; Korenberg, J.R.; Sharna, V.; Kukull, W.; Larson, E.; Heaton, L.L.; Martin,
Am. J. Hum. Genet. 51, 998-1014, 1992
A:Title: Linkage and mutational analysis of familial Alzheimer disease kindreds for the
A:Reference number: A44017; MUID:93035397; PMID:1415269
A:Accession: A44017
A:Molecule type: DNA
A:Residues: 687-692, 'G', 694-718 <KAM1>
A:Cross-references: GB:S45135; NID:g257377; PIDN:AAB23645.1; PID:g257378
A:Experimental source: familial Alzheimer disease family SB
A>Note: sequence extracted from NCBI backbone (NCBIP:115374)
A:Accession: B44017
A:Molecule type: DNA
A:Residues: 687-718 <KAM2>
A:Cross-references: GB:S45136; NID:g257379; PIDN:AAB23646.1; PID:g257380
A:Experimental source: familial Alzheimer disease family LIT
A>Note: sequence extracted from NCBI backbone (NCBIP:115376)
A:Title: this sequence has a silent mutation
R:Kang, J.; Lemaire, H.G.; Unterbeck, A.; Salbaum, J.M.; Masters, C.L.; Grzeschik, K.H.;
Nature 325, 733-736, 1987
A:Title: The precursor of Alzheimer's disease amyloid A4 protein resembles a cell-surfac
A:Reference number: A03134; MUID:87144572; PMID:2881207
A:Accession: A03134
A:Molecule type: mRNA
A:Residues: 1-288, 'V', 365-770 <KAN>
A:Cross-references: GB:Y00264; NID:g28525; PIDN:CAA68374.1; PID:g28526
A>Note: alternative splice form APP(695)
R:Robakis, N.K.; Ramakrishna, N.; Wolfe, G.; Wisniewski, H.M.
Proc. Natl. Acad. Sci. U.S.A. 84, 4190-4194, 1987
A:Title: Molecular cloning and characterization of a cDNA encoding the cerebrovascular s
A:Reference number: A29030; MUID:87231971; PMID:3035574
A:Accession: A29030
A:Molecule type: mRNA
A:Residues: 284-288, 'V', 365-646, 'E', 648-770 <ROB>
A:Cross-references: GB:M16765; NID:g178539; PIDN:AAA51722.1; PID:g178540
A>Note: the authors translated the codon GAG for residue 647 as Asp
R:Goldgaber, D.; Lerman, M.I.; McBride, O.W.; Saffiotti, U.; Gajdusek, D.C.
Science 235, 877-880, 1987
A:Title: Characterization and chromosomal localization of a cDNA encoding brain amyloid
A:Reference number: A47584; MUID:87120328; PMID:3810169
A:Accession: A47584

A:Molecule type: mRNA
A:Residues: 674-756, 'S', 758-770 <GOL>
A:Cross-references: GB:M15533; NID:g178706; PIDN:AAA35540.1; PID:g178707
A:Experimental source: brain
R:Tanzi, R.E.; Gusella, J.F.; Watkins, P.C.; Bruns, G.A.P.; St George-Hyslop, P.; Van Ke
Science 235, 880-884, 1987
A:Title: Amyloid beta protein gene: cDNA, mRNA distribution, and genetic linkage near th
A:Reference number: A47585; MUID:87120329; PMID:2949367
A:Accession: A47585
A:Molecule type: mRNA
A:Residues: 674-703 <TANI>
A:Cross-references: GB:M15532; NID:g177957; PIDN:AAA51564.1; PID:g177958
R:Dyrks, T.; Weidemann, A.; Multhaup, G.; Salbaum, J.M.; Lemaire, H.G.; Kang, J.; Muelle
EMBO J. 7, 949-957, 1988
A:Title: Identification, transmembrane orientation and biogenesis of the amyloid A4 prec
A:Reference number: S02638; MUID:88296437; PMID:2900137
A:Accession: S02638
A:Molecule type: mRNA
A:Residues: 672-678 <DYR>
R:Tanzi, R.E.; McClatchey, A.I.; Lamperti, E.D.; Villa-Komaroff, L.; Gusella, J.F.; Neve
Nature 331, 528-530, 1988
A:Title: Protease inhibitor domain encoded by an amyloid protein precursor mRNA associat
A:Reference number: S00707; MUID:88122640; PMID:2893290
A:Accession: S00707
A:Molecule type: mRNA
A:Residues: 286-344, 'I', 365-366 <TAN2>
A:Cross-references: EMBL:X06982; NID:g28817; PIDN:CAA30042.1; PID:g929612
A:Experimental source: promyelocytic leukemia cell line HL60
A>Note: alternative splice form APP(751)
R:Ponte, P.; Gonzalez-Dewhitt, P.; Schilling, J.; Miller, J.; Hsu, D.; Greenberg, B.; Da
Nature 331, 525-527, 1988
A:Title: A new A4 amyloid mRNA contains a domain homologous to serine proteinase inhibit
A:Reference number: S00925; MUID:88122639; PMID:2893289
A:Accession: S00925
A:Molecule type: mRNA
A:Residues: 1-344, 'I', 365-770 <PO2>
A:Cross-references: GB:X06989; EMBL:X00297; NID:g28720; PIDN:CAA30050.1; PID:g28721
A>Note: alternative splice form APP(751)
R:Kitaguchi, N.; Takahashi, Y.; Tokushima, Y.; Shiojiri, S.; Ito, H.
Nature 331, 530-532, 1988
A:Title: Novel precursor of Alzheimer's disease amyloid protein shows protease inhibitor
A:Reference number: A38949; MUID:88122641; PMID:2893291
A:Accession: A38949
A:Molecule type: mRNA
A:Residues: 287-367 <KIT>
A:Cross-references: GB:X06981; NID:g28816; PIDN:CAA30041.1; PID:g929611
A:Experimental source: glioblastoma cell line
A>Note: alternative splice form APP(770)
R:Vitek, M.P.; Rasool, C.G.; de Sauvage, F.; Vitek, S.M.; Bartus, R.T.; Beer, B.; Ashtot
Brain Res. Mol. Brain Res. 4, 121-131, 1988
A:Title: Absence of mutation in the beta-amyloid cDNAs cloned from the brains of three i
A:Reference number: A30320
A:Accession: A30320
A>Status: not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 284-288, 'V', 365-770 <VIT1>
A:Accession: B30320
A>Status: not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 122-288, 'V', 365-770 <VIT2>
A:Accession: C30320
A>Status: not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 606-770 <VIT3>
R:Zain, S.B.; Salim, M.; Chou, W.G.; Sajdel-Sulkowska, E.M.; Majocha, R.E.; Marotta, C.
Proc. Natl. Acad. Sci. U.S.A. 85, 929-933, 1988
A:Title: Molecular cloning of amyloid cDNA derived from mRNA of the Alzheimer disease b
A:Reference number: A31087; MUID:88124954; PMID:2893379
A:Accession: A31087
A:Molecule type: mRNA
A:Residues: 507-770 <ZAI>
A:Cross-references: GB:M18734; NID:g178572; PIDN:AAA51726.1; PID:g178573
A>Note: the authors translated the codon GAA for residue 599 as Gly, ACC for residue 60

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8 as Val, GTG for residue 609 as Asn, AAT for residue 610 as Gly, and GGT for residue 65
A>Note: the cited Genbank accession number, J03594, is not in release 101.0
R:Masters, C.L.; Multhaup, G.; Simms, G.; Pottgiesser, J.; Martins, R.N.; Beyreuther, K.

Query Match      48.7%; Score 147; DB 1; Length 770;
Best Local Similarity 47.1%; Pred. No. 7.4e-10;
Matches 24; Conservative 5; Mismatches 22; Indels 0; Gaps 0;

Qy      1 CSMPOEAGPCLASIPHHWYNNKTKICSEFIYGGCGGNNNFQTEAICLVTC 51
Db      291 CSEAGTGPCRAMISRWYFDVTEGKCAPFFYGGCGGNNNFDESYCNMAVC 341

RESULT 16
S41082
amyloid precursor protein homolog - human (fragment)
C:Species: Homo sapiens (man)
C>Date: 25-Dec-1994 #sequence_revision 03-Aug-1995 #text_change 09-Jul-2004
C:Accession: S41082
R:Peterson, L.C.; Bjorn, S.E.; Norris, F.; Norris, K.; Sprecher, C.; Foster, D.C.
FEBS Lett. 338, 53-57, 1994
A>Title: Expression, purification and characterization of a Kunitz-type protease inhibitor
A:Reference number: S41082; MUID:94139895; PMID:8307156
A:Accession: S41082
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-111 <P>
A:Cross-references: UNIPROT:Q7M4L3
F:59-109/Domain: animal Kunitz-type proteinase inhibitor homology <BPI>

Query Match      48.3%; Score 146; DB 2; Length 111;
Best Local Similarity 45.1%; Pred. No. 1.5e-10;
Matches 23; Conservative 7; Mismatches 21; Indels 0; Gaps 0;

Qy      1 CSMPOEAGPCLASIPHHWYNNKTKICSEFIYGGCGGNNNFQTEAICLVTC 51
Db      59 CSQEAHTGPCRAVMPRWYFDLSKGCVRFIYGGCGGNNNFSESDYCNMAVC 109

RESULT 17
A49974
beta-amyloid precursor protein 2 homolog APLP2 - mouse
C:Species: Mus musculus (house mouse)
C>Date: 06-Oct-1994 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
C:Accession: A49974
R:Slunt, H.H.; Thinakaran, G.; Von Koch, C.; Lo, A.C.; Tanzi, R.E.; Sisodia, S.S.
J. Biol. Chem. 269, 2637-2644, 1994
A>Title: Expression of a ubiquitous, cross-reactive homologue of the mouse beta-amyloid
A:Reference number: A49974; MUID:94132029; PMID:8300594
A:Accession: A49974
A>Status: preliminary; not compared with conceptual translation
A:Molecule type: nucleic acid
A:Residues: 1-751 <SLU>
A:Cross-references: UNIPROT:Q60709; GB:U15571; NID:G558467; PIDN:AAA50603.1; PID:G558468
A>Note: sequence extracted from NCBI backbone (NCBI:P144636)
C:Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase i
F:310-360/Domain: animal Kunitz-type proteinase inhibitor homology <BPI>

Query Match      48.3%; Score 146; DB 2; Length 751;
Best Local Similarity 45.1%; Pred. No. 9.6e-10;
Matches 23; Conservative 7; Mismatches 21; Indels 0; Gaps 0;

Qy      1 CSMPOEAGPCLASIPHHWYNNKTKICSEFIYGGCGGNNNFQTEAICLVTC 51
Db      310 CSQEAHTGPCRAVMPRWYFDLSKGCVRFIYGGCGGNNNFSESDYCNMAVC 360

RESULT 18
A49321
amyloid beta (A4) homolog 2 precursor - human
N:Alternate names: CDEI-binding protein
C:Species: Homo sapiens (man)
C>Date: 24-Feb-1994 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
```

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C:Accession: A49321; S34644; S40519
R:Sprecher, C.A.; Grant, F.J.; Grimm, G.; O'Hara, P.J.; Norris, F.; Norris, K.; Foster,
Biochemistry 32, 4481-4486, 1993
A>Title: Molecular cloning of the cDNA for a human amyloid precursor protein homolog: ev
A:Reference number: A49321; MUID:93250009; PMID:8485127
A:Accession: A49321
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-763 <SPR>
A:Cross-references: UNIPROT:Q06481; GB:S60099; NID:G300168; PIDN:AAC60589.1; PID:G300168
A:Experimental source: placenta
A>Note: sequence extracted from NCBI backbone (NCBIN:131198, NCBI:P131199)
A>Note: expression was shown in placenta, brain, heart, lung, liver, and kidney
R:von der Kammer, H.; Klaudiny, J.; Hanes, J.; Scheit, K.H.
submitted to the EMBL Data Library, April 1993
A:Description: The human homologue of the murine CDEI binding protein is an amyloid prec
A:Reference number: S34644
A:Accession: S34644
A:Molecule type: mRNA
A:Residues: 1-763 <VON>
A:Cross-references: EMBL:Z22572; NID:G394763; PIDN:CAA80295.1; PID:G394764
R:Wasco, W.; Gurubhagavata, S.; Paradis, M.; Romano, D.W.; Sisodia, S.S.; Hyman, B.T.;
Nature Genet. 5, 95-99, 1993
A>Title: Isolation and characterization of APLP2 encoding a homologue of the Alzheimer's
A:Reference number: S40519; MUID:94035131; PMID:8220435
A:Accession: S40519
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-763 <WAS>
A:Cross-references: GB:L27631; NID:G450391; PIDN:AAC41701.1; PID:G450392
C:Genetics:
A:Gene: GDB:APLP2; APLP2
A:Cross-references: GDB:139159; OMIM:104776
A:Map position: 11q23-11q25
C:Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase i
C:Keywords: alternative splicing; transmembrane protein
F:310-360/Domain: animal Kunitz-type proteinase inhibitor homology <BPI>

Query Match      48.3%; Score 146; DB 2; Length 763;
Best Local Similarity 45.1%; Pred. No. 9.7e-10;
Matches 23; Conservative 7; Mismatches 21; Indels 0; Gaps 0;

Qy      1 CSMPOEAGPCLASIPHHWYNNKTKICSEFIYGGCGGNNNFQTEAICLVTC 51
Db      310 CSQEAHTGPCRAVMPRWYFDLSKGCVRFIYGGCGGNNNFSESDYCNMAVC 360

RESULT 19
S42880
amyloid precursor-like protein - rat
C:Species: Rattus norvegicus (Norway rat)
C>Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 09-Jul-2004
C:Accession: S42880; S47528
R:Sandbrink, R.; Masters, C.L.; Beyreuther, K.
submitted to the EMBL Data Library, March 1994
A:Description: Complete nucleotide ad deduced amino acid sequence of rat amyloid precurs
A:Reference number: S42880
A:Accession: S42880
A:Molecule type: mRNA
A:Residues: 1-765 <SAN>
A:Cross-references: UNIPROT:P15943; EMBL:X77934
R:Sandbrink, R.; Masters, C.L.; Beyreuther, K.
Biochim. Biophys. Acta 1219, 167-170, 1994
A>Title: Complete nucleotide and deduced amino acid sequence of rat amyloid protein prec
A:Reference number: S47528; MUID:94368849; PMID:8086458
A:Accession: S47528
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-765 <SA2>
A:Cross-references: EMBL:X77934
C:Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase i
C:Keywords: alternative splicing
F:312-362/Domain: animal Kunitz-type proteinase inhibitor homology <BPI>
```

C>Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004

C:Accession: T16210
R:Pauley, A.; Stelliyes, L.
submitted to the EMBL Data Library, June 1995
A:Description: The sequence of C. elegans cosmid F30H5.
A:Reference number: Z18478
A:Accession: T16210
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-1599 <PAU>
A:Cross-references: UNIPROT:Q09983; EMBL:U29096; PID:g861393; PIDN:AAA68408
A:Experimental source: strain Bristol N2
C:Genetics:
A:Gene: CBSP:F30H5.3
A:Introns: 12/1; 59/2; 85/3; 124/3; 217/2; 534/3; 560/1; 1549/1

Query Match 48.0%; Score 145; DB 2; Length 1599;
Best Local Similarity 49.0%; Pred. No. 2.6e-09;
Matches 25; Conservative 5; Mismatches 21; Indels 0; Gaps 0;

QY 1 CSMPOAGPCLASIPHHWYNNKTKICSFYIYGGCGGNNNFQTEAICLVTC 51
DB 563 CSQPLRLGDKQVRRYYNVAVTRACIFDYTGCGQGNNDNNFETLLEQCNTC 613

RESULT 23

S01802
chymotrypsin inhibitor I - silkworm
C:Species: Bombyx mori (silkworm)
C>Date: 30-Sep-1989 #sequence_revision 30-Sep-1989 #text_change 09-Jul-2004
C:Accession: S01802
R:Sasaki, T.
Biol. Chem. Hoppe-Seyler 369, 1235-1241, 1988
A:Title: Amino-acid sequences of two basic chymotrypsin inhibitors from silkworm larval
A:Reference number: S01802; MUID:89228538; PMID:3072972
A:Accession: S01802
A:Molecule type: protein
A:Residues: 1-62 <SAS>
A:Cross-references: UNIPROT:P10831
C:Superfamily: basic proteinase inhibitor; animal Kunitz-type proteinase inhibitor homol
C:Keywords: serine proteinase inhibitor
F;9-60/Domain: animal Kunitz-type proteinase inhibitor homology <BPI>

Query Match 47.7%; Score 144; DB 2; Length 62;
Best Local Similarity 60.0%; Pred. No. 1.5e-10;
Matches 27; Conservative 4; Mismatches 14; Indels 0; Gaps 0;

QY 7 AGCPCLASIPHHWYNNKTKICSFYIYGGCGGNNNFQTEAICLVTC 51
DB 16 SGPCFAYIKLYSYNOKTKCEBFYIYGGCGGNNDNNFETLLEQCNTC 60

RESULT 24

S04855
Alzheimer's disease amyloid A4 protein - mouse (fragment)
C:Species: Mus musculus domesticus (western European house mouse)
C>Date: 28-Feb-1990 #sequence_revision 28-Feb-1990 #text_change 09-Jul-2004
C:Accession: S04855
R:Fukuchi, K.I.; Martin, G.M.; Deeb, S.S.
Nucleic Acids Res. 17, 5396, 1989
A:Title: Sequence of the protease inhibitor domain of the A4 amyloid protein precursor
A:Reference number: S04855; MUID:89345111; PMID:2569710
A:Accession: S04855
A:Molecule type: mRNA
A:Residues: 1-76 <PUK>
A:Cross-references: UNIPROT:P12023; EMBL:X15210; NID:949965; PIDN:CAA33280.1; PID:G93013
A:Note: The authors translated the codon GAT for residue 74 as Val
C:Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase i
C:Keywords: alternative splicing; serine proteinase inhibitor; transmembrane protein
F;3-53/Domain: animal Kunitz-type proteinase inhibitor homology <BPI>

Query Match 47.7%; Score 144; DB 2; Length 76;
Best Local Similarity 47.1%; Pred. No. 1.9e-10;

Query Match 47.0%; Score 142; DB 1; Length 61;
Best Local Similarity 47.1%; Pred. No. 2.6e-10;
Matches 24; Conservative 9; Mismatches 18; Indels 0; Gaps 0;

QY 1 CSMPOEAGPCLASIPHHWYNNKTKICSEFIYGGCGGNNNNFQTEAICLVTC 51
DB 235 CNAEPDAGPCFTGVRHFYNNSSMACQLFTYGGCGGNNNNFVTERECLOSC 285

RESULT 33
TIPGBI
Alpha-1-microglobulin/inter-alpha-trypsin inhibitor precursor - pig (fragment)
N:Alternate names: bikunin; ITI; PI-14 (inhibitory fragment of ITI)
C:Species: Sus scrofa domestica (domestic pig)
C:Date: 30-Jun-1987 #sequence_revision 04-Feb-2000 #text_change 09-Jul-2004
C:Accession: S11066; S13493; A01208
R:Gebhard, W.; Schreitmuller, T.; Vetr, H.; Wachter, E.; Hochstrasser, K.
FEBS Lett. 269, 32-36, 1990
A:Title: Complementary DNA and deduced amino acid sequences of porcine alpha1-microglobulin
A:Reference number: S11066; MUID:90353595; PMID:1696914
A:Accession: S11066
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-337 <GB>
A:Cross-references: UNIPROT:P04366; EMBL:X53685; NID:g1877; PIDN:CAA37725.1; PID:g1878
R:Tavakkol, A.
Biochim. Biophys. Acta 1088, 47-56, 1991
A:Title: Molecular cloning of porcine alpha(1)-microglobulin/HI-30 reveals developmental
A:Reference number: S13493; MUID:91113729; PMID:1703444
A:Accession: S13493
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 'M', 3-48, 'M', 50-337 <TAV>
A:Cross-references: GB:X52087; NID:g1881; PIDN:CAA36306.1; PID:g1882
A:Note: the authors translated the codon GTG for residue 2 as a Met initiation codon
R:Hochstrasser, K.; Wachter, E.; Albrecht, G.J.; Reisinger, P.
Biol. Chem. Hoppe-Seyler 366, 473-478, 1985
A:Title: Kunitz-type proteinase inhibitors derived by limited proteolysis of the inter-alpha
A:Reference number: A90685; MUID:85225967; PMID:2408637
A:Accession: A01208
A:Molecule type: protein
A:Residues: 212-258, 'Q', 260-269, 'S', 271-277, 'Q', 279-282, 'A', 284, 'IR', 287-292, 'A', 294-310
C:Comment: This inhibitory fragment, released from native ITI after limited proteolysis of first domain interacts weakly with PMN-granulocytic elastase and not at all with pancreas

Query Match 47.0%; Score 142; DB 1; Length 337;
Best Local Similarity 47.1%; Pred. No. 1.4e-09;
Matches 24; Conservative 5; Mismatches 22; Indels 0; Gaps 0;

QY 1 CSMPOEAGPCLASIPHHWYNNKTKICSEFIYGGCGGNNNNFQTEAICLVTC 51
DB 216 COLGYSQGPCLGIMKRYFYNGSSMACETFYGGCGGNGNPFVSEKELQTC 266

RESULT 35
TIPGBI
Alpha-1-microglobulin / inter-alpha-trypsin inhibitor precursor [validated] - bovine
N:Alternate names: BI-14 (inhibitory fragment of ITI); bikunin; ITI
C:Species: Bos primigenius taurus (cattle)
C:Date: 25-Feb-1985 #sequence_revision 04-Feb-2000 #text_change 09-Jul-2004
C:Accession: S68149; A91717; A90685; S31219; A01209
R:Lindqvist, A.; Akerstroem, B.
Biochim. Biophys. Acta 1306, 98-106, 1996
A:Title: Bovine alpha(1)-microglobulin/bikunin. Isolation and characterization of liver
A:Reference number: S68149; MUID:96201710; PMID:8611630
A:Accession: S68149
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-352 <LIN>
A:Cross-references: UNIPROT:P00978; EMBL:U35642; NID:g1016297; PIDN:AAB07599.1; PID:g101
R:Hochstrasser, K.; Wachter, E.
Hoppe-Seyler's Z. Physiol. Chem. 364, 1679-1687, 1983
A:Title: Kunitz-type proteinase inhibitors derived by limited proteolysis of the inter-alpha
A:Reference number: A91717; MUID:84133807; PMID:6199275
A:Accession: A91717
A:Molecule type: protein
A:Residues: 227-267, 'L', 269-273, 'Q', 275-297, 'AF', 300-329, 'Q', 331-345, 'R', 347-348 <HOC>
R:Hochstrasser, K.; Wachter, E.; Albrecht, G.J.; Reisinger, P.
Biol. Chem. Hoppe-Seyler 366, 473-478, 1985
A:Title: Kunitz-type proteinase inhibitors derived by limited proteolysis of the inter-alpha
A:Reference number: A90685; MUID:85225967; PMID:2408637
A:Accession: A90685
A:Molecule type: protein
A:Residues: 347-349 <HOC2>
R:Hochstrasser, K.; Albrecht, G.J.; Schonberger, O.L.; Wachter, E.
Hoppe-Seyler's Z. Physiol. Chem. 364, 1689-1696, 1983
A:Title: Kunitz-type proteinase inhibitors derived by limited proteolysis of the inter-alpha
A:Reference number: A91718; MUID:84133808; PMID:6199276
A:Contents: annotation; reactive sites
R:Castillo, G.M.; Templeton, D.M.
FEBS Lett. 318, 292-296, 1993
A:Title: Subunit structure of bovine EGF (extracellular-matrix stabilizing factor(s)).
A:Reference number: S31219; MUID:93178646; PMID:7680011
A:Accession: S31219
A:Status: preliminary
A:Molecule type: protein
A:Residues: 206-214, 'X', 216, 'X', 218-220 <CAS>
R:Superfamily: alpha-1-microglobulin and inter-alpha-trypsin inhibitor light chain prec
C:Keywords: duplication; glycoprotein; plasma; serine proteinase inhibitor
F:35-188/Domain: lipocalin homology <LIP>
F:231-281/Domain: animal Kunitz-type proteinase inhibitor homology <BP1>
F:287-337/Domain: animal Kunitz-type proteinase inhibitor homology <BP2>
F:241/Inhibitory site: Leu (chymotrypsin, elastase) #status experimental
F:250/Binding site: carbohydrate (Asn) (covalent) #status experimental
F:297/Inhibitory site: Arg (trypsin) #status experimental

A:Molecule type: protein
A:Residues: 1-61 <NAK>
A:Cross-references: UNIPROT:P16044
A:Experimental source: hemocytes
A:Comment: The inhibitory activity is similar to bovine basic proteinase inhibitor.
C:Superfamily: basic proteinase inhibitor; animal Kunitz-type proteinase inhibitor homolog
C:Keywords: serine proteinase inhibitor
F:8-58/Domain: animal Kunitz-type proteinase inhibitor homolog <BPI>
F:18/Inhibitory site: Arg (chymotrypsin, elastase, trypsin, plasmin, plasma kallikrein)
Query Match 45.7%; Score 138; DB 1; Length 61;
Best Local Similarity 45.1%; Pred. No. 8e-10;
Matches 23; Conservative 7; Mismatches 21; Indels 0; Gaps 0;
QY 1 CSMQEQAGPCLASIPHHWYKTKICSEFIYGGCGGNNNNFQTEAICLVTC 51
DB 8 CTSPPVTGCRAGFRKYRNTYNTKQCEPFYGGCKGNRYKSEQDCLDAC 58
RESULT 41
TIHOBI
Alpha-1-microglobulin/inter-alpha-trypsin inhibitor - horse (fragment)
N:Alternate names: EI-14 (inhibitory fragment of ITI); ITI; trypsin inhibitor, E-UTI
C:Species: Equus caballus (domestic horse)
C:Date: 30-Jun-1987 #sequence_revision 04-Feb-2000 #text_change 09-Jul-2004
C:Accession: A01210; A45653
R:Hochstrasser, K.; Wachtel, E.; Albrecht, G.J.; Reisinger, P.
Biol. Chem. Hoppe-Seyler 366, 473-478, 1985
A:Title: Kunitz-type proteinase inhibitors derived by limited proteolysis of the inter-alpha-1-trypsin inhibitor
A:Reference number: A90685; UID:85225967; PMID:2408637
A:Accession: A01210
A:Molecule type: protein
A:Residues: 3-125 <HOC>
A:Cross-references: UNIPROT:P04355
R:Veeraragavan, K.; Singh, K.; Wachtel, E.; Hochstrasser, K.
Biochem. Int. 26, 405-413, 1992
A:Title: Characterization of a trypsin inhibitor from equine urine.
A:Reference number: A45653; UID:92328813; PMID:1627153
A:Accession: A45653
A>Status: preliminary
A:Molecule type: protein
A:Residues: 1-12, 'E', 14-33 <VEE>
A:Cross-references: PIDN:AAB22430.1; PID:G250858
A:Experimental source: urine
A:Note: sequence extracted from NCBI backbone (NCBIP:107966)
C:Comment: This inhibitory fragment, released from native ITI after limited proteolysis of first domain interacts weakly with PMN-granulocytic elastase and not at all with pancreatic elastase. The amino acid at position P2' (19-Met) appears to determine the specificity of elastase; those with leucine interact strongly.
C:Superfamily: alpha-1-microglobulin and inter-alpha-trypsin inhibitor light chain precursor
C:Keywords: duplication; glycoprotein; plasma; serine proteinase inhibitor
F:7-57/Domain: animal Kunitz-type proteinase inhibitor homolog <BPI>
F:63-113/Domain: animal Kunitz-type proteinase inhibitor homolog <BP2>
F:7-57, 16-40, 32-53, 63-113, 72-96, 88-109/Diulfide bonds: #status predicted
F:17/Inhibitory site: Leu (chymotrypsin, elastase) #status predicted
F:26/Binding site: carbohydrate (Asn) (covalent) #status experimental
F:73/Inhibitory site: Arg (trypsin) #status predicted
Query Match 45.7%; Score 138; DB 1; Length 125;
Best Local Similarity 45.1%; Pred. No. 1.6e-09;
Matches 23; Conservative 6; Mismatches 22; Indels 0; Gaps 0;
QY 1 CSMQEQAGPCLASIPHHWYKTKICSEFIYGGCGGNNNNFQTEAICLVTC 51
DB 7 CQLDHAQGPCLGIMISRYFYNGTSMACETFOYGGCLGNGNMFASQKECLQC 57
RESULT 42
A53390
Kunitz-type proteinase inhibitor precursor - sheep
C:Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
C:Date: 27-Jun-1994 #sequence_revision 27-Jun-1994 #text_change 09-Jul-2004

C:Accession: A53390
R:Kramer, K.K.; Duffy, J.Y.; Klemann, S.W.; Bixby, J.A.; Low, B.G.; Pope, W.F.; Roberts, J. Biol. Chem. 269, 7255-7261, 1994
A:Title: Selective cloning of cDNA for secretory proteins of early embryos. Identification of a novel Kunitz-type proteinase inhibitor
A:Reference number: A53390; UID:94171738; PMID:7510284
A:Accession: A53390
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-265 <KRA>
A:Cross-references: UNIPROT:Q29428; GB:U00165; NID:G501024; PIDN:AAA19108.1; PID:G992040
C:Keywords: serine proteinase inhibitor
F:208-258/Domain: animal Kunitz-type proteinase inhibitor homolog <BPI>
Query Match 45.7%; Score 138; DB 2; Length 265;
Best Local Similarity 41.2%; Pred. No. 3.3e-09;
Matches 21; Conservative 12; Mismatches 18; Indels 0; Gaps 0;
QY 1 CSMQEQAGPCLASIPHHWYKTKICSEFIYGGCGGNNNNFQTEAICLVTC 51
DB 208 CLPEKVTGDCNATWRYFYNTQTGLCEQFVYTGCGNGNFFENLEDCKMTC 258
RESULT 43
A54951
Tissue factor pathway inhibitor-2 precursor - human
N:Alternate names: placental protein 5 (PF5)
C:Species: Homo sapiens (man)
C:Date: 31-May-1996 #sequence_revision 31-May-1996 #text_change 09-Jul-2004
C:Accession: A54951; I55185; A34029; B34029
R:Spracher, C.A.; Kiesel, W.; Mathewes, S.; Foster, D.C.
Proc. Natl. Acad. Sci. U.S.A. 91, 3353-3357, 1994
A:Title: Molecular cloning, expression, and partial characterization of a second human tissue factor pathway inhibitor
A:Reference number: A54951; UID:94211862; PMID:8159751
A:Accession: A54951
A>Status: translated from GB/EMBL/DDBJ
A:Molecule type: mRNA
A:Residues: 1-235 <RES>
A:Cross-references: UNIPROT:P48307; GB:I27624; NID:G441149; PIDN:AAA20094.1; PID:G44115
A:Experimental source: placenta
R:Miyagi, Y.; Koshikawa, N.; Yasumitsu, H.; Miyagi, E.; Hirahara, F.; Aoki, I.; Muegi, J. Biochem. 116, 939-942, 1994
A:Title: cDNA cloning and mRNA expression of a serine proteinase inhibitor secreted by human placenta
A:Reference number: I55185; UID:95204397; PMID:7896752
A:Accession: I55185
A>Status: nucleic acid sequence not shown; translation not shown; translated from GB/EMBL/DDBJ
A:Molecule type: mRNA
A:Residues: 1-235 <RE2>
A:Cross-references: GB:D29992; NID:G484050; PIDN:BAA06272.1; PID:G484051
A:Note: parts of this sequence, including the amino end of the mature protein, were determined by the authors.
R:Buetzow, R.; Huhtala, M.L.; Bohn, H.; Virtanen, I.; Seppälä, M.
Biochem. Biophys. Res. Commun. 150, 483-490, 1988
A:Title: Purification and characterization of placental protein 5.
A:Reference number: A34029; UID:88106628; PMID:3276312
A:Accession: A34029
A:Molecule type: protein
A:Residues: 'A', 24-33, 'X', 35 <BUB>
A:Accession: C34029
A:Molecule type: protein
A:Residues: 47-50, 'X', 52-53 <BU2>
A:Accession: B34029
A:Molecule type: protein
A:Residues: 133, 'X', 135-137, 'X', 139-140, 'X', 142-144, 'X', 146 <BU3>
C:Genetics:
A:Gene: GDB:TFPI2
A:Cross-references: GDB:354485
C:Superfamily: tissue factor pathway inhibitor; animal Kunitz-type proteinase inhibitor
C:Keywords: anticoagulant; blood coagulation; duplication; glycoprotein; heparin binding
F:1-22/Domain: signal sequence #status predicted <SIG>
F:23-235/Product: tissue factor pathway inhibitor-2 #status predicted <MAT>
F:36-86/Domain: animal Kunitz-type proteinase inhibitor homolog <BPI>
F:96-149/Domain: animal Kunitz-type proteinase inhibitor homolog <BP2>
F:158-208/Domain: animal Kunitz-type proteinase inhibitor homolog <BP3>
F:36-86, 45-69, 61-82, 96-149, 106-130, 122-145, 158-208, 167-191, 183-204/Diulfide bonds: #status predicted

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 21, 2005, 15:41:33 ; Search time 28.1327 Seconds
(without alignments)
928.315 Million cell updates/sec

Title: US-10-807-204-1_COPY_77_127

Perfect score: 302
Sequence: 1 CSMPEAGPCLASIPHHWYN.....GCGQNNNNFQTEAICLVTC 51

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 50 summaries

Database : Uniprot_03:*

1: uniprot_sprot:*

2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	247	81.8	137	2	Q9BDL0
2	223	73.8	182	2	Q6IE19
3	219	72.5	133	1	EPPI_HUMAN
4	219	72.5	143	2	Q86TP9
5	216	71.5	133	2	Q8HZ45
6	211	69.9	133	1	EPPI_MACMU
7	188	62.3	134	1	EPPI_MOUSE
8	170	56.3	110	1	IBP_CARCR
9	169	56.0	571	2	Q7TQX3
10	166	55.0	86	2	Q9GP15
11	166	55.0	169	2	Q9N0X7
12	165	54.6	131	1	WFD6_HUMAN
13	165	54.6	750	2	Q6DJB6
14	163	54.0	67	1	IBPC_BOVIN
15	160	53.0	83	2	Q6ITB9
16	160	53.0	252	1	SPT2_MOUSE
17	160	53.0	283	2	Q6ZNI4
18	160	53.0	576	2	Q8TEU8
19	160	53.0	576	2	Q6UXZ9
20	160	53.0	2419	2	Q7PXZ1
21	159	52.6	80	2	Q8T3S7
22	159	52.6	2174	2	Q9GGR0
23	159	52.6	2772	2	Q9VAV4
24	159	52.6	2776	2	Q869A0
25	159	52.6	2894	2	Q7KRX2
26	159	52.6	2898	2	Q86BZ9
27	158	52.3	62	1	IVBT_OXYSC
28	158	52.3	69	1	CRPT_BOOMI
29	158	52.3	142	2	Q6B8G1
30	157	52.0	83	2	Q6ITB4
31	157	52.0	83	2	Q6ITB5

ALIGNMENTS

RESULT 1

Q9BDL0 PRELIMINARY; PRT; 137 AA.
AC Q9BDL0; DT 01-JUN-2001 (Tremblrel. 17, Created)
DT 01-JUN-2001 (Tremblrel. 17, Last sequence update)
DT 01-MAR-2004 (Tremblrel. 26, Last annotation update)
DE Eppin.
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Testis;
RX MEDLINE=22791380; PubMed=12909348; DOI=10.1016/S0378-1119(03)00608-5;
RA Sivashanmugam P., Hall S.H., Hamil K.G., French F.S., O'Rand M.G.,
RA Richardson R.T.;
RT "Characterization of mouse Eppin and a gene cluster of similar
RT protease inhibitors on mouse chromosome 2.";
RL Gene 312:125-134(2003).
CC -1- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.
DR EMBL; AF346415; AAK31337.1; -.
DR HSSP; Q16019; IAP.
DR GO; GO:0004867; F:serine-type endopeptidase inhibitor activity; IEA.
DR InterPro; IPR002223; Prot_Inh_Kunz-m.
DR InterPro; IPR008197; WAP.
DR Pfam; PF00014; Kunitz_BPTI; 1.
DR Pfam; PF00095; WAP; 1.
DR PRINTS; PRO0003; 4DISULPHCORE.
DR PRINTS; PRO0759; BASICPTASE.
DR ProDom; PD000222; Prot_Inh_Kunz-m; 1.
DR SMART; SM00131; KU; 1.
DR SMART; SM00217; WAP; 1.
DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
DR PROSITE; PS50279; BPTI_KUNITZ_2; 1.
SQ SEQUENCE 137 AA; 15773 MW; F397AF4E065D626B CRC64;

Query Match 81.8%; Score 247; DB 2; Length 137;

Best Local Similarity 78.4%; Pred. No. 1.1e-22;
Matches 40; Conservative 5; Mismatches 6; Indels 0; Gaps 0;

QY 1 CSMPEAGPCLASIPHHWYNKKTKTCSEFIYGGCGGNNNNFQTEAICLVTC 51

Db 77 CSMPEKGTGCLAFIPRWYDKEREICTEFIYGGCGGNNNNFQTEAICLVIC 127

RESULT 2

Q6IE19

```

ID AC Q6IE19 PRELIMINARY; PRT; 182 AA.
AC Q6IE19;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE WAP four-disulfide core 6-like 1.
GN Name=wfd6c11;
OS Rattus norvegicus (Rat)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Sprague-Dawley;
RX PubMed=15060002; DOI=10.1101/gr.1946304;
RA Fuente X.S., Lopez-Otin C.;
RT "A genomic analysis of rat proteases and protease inhibitors.";
RL Genome Res. 14:609-622(2004).
CC -!- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.
CC -!- MISCELLANEOUS: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ third party annotation (TPA) entry.
DR EMBL; BN000374; CAES1900.1; -.
DR HSP; P00974; I6K6.
DR GO; GO:0004867; F:serine-type endopeptidase inhibitor activity; IEA.
DR InterPro; IPR002223; Prot_Inh_Kunz-m.
DR InterPro; IPR008197; WAP.
DR Pfam; PF00014; Kunitz_BPTI; 1.
DR Pfam; PF00095; WAP; 1.
DR PRINTS; PR00003; 4DISULPHCORE.
DR PRINTS; PR00759; BASICPTASE.
DR ProDom; PD000222; Prot_Inh_Kunz-m; 1.
DR SMART; SM00131; KU; 1.
DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
DR PROSITE; PS02279; BPTI_KUNITZ_2; 1.
SQ SEQUENCE 182 AA; 21018 MW; EB12D7BFF756707E CRC64;

Query Match 73.8%; Score 223; DB 2; Length 182;
Best Local Similarity 66.7%; Pred. No. 1.3e-19;
Matches 34; Conservative 8; Mismatches 9; Indels 0; Gaps 0;

Qy 1 CSMPOEAGPCIASIPHHWNKKIKCSFFIYGGCGGNNNFQTRAILCVTC 51
Dd 77 CSLPDQAGPCPLAYLPWWYNNKTNLTQFIYGGCGGNNTNFKSLDKICTSIC 127

RESULT 3
EPPI HUMAN STANDARD; PRT; 133 AA.
AC Q95925; Q96SD7; Q9HD30;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE EpPin precursor (Epидidymal protease inhibitor) (Serine protease
DE inhibitor-like with Kunitz and WAP domains 1) (WAP four-disulfide core
DE domain protein 7) (Protease inhibitor WAP7).
GN Name=SPINLW1; Synonyms=WAP7, WFDCT;
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Carnithini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
RC TISSUE=Epидidymis, and Testis;
RX MEDLINE=21297183; PubMed=11404006; DOI=10.1016/S0378-1119(01)00462-0;
RA Richardson R.T., Sivashanmugam P., Hall S.H., Hamil K.G., Moore P.A.,
RA Ruben S.M., French P.S., O'Rand M.G.;
RT "Cloning and sequencing of human EpPin: a novel family of protease
RT inhibitors expressed in the epидidymis and testis.";
RL Gene 270:93-102(2001).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RA Stavrides G.S., Huckle E.J., Deloukas P.;
RA Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=21639749; PubMed=11780052; DOI=10.1038/414865a;
RA Deloukas P., Matthews L.H., Ashurst J.L., Burton J., Gilbert J.G.R.,
RA Jones M., Stavrides G., Almeida J.P., Babbage A.K., Bagguley C.L.,
RA Bailey J., Barlow K.F., Bates K.N., Bead L.M., Beare D.M.,
RA Beasley O.P., Bird C.P., Blakey S.E., Bridgeman A.M., Brown A.J.,
RA Buck D., Burrill W.D., Butler A.P., Carder C., Carter N.P.,
RA Chapman J.C., Clamp M., Clark G., Clark L.N., Clark S.Y., Clee C.M.,
RA Clegg S., Cobley V.E., Collier R.E., Connor R.E., Corby N.R.,
RA Coulson A., Coville G.J., Deadman R., Dhami P.D., Dunn M.,
RA Ellington A.G., Frankland J.A., Fraser A., French L., Garner P.,
RA Grafham D.V., Griffiths C., Griffiths M.N.D., Gwilliam R., Hall R.E.,
RA Hammond S., Harley J.L., Heath P.D., Ho S., Holden J.L., Howden P.J.,
RA Huckle E., Hunt A.R., Hunt S.E., Jekosch K., Johnson C.M., Johnson D.,
RA Kay M.P., Kimberley A.M., King A., Knights A., Laird G.K., Lawlor S.,
RA Lehaealho M.H., Leversha M.A., Lloyd C., Lloyd D.M., Lovell J.D.,
RA Marsh V.L., Martin S.L., McConachie L.J., McIay K., McMurray A.A.,
RA Milne S.A., Mistry D., Moore M.J.F., Mullikin J.C., Nickerson T.,
RA Oliver K., Parker A., Patel R., Pearce T.A.V., Peck A.I.,
RA Phillimore B.J.C.T., Prathalingam S.R., Plumb R.W., Ramsay H.,
RA Rice C.M., Ross M.T., Scott C.E., Senra H.K., Shownkeen R., Sims S.,
RA Skuce C.D., Smith M.L., Soderlund C., Steward C.A., Suleston J.E.,
RA Swann R.M., Sycamore N., Taylor R., Tee L., Thomas D.W., Thorpe A.,
RA Tracey A., Tromans A.C., Vaudin M., Wall M., Wallis J.M.,
RA Whitehead S.L., Whittaker P., Willey D.L., Williams L., Williams S.A.,
RA Wilming L., Wray P.W., Hubbard T., Durbin R.M., Bentley D.R., Beck S.,
RA Rogers J.;
RT "The DNA sequence and comparative analysis of human chromosome 20.";
RL Nature 414:865-871(2001).
RN [4]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RC TISSUE=Brain;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heieh F.,
RA Datchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.P., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Pahey J., Helton E., Kettaman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko I., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butcherfield Y.S.N., Krzywinski M.I., Skaleka U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC -!- SUBCELLULAR LOCATION: Secreted (Potential).
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=1;
CC IsoId=O95925-1; Sequence=Displayed;
CC Name=2;
CC IsoId=O95925-2; Sequence=VSP_006755;
CC -!- TISSUE SPECIFICITY: Expressed in epидidymis and testis.
CC -!- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.
CC -!- SIMILARITY: Contains 1 WAP-type domain.
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CC or send an email to license@isb-sib.ch).
CC -----
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RA	Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.
RA	Fahy J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S., Krzywinski A.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E., Jones S.J., Marra M.A.;
RA	"Generation and initial analysis of more than 15,000 full-length human
RT	and mouse cDNA sequences";
RL	Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN	[2]
RP	SEQUENCE FROM N.A.
RC	TISSUE=Brain;
RA	Straussberg R.;
RL	Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
CC	- I- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.
DR	EMBL; BC044829; AAH44829.1; -.
DR	HSP; P00974; IUUA.
DR	GO; GO:0004867; F:serine-type endopeptidase inhibitor activity; IEA.
DR	InterPro; IPR002223; Prot_inh_Kunz-m.
DR	InterPro; IPR008197; WAP.
DR	Pfam; PF00014; Kunitz_BPTI; 1.
DR	Pfam; PF00095; WAP; 1.
DR	PRINTS; PR00003; 4DISULPHCORE.
DR	PRINTS; PRO0759; BASICPTASE.
DR	PRODOM; PD000222; Prot_inh_kunzm; 1.
DR	SMART; SM00131; KU; 1.
DR	SMART; SM00217; WAP; 1.
DR	PROSITE; PS00317; 4_DISULFIDE_CORE; 1.
DR	PROSITE; PS00280; BPTI_KUNITZ_1; 1.
DR	PROSITE; PS00279; BPTI_KUNITZ_2; 1.
FT	NON_TER 1
SQ	SEQUENCE 143 AA; 16506 MW; 92BF56C2B7977508 CRC64;
Query Match 72.5%; Score 219; DB 2; Length 143;	
Best Local Similarity 68.6%; Pred. No. 3.3e-19;	
Matches 35; Conservative 5; Mismatches 11; Indels 0; Gaps	
QY	1 CSMPOEAGPCLASIPHHWYNKTKICSEFYVGGCGGNNNFQTEAICLVTC 51 : : : : : : : : : : : :
Db	87 CEMPETGETGLAYFLHWYDKDCTCMFVVGCGGNNNFQSKANCLNTC 137 : : : : : : : : : : : :
RESULT 5	
Q8HZ45	ID Q8HZ45 PRELIMINARY; PRT; 133 AA.
AC	Q8HZ45;
DT	01-MAR-2003 (TrEMBLrel. 23, Created)
DT	01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT	01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE	Epididymal protease inhibitor 1.
GN	Name=Eppin;
OS	Papio papio. (Guinea baboon).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae;
OC	Cercopithecinae; Papio.
OX	NCBI_TaxID=100937;
EN	[1]
RP	SEQUENCE FROM N.A.
RC	TISSUE=Testis;
RA	Sivadamugam P., O'Rand M.G., Richardson R.T.;
RL	Submitted (AUG-2002) to the EMBL/GenBank/DBJ databases.
CC	- I- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.
DR	EMBL; AV141973; AAN08507.1; -.
DR	HSP; P00974; IUUA.
DR	GO; GO:0008233; F:peptidease activity; IEA.
DR	GO; GO:0004867; F:serine-type endopeptidase inhibitor activity; IEA.
DR	InterPro; IPR002223; Prot_inh_Kunz-m.
DR	InterPro; IPR008197; WAP.
DR	Pfam; PF00014; Kunitz_BPTI; 1.
DR	Pfam; PF00095; WAP; 1.
DR	PRINTS; PRO0759; BASICPTASE.

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DR ProDom; P000222; Prot_Inh_Kunz-m; 1.
DR SMART; SM00131; KU; 1.
DR SMART; SM00217; WAP; 1.
DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
DR PROSITE; PS00279; BPTI_KUNITZ_2; 1.
KW Protease.
SQ SEQUENCE 133 AA; 15277 MW; B33AEB57ECBEBE84 CRC64;

Query Match          71.5%; Score 216; DB 2; Length 133;
Best Local Similarity 68.6%; Pred. No. 7.2e-19;
Matches 35; Conservative 3; Mismatches 13; Indels 0; Gaps 0;

Qy 1 CSMPOEAGPCLASIPHWYNNKTKICSEFIYGGCGQNNNNFQTEAICLVTC 51
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 77 CEMNETGPCLAFFIRWYDKKNTCTSTFVHGCGQNNNNFQSEANCLNTC 127

RESULT 6
EPPI_MACMU
ID EPPI_MACMU STANDARD; PRT; 133 AA.
AC Q9BDL1.
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DE 05-JUL-2004 (Rel. 44, Last annotation update)
DE Eppin precursor (Epidiidymal protease inhibitor) (Serine protease
DE inhibitor-like with Kunitz and WAP domains 1).
GN Name=SPINLW1;
OS Macaca mulatta (Rhesus macaque).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae;
OC Cercopitheciinae; Macaca.
OX NCBI_TaxID=9544;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Epidiidymis, and Testis;
RA Sivashanmugam P., Hall S.H., Hamil K.G., French F.S., O'Rand M.G.,
RA Richardson R.T.;
RT "Characterization of monkey and mouse Eppin, a protease inhibitor from
RT epidiidymis and testis.";
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
CC -! SUBCELLULAR LOCATION: Secreted (Potential).
CC -! TISSUE SPECIFICITY: Expressed in epidiidymis and testis.
CC -! SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.
CC -! SIMILARITY: Contains 1 WAP-type domain.
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; AF346414; AAK31336.1; -.
DR HSSP; P00974; 1BPTI.
DR InterPro; IPR002223; Prot_Inh_Kunz-m.
DR InterPro; IPR008197; WAP.
DR Pfam; PF00014; Kunitz_BPTI; 1.
DR Pfam; PF00095; WAP; 1.
DR PRINTS; PR00759; BASICPTASE.
DR ProDom; P000222; Prot_Inh_Kunz-m; 1.
DR SMART; SM00131; KU; 1.
DR SMART; SM00217; WAP; 1.
DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
DR PROSITE; PS00279; BPTI_KUNITZ_2; 1.
KW Serine protease inhibitor; Signal.
SIGNAL 1 21 Potential.
FT CHAIN 22 133 Eppin.
FT DOMAIN 29 73 WAP.
FT DOMAIN 77 127 BPTI/Kunitz inhibitor.
FT DISULFID 33 61 By similarity.
FT DISULFID 40 65 By similarity.
FT DISULFID 48 60 By similarity.

us-10-807-204-1_copy_77_127_std.rup
Page 4
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OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM 2).
RX MEDLINE=22304654; PubMed=12206714; DOI=10.1042/BJ20020869;
RA Clauss A., Lilja H., Lundwall A.;
RT "A locus on human chromosome 20 contains several genes expressing
RL protease inhibitor domains with homology to whey acidic protein."; Biochem. J. 368:233-242(2002).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RX MEDLINE=21638749; PubMed=11780052; DOI=10.1038/414865a;
RA Deloukas P., Matthews L.H., Anisuris J.L., Burton J., Gilbert J.G.R., Jones M., Stavrides G., Almeida J.P., Babbage A.K., Bagguley C.L., Bailey J., Barlow K.F., Bates K.N., Beard L.M., Beare D.M., Beasley O.P., Bird C.P., Blake S.E., Bridgeman A.M., Brown A.J., Buck D., Burrill W.D., Butler A.P., Carder C., Carter N.P., Clee C.M., Chapman J.C., Clamp M., Clark G., Clark L.N., Clark S.Y., Clegg S., Clegg S., Cobley V.E., Collier R.E., Connor R.E., Corby N.R., Coulson A., Coville G.J., Deadman R., Dhani P.D., Dunn M., Ellington A.G., Frankland J.A., Fraser A., French L., Garner P., Graffham D.V., Griffiths C., Griffiths M.N.D., Gwilliam R., Hall R.E., Hammond S., Harley J.L., Heath P.D., Ho S., Holden J.L., Howden P.J., Huckle E., Hunt A.R., Hunt S.E., Jekosch K., Johnson C.M., Johnson D., Kay M.P., Kimberley A.M., King A., Knights A., Laird G.K., Lawlor S., Lehaegslaitho M.H., Leversha M.A., Lloyd C., Lloyd D.M., Lovell J.D., Marsh V.L., Martin S.L., McConachie L.J., McLay K., McMurray A.A., Milne S.A., Mistry D., Moore M.J.F., Mullikin J.C., Nickerson T., Oliver K., Parker A., Patel R., Pearce T.A.V., Peck A.I., Phillimore B.J.C.F., Prathalingam S.R., Plumb R.W., Ramsay H., Rice C.M., Ross M.T., Scott C.E., Sehra H.K., Showkneen R., Sims S., Skuce C.D., Smith M.L., Soderlund C., Steward C.A., Sulston J.E., Swann R.M., Sycamore N., Taylor R., Tee L., Thomas D.W., Thorpe A., Tracey A., Tromans A.C., Vaudin M., Wall M., Wallis J.M., Whitehead S.L., Whitaker P., Willey D.L., Williams L., Williams S.A., Wilming L., Wray P.W., Hubbard T., Durbin R.M., Bentley D.R., Beck S., Rogers J.;
RT "The DNA sequence and comparative analysis of human chromosome 20."; Nature 414:865-871(2001).
RL Nature 414:865-871(2001).
CC -1- SUBCELLULAR LOCATION: Secreted (Potential).
CC -1- ALTERNATIVE PRODUCTS:
CC Name=1;
CC Event=Alternative splicing; Named isoforms=2;
CC Name=2;
CC IsoId=Q9BQY6-1; Sequences=Displayed;
CC IsoId=Q9BQY6-2; Sequences=VSP_007550, VSP_007551;
CC -1- TISSUE SPECIFICITY: Ubiquitously expressed, but the highest levels are found in epididymis, testis and trachea.
CC -1- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.
CC -1- SIMILARITY: Contains 1 WAP-type domain.
CC -----
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CC -----
CC EMBL; AF411861; AAN03684.1; -;
CC EMBL; AL031663; CAC36264.1; -;
CC HSP; P02760; 1B1K.
CC Genew; HGNC:16164; WPC6.
DR InterPro; IPR002223; Prot_Inh_Kunz-m.
DR InterPro; IPR008197; WAP.
DR Pfam; PF00014; Kunitz_BPTI; 1.
DR Pfam; PF00095; WAP; 1.
DR PRINTS; PR00759; BASICTPASE.
DR ProDom; PD000222; Prot_Inh_Kunz-m; 1.
DR SMART; SM00131; KU; 1.
DR SMART; SM00217; WAP; 1.
DR PROSITE; PS00317; 4 DISULFIDE CORE; FALSE NEG.
DR PROSITE; PS00280; BPTI_KUNITZ_1; FALSE NEG.
DR PROSITE; PS00279; BPTI_KUNITZ_2; 1.

KW Alternative splicing; Serine protease inhibitor; Signal.
FT SIGNAL 1 25 Potential.
FT CHAIN 26 131 WAP four-disulfide core domain protein 6.
FT DOMAIN 31 69 WAP.
FT DOMAIN 70 128 BPTI/Kunitz inhibitor.
FT DISULFID 33 61 By similarity.
FT DISULFID 48 60 By similarity.
FT DISULFID 54 69 By similarity.
FT VARSPLIC 75 86 IYAVCHRRRLAPA -> VSLTYHKKELE (in isoform 2).
FT /FTid=VSP_007550.
FT VARSPLIC 87 131 Missing (in isoform 2).
FT /FTid=VSP_007551.
SQ SEQUENCE 131 AA; 14626 MW; 2F6D06EF43EB7564 CRC64;
Query Match 54.6%; Score 165; DB 1; Length 131;
Best Local Similarity 96.8%; Pred. No. 1.5e-12;
Matches 30; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 21 KKTICSFYIYGGCGGNNNNFQTEAICLVTC 51
Db 97 KKTICSFYIYGGCGGNNNNFQTEAICLVTC 127
RESULT 13
Q6DJB6 PRELIMINARY; PRT; 750 AA.
AC Q6DJB6;
DT 25-OCT-2004 (TRENBLrel. 28, Created)
DT 25-OCT-2004 (TRENBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TRENBLrel. 28, Last annotation update)
DE App-prov protein.
GN Name=app-prov;
OS Xenopus tropicalis (Western clawed frog) (Silurana tropicalis).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8364;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Whole body;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnae.242603899;
RA Strausberg R.D., Feingold E.A., Grouse L.H., Derge J.G., Schuler G.D., Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D., Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh P., Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Diatchenko M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Fahy J., Hellon E., Kettner M., Madan A., Rodriguez S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.C., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S., Krzywinski M.I., Skalska U., Smalick D.E., Schnerch A., Schein J.E., Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences."; Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Whole body;
RC Klein S., Gerhard D.S.;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBSJ databases.
CC -1- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.
CC EMBL; BC075266; AAH75266.1; -;
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0005488; F:binding; IEA.
DR GO; GO:0004867; F:serine-type endopeptidase inhibitor activity; IEA.
DR InterPro; IPR008155; A4_APP.

ITOH H., KATAOKA H., HAMASUNA K., KITAHARA N., KOBAYASHI M.,
"Hepatocyte growth factor activator inhibitor type 2 lacking the first

RT Kunitz-type serine proteinase inhibitor domain is a predominant
RT product in mouse but not in human.;
RL Biochem. Biophys. Res. Commun. 255:740-748(1999).
CC !- FUNCTION: Inhibitor of HGF activator.
CC !- SUBCELLULAR LOCATION: Type I membrane protein (Potential).
CC !- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=3;
CC Name=1;
CC IsoId=Q9WU03-1; Sequence=Displayed;
CC Name=2;
CC IsoId=Q9WU03-2; Sequence=VSP_003034;
CC Name=3;
CC IsoId=Q9WU03-3; Sequence=VSP_003035, VSP_003036;
CC !- TISSUE SPECIFICITY: Isoform 2 is more predominantly expressed than
CC isoform 1.
CC !- DOMAIN: This inhibitor contains two inhibitory domains.
CC !- SIMILARITY: Contains 2 BPTI/Kunitz domains.
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CC -----
DR EMBL; AF099016; AAD22172.1; -;
DR EMBL; AF099019; AAD22173.1; -;
DR EMBL; AF099020; AAD22174.1; -;
DR HSSP; P00974; IK09.
DR MGD; MGI:1338031; Spint2.
DR InterPro; IPR002223; Prot_Inh_Kunz-m.
DR Pfam; PF00014; Kunitz BPTI; 2.
DR PRINTS; PR00759; BASICPTASE.
DR ProDom; PD000222; Prot_Inh_Kunz-m; 2.
DR SMART; SM00131; KU; 1.
DR PROSITE; PS00280; BPTI_KUNITZ_1; 2.
DR PROSITE; PS0279; BPTI_KUNITZ_2; 2.
KW Alternative splicing; Glycoprotein; Repeat; Serine protease inhibitor;
KW Signal; Transmembrane.
FT SIGNAL 1 27 Potential.
FT CHAIN 28 252 Kunitz-type protease inhibitor 2.
FT DOMAIN 28 197 Extracellular (Potential).
FT TRANSMEM 198 218 Potential.
FT DOMAIN 219 252 Cytoplasmic (Potential).
FT DOMAIN 38 88 BPTI/Kunitz inhibitor 1.
FT DOMAIN 133 183 BPTI/Kunitz inhibitor 2.
FT SITE 48 49 Reactive bond (By similarity).
FT SITE 143 144 Reactive bond (By similarity).
FT DISULFID 38 88 By similarity.
FT DISULFID 47 71 By similarity.
FT DISULFID 63 84 By similarity.
FT DISULFID 133 183 By similarity.
FT DISULFID 142 166 By similarity.
FT DISULFID 158 179 By similarity.
FT CARBOHYD 57 57 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 94 94 N-linked (GlcNAc...) (Potential).
FT VARSPPLIC 37 93 Missing (in isoform 2 and isoform 3).
FT VARSPPLIC 114 128 PRKQSAEDLSAIFN -> CFVELSVAALFLPYA (in
FT isoform 3).
FT VARSPPLIC 129 252 /FTId=VSP_003035.
FT VARSPPLIC 252 252 Missing (in isoform 3).
FT SEQUENCE 252 AA; 27914 MW; B2FF4B86924D4F8F CRC64;
Query Match 53.0%; Score 160; DB 1; Length 252;
Best Local Similarity 49.0%; Pred. No. 1.2e-11;
Matches 25; Conservative 7; Mismatches 19; Indels 0; Gaps 0;
QY 1 CSMQVAGPCLASIPHWYNNKTKICSEFIYGGCGGNNNFQTEAICLVTC 51
DB CGSVKVGKCRASIPRWYNNITDGSQPFVYGGCEGNGNYQSKBCLDKC 88

RESULT 17
Q6ZNI4
ID Q6ZNI4 PRELIMINARY; PRT; 283 AA.
AC Q6ZNI4;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE Hypothetical protein FLJ16032.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Tongue;
RA Nimmiya K., Wagatsuma M., Kanda K., Kondo H., Yokoi T., Kodaira H.,
RA Furuya T., Takahashi M., Kikkawa E., Omura Y., Abe K., Kamihara K.,
RA Katsuta N., Sato K., Tanikawa M., Yamazaki M., Sugiyama T., Irie R.,
RA Otsuki T., Sato H., Wakamatsu A., Ishii S., Yamamoto J., Isono Y.,
RA Kawai-Hio Y., Saito K., Nishikawa T., Kimura K., Yamashita H.,
RA Matsuoka K., Nakamura Y., Sekine M., Kikuchi H., Murakawa K.,
RA Kanehori K., Takahashi-Fujii A., Oshima A., Sugiyama A., Kawakami B.,
RA Suzuki Y., Sugano S., Nagahari K., Masuho Y., Nagai K., Isogai T.;
RL Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.
CC !- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.
DR EMBL; AK131196; BAD18391.1; -;
DR HSSP; P00974; IK09.
DR GO; GO:0004867; F:serine-type endopeptidase inhibitor activity; IEA.
DR InterPro; IPR001134; Netrin-C.
DR InterPro; IPR002223; Prot_Inh_Kunz-m.
DR InterPro; IPR008993; TIMP like.
DR Pfam; PF00014; Kunitz BPTI; 2.
DR PRINTS; PR00759; BASICPTASE.
DR ProDom; PD000222; Prot_Inh_Kunz-m; 2.
DR SMART; SM00131; KU; 1.
DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
DR PROSITE; PS0279; BPTI_KUNITZ_2; 1.
DR PROSITE; PS0189; NTR; 1.
SQ SEQUENCE 283 AA; 31291 MW; 86206E7309866D30 CRC64;
Query Match 53.0%; Score 160; DB 2; Length 283;
Best Local Similarity 49.0%; Pred. No. 1.3e-11;
Matches 25; Conservative 7; Mismatches 19; Indels 0; Gaps 0;
QY 1 CSMQVAGPCLASIPHWYNNKTKICSEFIYGGCGGNNNFQTEAICLVTC 51
DB 93 CSLPALQGPCKAYAPRWAYNSQTGQCOSFVYGGCEGNGNPFESRACBESC 143
RESULT 18
Q8TEU8
ID Q8TEU8 PRELIMINARY; PRT; 576 AA.
AC Q8TEU8;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Multivalent protease inhibitor protein.
GN Name=WF1KGNRP;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21173622; PubMed=11274388; DOI=10.1073/pnas.061028398;
RA Trexler M., Banyai L., Patthy L.;
RT "A human protein containing multiple types of protease-inhibitory
RT modules.";
RL Proc. Natl. Acad. Sci. U.S.A. 98:3705-3709(2001).
RN [2]
RP SEQUENCE FROM N.A.

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RA Trexler M., Banyai L., Paddy L.;
RT "Distinct expression pattern of two related human proteins containing
RL multiple types of protease-inhibitory modules.";
CC Biol. Chem. 383:0-0(2002).
DR -1- SIMILARITY: Contains 2 BPTI/Kunitz inhibitor domains.
DR HSSP; P00974; 1K09.
DR GO; GO:0008233; F:peptidase activity; IEA.
DR GO; GO:0004867; F:serine-type endopeptidase inhibitor activity; IEA.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003598; IG c2.
DR InterPro; IPR008993; TIMP_like.
DR Pfam; PF07648; Kazal_2; 1.
DR Pfam; PF00014; Kunitz_BPTI; 2.
DR PRINTS; PR00095; WAP; 1.
DR PRINTS; PR00003; 4DISULPHCORE.
DR PRODOM; PD000222; Prot_Inh_kunz-m; 2.
DR SMART; SM00408; IGC2; 1.
DR SMART; SM00280; KAZAL; 1.
DR SMART; SM00131; KU; 2.
DR SMART; SM00217; WAP; 1.
DR PROSITE; PS00317; 4_DISULFIDE_CORE; 1.
DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
DR PROSITE; PS02079; BPTI_KUNITZ_2; 1.
DR PROSITE; PS0835; IG LIKE; 1.
DR PROSITE; PS50189; NTR; 1.
KW Protease.
SQ SEQUENCE 576 AA; 63941 MW; 08B4F2EDBE121F81 CRC64;

Query Match 53.0%; Score 160; DB 2; Length 576;
Best Local Similarity 49.0%; Pred. No. 2.7e-11;
Matches 25; Conservative 7; Mismatches 19; Indels 0; Gaps 0;

Qy 1 CSMPEAGPCLASIPHHWYKTKICSEFIYGGCGGNNNFQTEAICLVTC 51
Db 386 CSLPALQGPCAYAPRWAYNSQTGCQSFYVGCGEGNNGNFESREACEESC 436

RESULT 19
Q6UXZ9
ID Q6UXZ9 PRELIMINARY; PRT; 576 AA.
AC Q6UXZ9;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Btkunin hlg.
GN ORFNames=UNQ9235;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
[1]
SEQUENCE FROM N.A.
RA Medline=22887296; PubMed=12975309; DOI=10.1101/gr.1293003;
RA Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D., Brush J.,
RA Chen J., Chow B., Chui C., Crowley C., Currell B., Deuel B., Dowd P.,
RA Eaton D., Foster J., Grimaldi C., Gu Q., Hass P.E., Heldens S.,
RA Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J.,
RA Lewis L., Liao D., Mark M., Robble E., Sanchez C., Schoenfeld J.,
RA Seshagiri S., Simmons L., Singh J., Smith V., Stinson J., Vagts A.,
RA Vandlen R., Watanabe C., Wieand D., Woods K., Xie M.H., Yansura D.,
RA Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A., Wood W.I.,
RA Godowski P.;
RT "The secreted protein discovery initiative (SPDI), a large-scale
RT effort to identify novel human secreted and transmembrane proteins: a
RT bioinformatics assessment.";
RL Genome Res. 13:2265-2270(2003).
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CC -1- SIMILARITY: Contains 2 BPTI/Kunitz inhibitor domains.
DR EMBL; AY358142; AAQ88509.1; -.
DR HSSP; P00974; 1K09.
DR GO; GO:0004867; F:serine-type endopeptidase inhibitor activity; IEA.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003598; IG c2.
DR InterPro; IPR001134; Netrin C.
DR InterPro; IPR002223; Prot_Inh_Kunz-m.
DR InterPro; IPR008993; TIMP_like.
DR InterPro; IPR008197; WAP.
DR Pfam; PF00014; Kunitz_BPTI; 2.
DR Pfam; PF00095; WAP; 1.
DR PRINTS; PR00003; 4DISULPHCORE.
DR PRINTS; PR00759; BASICPTASE.
DR PRODOM; PD000222; Prot_Inh_Kunz-m; 2.
DR SMART; SM00409; IG; 1.
DR SMART; SM00408; IGC2; 1.
DR SMART; SM00131; KU; 2.
DR SMART; SM00217; WAP; 1.
DR PROSITE; PS00317; 4_DISULFIDE_CORE; 1.
DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
DR PROSITE; PS02079; BPTI_KUNITZ_2; 1.
DR PROSITE; PS0835; IG LIKE; 1.
DR PROSITE; PS50189; NTR; 1.
SQ SEQUENCE 576 AA; 63912 MW; 08B42DD50C3CF81 CRC64;

Query Match 53.0%; Score 160; DB 2; Length 576;
Best Local Similarity 49.0%; Pred. No. 2.7e-11;
Matches 25; Conservative 7; Mismatches 19; Indels 0; Gaps 0;

Qy 1 CSMPEAGPCLASIPHHWYKTKICSEFIYGGCGGNNNFQTEAICLVTC 51
Db 386 CSLPALQGPCAYAPRWAYNSQTGCQSFYVGCGEGNNGNFESREACEESC 436

RESULT 20
Q7PXZ1
ID Q7PXZ1 PRELIMINARY; PRT; 2419 AA.
AC Q7PXZ1;
DT 01-MAR-2004 (TrEMBLrel. 26, Created)
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE AGCP12609 (Fragment).
GN Name=agCG49342; ORFNames=ENSANGG000000019572;
OS Anopheles gambiae str. PEST.
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Anopheles.
OX NCBI_TaxID=180454;
[1]
SEQUENCE FROM N.A.
RA STRAIN=PEST;
RA Anopheles Genome Sequencing Consortium;
RA Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Contains 9 BPTI/Kunitz inhibitor domains.
CC -1- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; AAA801008987; EAA01339.1; -.
DR HSSP; P10646; 1IRH.
DR GO; GO:0004867; F:serine-type endopeptidase inhibitor activity; IEA.
DR InterPro; IPR010294; ADAM spacer1.
DR InterPro; IPR006209; EGF-like.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR002223; Prot_Inh_Kunz-m.
DR InterPro; IPR000884; TSPI.
DR InterPro; IPR008197; WAP.
DR Pfam; PF05986; ADAM spacer1; 1.
DR Pfam; PF00014; Kunitz_BPTI; 9.
DR Pfam; PF00090; TSP_1; 7.
DR Pfam; PF00095; WAP; 1.
DR PRINTS; PR00003; 4DISULPHCORE.
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DR PRINTS; PR00759; BASICPTASE.
 DR PRODOM; PD000222; Prot Inh Kunz-m; 9.
 DR PROSITE; PS00317; 4 DISULFIDE CORE; 1.
 DR PROSITE; PS00280; BPTI_KUNITZ_1; 8.
 DR PROSITE; PS00279; BPTI_KUNITZ_2; 9.
 DR PROSITE; PS00022; EGF_1; UNKNOWN_1.
 DR PROSITE; PS00835; IG_LIKE; 2.
 DR PROSITE; PS00900; PLAC; 1.
 DR PROSITE; PS00902; TSP1; 5.
 FT NON TER
 SQ SEQUENCE 2419 AA; 260249 MW; 58B0786609B3C946 CRC64;
 Query Match 53.0%; Score 160; DB 2; Length 2419;
 Best Local Similarity 49.0%; Pred. No. 1.2e-10;
 Matches 25; Conservative 7; Mismatches 19; Indels 0; Gaps 0;
 QY 1 CSMPOEAGPCLASIPHWYKTKICSEFIYGGCGNNNNFQTEAICLVTC 51
 DB 1576 CQPMWEGPCNGTFERWYDKTDACHPFYGGCKGNKNYPTEASCGYHC 1626
 RESULT 21
 Q8T3S7 PRELIMINARY; PRT; 80 AA.
 AC Q8T3S7
 DT 01-JUN-2002 (TrEMBLrel. 21, Created)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Toxin 1.
 OS Araneus ventricosus.
 OC Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Araneae;
 OC Araneomorphae; Entelegynae; Araneidae; Araneidae; Araneae.
 OX NCBI_TaxID=182803;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Jung E.H., Lee K.S., Han J.H., Je Y.H., Chang J.H., Roh J.Y.,
 RA Sohn H.D., Jin B.R.;
 RT "Molecular cloning of two cDNAs encoding an insecticidal toxin from
 RT the spider, Araneus ventricosus, and construction of a recombinant
 RT baculovirus expressing a spider toxin."
 RL Int. J. Ind. Entomol. 4:43-49(2002).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Chung E.H., Lee K.S., Han J.H., Sohn H.D., Jin B.R.;
 RA Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
 RL -!- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.
 CC EMBL; AY091482; AAW14403.1; -.
 DR HSSP; P12111; 1KTH.
 DR GO; GO:0004867; F:serine-type endopeptidase inhibitor activity; IEA.
 DR InterPro; IPR002223; Prot Inh Kunz-m.
 DR Pfam; PF00014; Kunitz BPTI; 1.
 DR PRINTS; PR00759; BASICPTASE.
 DR SMART; SM00131; KU; 1.
 DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
 DR PROSITE; PS00279; BPTI_KUNITZ_2; 1.
 SQ SEQUENCE 80 AA; 9275 MW; D07F5F9AC6B7BC10 CRC64;
 Query Match 52.6%; Score 159; DB 2; Length 80;
 Best Local Similarity 51.0%; Pred. No. 4.9e-12;
 Matches 26; Conservative 9; Mismatches 16; Indels 0; Gaps 0;
 QY 1 CSMPOEAGPCLASIPHWYKTKICSEFIYGGCGNNNNFQTEAICLVTC 51
 DB 27 CLLPKVTGPKASLTRYDDKTKACVEFIYGGCGNNNNFKKDECEKAC 77
 RESULT 22
 Q9GQRO PRELIMINARY; PRT; 2174 AA.
 ID Q9GQRO
 AC Q9GQRO; 01-MAR-2001 (TrEMBLrel. 16, Created)
 DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)

DE Extracellular matrix protein papilin precursor.
 GN Name=Ppn;
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 OX NCBI_TaxID=7227;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=dp cn bw;
 RA MEDLINE=20530499; PubMed=11076767;
 RA Kramerova I.A., Kawaguchi N., Nelson R.E., Fessler L.I., Chen Y.,
 RA Kramerov A.A., Kusche-Gullberg M., Kramer J.M., Ackley B.D.,
 RA Sieron A.L., Prockop D.O., Fessler J.H.;
 RT "Papilin in development; a pericellular protein with a homology to the
 RT ADAMTS metalloproteinases."
 RL Development 127:5475-5485(2000).
 CC -!- SIMILARITY: Contains 3 BPTI/Kunitz inhibitor domains.
 DR EMBL; AF205357; AAG37995.1; -.
 DR HSSP; P12111; 1KTH.
 DR FlyBase; FBgn0003137; Ppn.
 DR GO; GO:0005604; C:basement membrane; IDA.
 DR InterPro; IPR010294; ADAM spacer1.
 DR InterPro; IPR006209; EGF_Like.
 DR InterPro; IPR007110; Ig-Like.
 DR InterPro; IPR003598; Ig_c2.
 DR InterPro; IPR010909; PLAC.
 DR InterPro; IPR002223; Prot Inh Kunz-m.
 DR InterPro; IPR000884; TSP1.
 DR InterPro; IPR008197; WAP.
 DR Pfam; PF05986; ADAM_spacer1; 1.
 DR Pfam; PF00047; Ig; 1.
 DR Pfam; PF00014; Kunitz BPTI; 3.
 DR Pfam; PF00090; TSP 1; 5.
 DR Pfam; PF00095; WAP; 1.
 DR PRINTS; PR00003; 4DISULPHCORE.
 DR PRINTS; PR00759; BASICPTASE.
 DR SMART; SM00408; IGC2; 2.
 DR SMART; SM00131; KU; 3.
 DR SMART; SM00209; TSP1; 7.
 DR SMART; SM00217; WAP; 1.
 DR PROSITE; PS00317; 4 DISULFIDE CORE; 1.
 DR PROSITE; PS00280; BPTI_KUNITZ_1; 3.
 DR PROSITE; PS00279; BPTI_KUNITZ_2; 3.
 DR PROSITE; PS00022; EGF_1; UNKNOWN_1.
 DR PROSITE; PS00835; IG_LIKE; 2.
 DR PROSITE; PS00900; PLAC; 1.
 DR PROSITE; PS00902; TSP1; 5.
 KW Matrix protein; Signal.
 FT SIGNAL 1 26 Potential.
 SQ SEQUENCE 2174 AA; 231935 MW; 038F707952623120 CRC64;
 Query Match 52.6%; Score 159; DB 2; Length 2174;
 Best Local Similarity 47.1%; Pred. No. 1.4e-10;
 Matches 24; Conservative 7; Mismatches 20; Indels 0; Gaps 0;
 QY 1 CSMPOEAGPCLASIPHWYKTKICSEFIYGGCGNNNNFQTEAICLVTC 51
 DB 1730 CQPMWEGPCNGTFERWYDKTDACHPFYGGCKGNKNYPTEAHCNVC 1780
 RESULT 23
 Q9VAV4 PRELIMINARY; PRT; 2772 AA.
 ID Q9VAV4
 AC Q9VAV4; 09VAV3;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE CG33103-PB.
 GN Name=Ppn; ORFNames=CG33103;
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;

OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20196006; PubMed=10731132; DOI=10.1126/science.287.5461.2185;
RA Adams M.D., Celnikier S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.H., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Gabor G.L.,
RA Abril J.F., Agbayani A., An H.J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borokova D., Botchan M.R., Bouck J., Brokstein P., Brotter P.,
RA Burtis K.C., Buesam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferrieria S., Fleischmann W.,
RA Foster C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.H., Ibegwam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasbo P., Lei Y., Levitsky T.C., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattel B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusakern D.R., Pacleb J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E.C., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
RA Williams S.M., Woodgett, Worley K.C., Wu D., Yang S., Yao Q.A., Ye J.,
RA Zeng R.F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zeng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster.";
RL Science 287:2185-2195(2000).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=22426065; PubMed=12537568;
RA Celnikier S.E., Wheeler D.A., Kronmiller B., Carlson J.W., Halpern A.,
RA Patel S., Adams M., Champe M., Dugan S.P., Friese E., Hodgson A.,
RA George R.A., Hoskins R.A., Lavery T., Muzny D.M., Nelson C.R.,
RA Pacleb J.M., Park S., Pfeiffer B.D., Richards S., Sodergren E.J.,
RA Svirskas R., Tabor P.E., Wan K., Stapleton M., Sutton G.G., Venter C.,
RA Weinstock G., Scherer S.E., Myers E.W., Gibbs R.A., Rubin G.M.;
RT "Finishing a whole-genome shotgun: Release 3 of the Drosophila
melanogaster euchromatic genome sequence.";
RL Genome Biol. 3:RESEARCH0079-RESEARCH0079(2002).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=22426070; PubMed=12537573;
RA Kaminker J.S., Bergman C.M., Kronmiller B., Carlson J., Svirskas R.,
RA Patel S., Friese E., Wheeler D.A., Lewis S.E., Rubin G.M.,
RA Ashburner M., Celnikier S.E.;
RT "The transposable elements of the Drosophila melanogaster euchromatin:
a genomics perspective.";
RL Genome Biol. 3:RESEARCH0084-RESEARCH0084 (2002).
RN [4]
RP SEQUENCE FROM N.A.
RX MEDLINE=22426069; PubMed=12537572;
RA Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
RA Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochnik S.E.,
RA Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Berman B.P.,
RA Bettencourt B.R., Celnikier S.E., de Grey A.D., Drysdale R.A.,
RA Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,
RA Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,

RA Lewis S.E.;
RT "Annotation of the Drosophila melanogaster euchromatic genome: a
systematic review.";
RL Genome Biol. 3:RESEARCH0083-RESEARCH0083(2002).
RN [5]
RP SEQUENCE FROM N.A.
RX FlyBase;
RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
RN [6]
RP SEQUENCE FROM N.A.
RX FlyBase;
RL Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Contains 10 BPTI/Kunitz inhibitor domains.
EMBL; AE003765; AAF56794.3; -
DR HSPF; P12111; IKTH.
DR FlyBase; FBGN00031137; Ppn.
DR GO; GO:0005604; C:Basement membrane; IDA.
DR InterPro; IPR010294; ADAM spacer1.
DR InterPro; IPR006209; EGF Like.
DR InterPro; IPR007110; Ig-Like.
DR InterPro; IPR003598; Ig_c2.
DR InterPro; IPR010909; PLAC.
DR InterPro; IPR000884; TSP1.
DR InterPro; IPR008197; WAP.
DR Pfam; PF05986; ADAM_spacer1; 1.
DR Pfam; PF00047; Ig; 2.
DR Pfam; PF00014; Kunitz_BPTI; 10.
DR Pfam; PF00090; TSP_1; 5.
DR Pfam; PF00095; WAP; 1.
DR PRINTS; PR00003; 4DISULPHCORE.
DR ProDom; PD000222; Prot_Inh_Kunz-m; 10.
DR SMART; SM00408; IGC2; 3.
DR SMART; SM00131; KU; 10.
DR SMART; SM00209; TSP1; 7.
DR SMART; SM00217; WAP; 1.
DR PROSITE; PS00317; 4_DISULFIDE_CORE; 1.
DR PROSITE; PS00280; BPTI_KUNITZ_1; 9.
DR PROSITE; PS02079; BPTI_KUNITZ_2; 10.
DR PROSITE; PS00022; EGF_1; UNKNOWN_1.
DR PROSITE; PS50835; IG_Like; 3.
DR PROSITE; PS50900; PLAC; 1.
DR PROSITE; PS50092; TSP1; 5.
SQ SEQUENCE 2772 AA; 299154 MW; 3965DC92D30CCAAA CRC64;
Query Match 52.6%; Score 159; DB 2; Length 2772;
Best Local Similarity 47.1%; Pred. No. 1.8e-10;
Matches 24; Conservative 7; Mismatches 20; Indels 0; Gaps 0;
Qy 1 CSMQEGAGPCLASIPHHWYKTKICSEFIYGGCGNNNNFQFAICLVTC 51
Db 1730 CEQVESGPCAGNFERWYDNETDICRPFTYGGCKGNKNYPTFHACNYNC 1780
RESULT 24
Q869A0 PRELIMINARY; PRT; 2776 AA.
AC Q869A0;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Extracellular matrix protein papilin 2.
GN Name=Ppn;
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22552133; PubMed=12666201; DOI=10.1002/dvdy.10265;
RA Kramerova I.A., Kramerov A.A., Fessler J.H.;

RT "Alternative splicing of papilin and the diversity of Drosophila
 RL extracellular matrix during embryonic morphogenesis.";
 RL Dev. Dyn. 226:634-642(2003).
 RN [2]

RP SEQUENCE FROM N.A.
 RA Kramerova I., Fessler J.H.;
 RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
 CC -!- SIMILARITY: Contains 10 BPTI/Kunitz inhibitor domains.

DR EMBL; AF529179; AAO84907.1; -;
 DR HSSP; P12111; 1KTH.

DR FlyBase; FBgn0003137; Ppn.
 DR GO; GO:0005604; C:basement membrane; IDA.
 DR InterPro; IPR010294; ADAM spacer1.

DR InterPro; IPR006209; EGF like.
 DR InterPro; IPR007110; IGF-like.
 DR InterPro; IPR003598; Iq c2.

DR InterPro; IPR010309; PLAC.
 DR InterPro; IPR002223; Prot_Inh_Kunz-m.
 DR InterPro; IPR000884; TSP1.

DR InterPro; IPR008197; WAP.
 DR Pfam; PF05986; ADAM spacer1; 1.
 DR Pfam; PF00047; Iq; 2.

DR Pfam; PF00014; Kunitz_BPTI; 10.
 DR Pfam; PF00090; TSP1; 1.
 DR Pfam; PF00095; WAP; 1.

DR PRINTS; PR00003; 4DISULPHCORE.
 DR PRINTS; PR00759; BASICPTASE.
 DR PRODom; PD000222; Prot_inh_Kunz-m; 10.

DR SMART; SM00408; ICG2; 3.
 DR SMART; SM00131; KU; 10.
 DR SMART; SM00209; TSP1; 7.

DR SMART; SM00217; WAP; 1.
 DR PROSITE; PS00317; 4 DISULFIDE CORE; 1.
 DR PROSITE; PS00280; BPTI_KUNITZ_1; 9.

DR PROSITE; PS00279; BPTI_KUNITZ_2; 10.
 DR PROSITE; PS00022; EGF 1; UNKNOWN_1.
 DR PROSITE; PS00835; IGF LIKE; 3.

DR PROSITE; PS00900; PLAC; 1.
 DR PROSITE; PS00092; TSP1; 5.
 KW Matrix protein.

SQ SEQUENCE 2776 AA; 299741 MW; 92D38A17360D2D42 CRC64;
 Query Match 52.6%; Score 159; DB 2; Length 2776;
 Best Local Similarity 47.1%; Pred. No. 1.8e-10;

Matches 24; Conservative 7; Mismatches 20; Indels 0; Gaps 0;
 QY 1 CSMPQAGCLASIPHWNTKTKICSEFIYGCQGNWNNFOTELCLVTC 51
 DB 1730 CEQPVESGPGAGNFERWYDNETDICRPTYGCKGNKNYPTEHACNYNC 1780

RESULT 25
 Q7KRX2 PRELIMINARY; PRT; 2894 AA.
 AC Q7KRX2

DT 05-JUL-2004 (TEMBLrel. 27, Created)
 DT 05-JUL-2004 (TEMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TEMBLrel. 27, Last annotation update)

DE G33103-PA.
 GN NamesPpn; ORFNames=CG33103;
 OS Drosophila melanogaster (fruit fly).

OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.

OX NCBI_TaxID=7227;
 RN [1]
 RP SEQUENCE FROM N.A.

RX MEDLINE=20196006; PubMed=10731132; DOI=10.1126/science.287.5461.2185;
 RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Amanatides P.G., Scher S.E., Li P.W., Hoskins R.A., Galle R.F.,

RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
 RA Brandon R.C., Rogers Y.H., Blazej R.G., Champe M., Pfeiffer B.D.,

RA Winkler D.A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
 RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
 RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,

RA Burtis K.C., Buseam D.A., Butler H., Cadieu E., Center A., Chandra I.,
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
 RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,

RA Dodson K.J., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
 RA Floer C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,

RA Glodok A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.B., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
 RA Hostin D., Houston K.A., Howland T.J., Wei M.H., Ibgwam C.,

RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 RA Laoko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,

RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,

RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Reinert K., Remington K., Saunders R.D., Scheeler F., Shen H.,

RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E., Wang X.,
 RA Svirska R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,

RA Wang Z.Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
 RA Williams S.M., Woodruff, Worley K.C., Wu D., Yang S., Yao Q.A., Ye J.,
 RA Yeh R.F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,

RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 RT "The genome sequence of Drosophila melanogaster.";
 RN Science 287:2185-2195(2000).
 RN [2]

RP SEQUENCE FROM N.A.
 RX MEDLINE=2426065; PubMed=12537568;
 RA Celniker S.E., Wheeler D.A., Krommiller B., Carlson J.W., Halpern A.,

RA Patel S., Adams M., Champagne M., Dugan S.P., Friese E., Hodgson A.,
 RA George R.A., Hoskins R.A., Lavery T., Muzny D.M., Nelson C.R.,
 RA Pacleb J.M., Park S., Pfeiffer B.D., Richards S., Sodergren E.J.,

RA Svirska R., Tabor P.E., Wan K., Stapleton M., Sutton G.G., Venter C.,
 RA Weinstock G., Scherer S.E., Myers E.W., Gibbs R.A., Rubin G.M.,
 RT "Finishing a whole-genome shotgun: Release 3 of the Drosophila
 melanogaster euchromatic genome sequence.";
 RN Genome Biol. 3:RESEARCH0079-RESEARCH0079(2002).
 RN [3]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=2426070; PubMed=12537573;
 RA Kaminker J.S., Bergman C.M., Krommiller B., Carlson J., Svirska R.,
 RA Patel S., Friese E., Wheeler D.A., Lewis S.E., Rubin G.M.,
 RA Ashburner M., Celniker S.E.;
 RT "The transposable elements of the Drosophila melanogaster euchromatin:
 a genomics perspective.";
 RN Genome Biol. 3:RESEARCH0084-RESEARCH0084(2002).
 RN [4]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=2426069; PubMed=12537572;
 RA Mixa S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
 RA Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochnik S.E.,
 RA Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Berman B.P.,
 RA Bettencourt B.R., Celniker S.E., de Grey A.D., Drysdale R.A.,
 RA Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.O.,
 RA Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
 RA Lewis S.E.;
 RT "Annotation of the Drosophila melanogaster euchromatic genome: a
 systematic review.";
 RN Genome Biol. 3:RESEARCH0083-RESEARCH0083(2002).
 RN [5]
 RP SEQUENCE FROM N.A.
 RG FlyBase;
 RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
 RL [6]
 RP SEQUENCE FROM N.A.

RG FlyBase;
 RL Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.
 CC -!- SIMILARITY: Contains 12 BPTI/Kunitz inhibitor domains.
 DR EMBL; AE003765; AAF56795.3; -.
 DR HSSP; P10646; 1ADZ.
 DR GO; GO:0004867; F:serine-type endopeptidase inhibitor activity; IEA.
 DR InterPro; IPR010294; ADAM_spacer1.
 DR InterPro; IPR006209; EGF_Like.
 DR InterPro; IPR003599; IG.
 DR InterPro; IPR007110; IG_Like.
 DR InterPro; IPR003598; IG_c2.
 DR InterPro; IPR010909; PLAC.
 DR InterPro; IPR002223; Prot_Inh_Kunz-m.
 DR InterPro; IPR000884; TSP1.
 DR InterPro; IPR008197; WAP.
 DR Pfam; PF05986; ADAM_spacer1; 1.
 DR Pfam; PF00047; IG; 2.
 DR Pfam; PF00014; Kunitz_BPTI; 12.
 DR Pfam; PF00090; TSP_1; 5.
 DR Pfam; PF00095; WAP; 1.
 DR PRINTS; PR00003; 4DISULPHCORE.
 DR PRODOM; PD000222; Prot_Inh_Kunz-m; 12.
 DR SMART; SM00409; IGC2; 3.
 DR SMART; SM00131; KU; 12.
 DR SMART; SM00209; TSP1; 7.
 DR SMART; SM00217; WAP; 1.
 DR PROSITE; PS00317; 4_DISULFIDE_CORE; 1.
 DR PROSITE; PS00280; BPTI_KUNITZ_1; 11.
 DR PROSITE; PS50279; BPTI_KUNITZ_2; 12.
 DR PROSITE; PS00022; EGF_1; UNKNOWN_1.
 DR PROSITE; PS50835; IG_Like; 3.
 DR PROSITE; PS50900; PLAC; 1.
 DR PROSITE; PS50092; TSP1; 5.
 DR PROSITE; PS50092; TSP1; 5.
 KW Matrix protein.
 SQ SEQUENCE 2894 AA; 312663 MW; A1BPE1BAD9B214BC CRC64;
 Query Match 52.6%; Score 159; DB 2; Length 2894;
 Best Local Similarity 47.1%; Pred. No. 1.9e-10;
 Matches 24; Conservative 7; Mismatches 20; Indels 0; Gaps 0;
 OY 1 CSMPOEAGPCLASIPHWYNNKTKICSEFIYGGCGGNNNFQTEAICLVTC 51
 DB 1730 CEQVESPAGCAGNFERWYDNETDICRPFTYGGCKGNKNYPTEHACNYNC 1780

RESULT 26
 ID Q86829 PRELIMINARY; PRT; 2898 AA.
 AC Q86829;
 DT 01-JUN-2003 (TrEMBLrel. 24, Created)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Extracellular matrix protein papilin 3.
 GN Name=Ppn;
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 OC NCBI_TaxID=7227;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA MEDLINE=2255133; PubMed=12666201; DOI=10.1002/dvdy.10265;
 RA Kramerova I.A., Kramerov A.A., Fessler J.H.;
 RT "Alternative splicing of papilin and the diversity of *Drosophila*
 RT extracellular matrix during embryonic morphogenesis.";
 RL Dev. Dyn. 226:634-642(2003).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Kramerova I., Fessler J.H.;
 RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
 CC -!- SIMILARITY: Contains 12 BPTI/Kunitz inhibitor domains.
 DR EMBL; AF529180; AAO84908.1; -.

DR HSSP; P12111; 1KTH.
 DR FlyBase; FBgn0003137; Ppn.
 DR GO; GO:0005604; C:basement membrane; IDA.
 DR InterPro; IPR010294; ADAM_spacer1.
 DR InterPro; IPR006209; EGF_Like.
 DR InterPro; IPR007110; IG_Like.
 DR InterPro; IPR003598; IG_c2.
 DR InterPro; IPR010909; PLAC.
 DR InterPro; IPR002223; Prot_Inh_Kunz-m.
 DR InterPro; IPR000884; TSP1.
 DR InterPro; IPR008197; WAP.
 DR Pfam; PF05986; ADAM_spacer1; 1.
 DR Pfam; PF00047; IG; 2.
 DR Pfam; PF00014; Kunitz_BPTI; 12.
 DR Pfam; PF00090; TSP_1; 5.
 DR Pfam; PF00095; WAP; 1.
 DR PRINTS; PR00003; 4DISULPHCORE.
 DR PRODOM; PD000222; Prot_Inh_Kunz-m; 12.
 DR SMART; SM00408; IGC2; 3.
 DR SMART; SM00131; KU; 12.
 DR SMART; SM00209; TSP1; 7.
 DR SMART; SM00217; WAP; 1.
 DR PROSITE; PS00317; 4_DISULFIDE_CORE; 1.
 DR PROSITE; PS00280; BPTI_KUNITZ_1; 11.
 DR PROSITE; PS50279; BPTI_KUNITZ_2; 12.
 DR PROSITE; PS00022; EGF_1; UNKNOWN_1.
 DR PROSITE; PS50835; IG_Like; 3.
 DR PROSITE; PS50900; PLAC; 1.
 DR PROSITE; PS50092; TSP1; 5.
 KW Matrix protein.
 SQ SEQUENCE 2898 AA; 313250 MW; 2F992742P2D64A00 CRC64;
 Query Match 52.6%; Score 159; DB 2; Length 2898;
 Best Local Similarity 47.1%; Pred. No. 1.9e-10;
 Matches 24; Conservative 7; Mismatches 20; Indels 0; Gaps 0;
 OY 1 CSMPOEAGPCLASIPHWYNNKTKICSEFIYGGCGGNNNFQTEAICLVTC 51
 DB 1730 CEQVESPAGCAGNFERWYDNETDICRPFTYGGCKGNKNYPTEHACNYNC 1780

RESULT 27
 ID IVBT_OYXSC STANDARD; PRT; 62 AA.
 AC Q7LZE4;
 DT 05-JUL-2004 (Rel. 44, Created)
 DT 05-JUL-2004 (Rel. 44, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Taicotoxin, serine protease inhibitor component (TCX).
 OS Oxyuranus scutellatus scutellatus (Australian taipan).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Lepidodermata; Squamata; Scleroglossa; Serpentes; Colubroidea;
 OC Elapidae; Acanthophilineae; Oxyuranus.
 OC NCBI_TaxID=8667;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Venom;
 RX PubMed=1485334; DOI=10.1016/0041-0101(92)90511-3;
 RA Possani L.D., Martin B.M., Yatani A., Mochca-Morales J., Zamudio F.Z.,
 RA Gurrola G.B., Brown A.M.;
 RT "Isolation and physiological characterization of taicotoxin, a complex
 RT toxin with specific effects on calcium channels.";
 RL Toxicon 30:1343-1364(1992).
 CC -!- FUNCTION: Taicotoxin blocks the high threshold calcium channel
 CC current of excitable membranes in heart and does not affect the
 CC low threshold calcium channel current. The block is selective for
 CC calcium channels, reversible, does not affect single channel
 CC conductance but only changes channel gating, and is voltage
 CC dependent with higher affinity for inactivated channels. Is very
 CC toxic to mice.
 CC -!- SUBUNIT: Linked to an alpha-neurotoxin-like peptide of 8000 Da and
 CC a neurotoxic phospholipase of 16000 Da by non-covalent bonds. The

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CC ratio is approximately one phospholipase and one neurotoxin for
CC four protease inhibitors.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- TISSUE SPECIFICITY: Expressed by the venom gland.
CC -1- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.
CC
DR PIR: A44180; A44180.
DR InterPro: IPR002223; Prot_Inh_Kunz-m.
DR PRINTS: PR00759; BASICPTASE.
DR PRODOM: PD000222; Prot_Inh_Kunz-m; 1.
DR PROSITE: PS00280; BPTI_KUNITZ_1; 1.
DR PROSITE: PS50279; BPTI_KUNITZ_2; 1.
DR Calcium channel inhibitor; Direct protein sequencing; Toxin.
KW Ionic channel inhibitor; Neurotoxin; Serine protease inhibitor; Toxin.
FT DISULFID 7 57 By similarity.
FT DISULFID 16 40 By similarity.
FT DISULFID 32 53 By similarity.
SQ SEQUENCE 62 AA; 7045 MW; A5E0BEPFD1990605 CRC64;

Query Match 52.3%; Score 158; DB 1; Length 62;
Best Local Similarity 51.0%; Pred. No. 5.1e-12;
Matches 26; Conservative 8; Mismatches 17; Indels 0; Gaps 0;

QY 1 CSMQPEAGPCLASIPHWYNNKTKICSEFIYGGCGGNNNNFQTEAICLVTC 51
   : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 7 CHLPKPGPCRAIIPRYFYNNPHSKQCEFIYGGCHGNANKFKTPDECNYTC 57

RESULT 28
CRPT_BOOMI
ID CRPT_BOOMI STANDARD; PRT; 69 AA.
AC P81162;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Protease inhibitor carboxatin.
OS Boophilus microplus (Cattle tick).
OC Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Acari;
OC Parasitiformes; Ixodida; Ixodoidea; Ixodidae; Boophilus.
OX NCBI_TaxID=6941;
RN [1]
RP SEQUENCE.
RA Fuentes-Prior P., Pereira P.J.B., Mentele R., Bode W.;
RL Submitted (JAN-1998) to Swiss-Prot.
CC -1- FUNCTION: Serine protease inhibitor.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.
CC
DR HSSP: P00980; 1DTX.
DR InterPro: IPR002223; Prot_Inh_Kunz-m.
DR Pfam: PF00014; Kunitz_BPTI; 1.
DR PRINTS: PR00759; BASICPTASE.
DR PRODOM: PD000222; Prot_Inh_Kunz-m; 1.
DR SMART: SM00131; KU; 1.
DR PROSITE: PS00280; BPTI_KUNITZ_1; 1.
DR PROSITE: PS50279; BPTI_KUNITZ_2; 1.
KW Direct protein sequencing; Serine protease inhibitor.
FT SITE 18 19 Reactive bond (By similarity).
FT DISULFID 8 58 By similarity.
FT DISULFID 17 41 By similarity.
FT DISULFID 33 54 By similarity.
SQ SEQUENCE 69 AA; 7842 MW; E0B14312AC1533BB CRC64;

Query Match 52.3%; Score 158; DB 1; Length 69;
Best Local Similarity 51.0%; Pred. No. 5.6e-12;
Matches 26; Conservative 6; Mismatches 19; Indels 0; Gaps 0;

QY 1 CSMQPEAGPCLASIPHWYNNKTKICSEFIYGGCGGNNNNFQTEAICLVTC 51
   : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 8 CVPTADPGCKGPMWYNNIFTSQCEFIYGGCGGNDNRRTKEECDKTC 58

RESULT 29
Q6B8G1
ID Q6B8G1 PRELIMINARY; PRT; 142 AA.
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AC Q6B8G1;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE KUN-5 (Fragment).
OS Ixodes pacificus (western blacklegged tick).
OC Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Acari;
OC Parasitiformes; Ixodida; Ixodoidea; Ixodidae; Ixodes.
OX NCBI_TaxID=29930;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Salivary gland;
RA Ribeiro J.M.C.;
RT "An insight into the transcriptome of the salivary glands of the adult female tick, Ixodes pacificus.";
RL Submitted (AUG-2004) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Salivary gland;
RA Francischetti I.M., Lane R.S., Pham V.M., Ribeiro J.M.C.;
RL Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Contains 2 BPTI/Kunitz inhibitor domains.
DR EMBL: AV674183; AAT92116.1; -.
DR GO: GO:0004867; F.serine-type endopeptidase inhibitor activity; IEA.
DR InterPro: IPR002223; Prot_Inh_Kunz-m.
DR Pfam: PF00014; Kunitz_BPTI; 1.
DR PRINTS: PR00759; BASICPTASE.
DR PRODOM: PD000222; Prot_Inh_Kunz-m; 1.
DR SMART: SM00131; KU; 2.
DR PROSITE: PS00280; BPTI_KUNITZ_1; 1.
DR PROSITE: PS50279; BPTI_KUNITZ_2; 2.
FT NON_TER 142 142
SQ SEQUENCE 142 AA; 16458 MW; A618B845CB812C4B CRC64;

Query Match 52.3%; Score 158; DB 2; Length 142;
Best Local Similarity 52.9%; Pred. No. 1.2e-11;
Matches 27; Conservative 7; Mismatches 17; Indels 0; Gaps 0;

QY 1 CSMQPEAGPCLASIPHWYNNKTKICSEFIYGGCGGNNNNFQTEAICLVTC 51
   : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 29 CTEVVDEGPCRALIPRYFYNNMETECSEFDYGGYGNNNFNFSSCTSTC 79

RESULT 30
Q6ITB4
ID Q6ITB4 PRELIMINARY; PRT; 83 AA.
AC Q6ITB4;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Microlepidin-2.
OS Oxyuranus microlepidotus (Inland taipan).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC Elapidae; Acanthophiinae; Oxyuranus.
OX NCBI_TaxID=111177;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Venom gland;
RA Filippovich I.V., Sorokina N.I.;
RL Submitted (MAY-2004) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.
DR EMBL: AV626931; AAT45407.1; -.
DR HSSP: P10646; 1ADZ.
DR GO: GO:0004867; F.serine-type endopeptidase inhibitor activity; IEA.
DR InterPro: IPR002223; Prot_Inh_Kunz-m.
DR Pfam: PF00014; Kunitz_BPTI; 1.
DR PRINTS: PR00759; BASICPTASE.
DR PRODOM: PD000222; Prot_Inh_Kunz-m; 1.
DR SMART: SM00131; KU; 1.
DR PROSITE: PS00280; BPTI_KUNITZ_1; 1.
DR PROSITE: PS50279; BPTI_KUNITZ_2; 1.
SQ SEQUENCE 83 AA; 9074 MW; 3145B51757014221 CRC64;
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Query Match          52.0%; Score 157; DB 2; Length 83;
Best Local Similarity 51.0%; Pred. No. 9.1e-12;
Matches 26; Conservative 6; Mismatches 19; Indels 0; Gaps 0;

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Qy 1 CSMPQEAGPCLASIPHWYNNKTKICSEFIYGGCGGNNNFQTEAICLVTC 51
| : | | | | : | | | | | : | | | | : | |
D6 31 CELPADTGPcRVGFPSPFYNDPEKKCLEFIYGGCEGNANFNITKEECSTC 81

RESULT 31	
Q6ITB5	PRELIMINARY; PRT; 83 AA.
ID Q6ITBS;	
AC DT 05-JUL-2004	(TReMBLrel_27, Created)
CD DT 05-JUL-2004	(TReMBLrel_27, Last sequence update)
DT DT 05-JUL-2004	(TReMBLrel_27, Last annotation update)
DE Microlepudin-1.	
OS Oxyuranus microlepidotus (Inland taipan).	
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutelestomi;	
OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;	
OC Elapidae; Acanthophinae; Oxyuranus.	
OX NCBI_TaxID=111177;	
[1] SEQUENCE FROM N.A.	
RN TISSUE=Venom gland;	
RC Filippovich I.V., Sorokina N.I.;	
RL Submitted (MAY-2004) to the EMBL/GenBank/DBJ databases.	
- - SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.	
CC EMBL; AY626930; AAT5406.1; -. HSP; P10646; 1ADZ.	
DR GO; GO:0004867; F:serine-type endopeptidase inhibitor activity; IEA.	
DR InterPro; IPRO02223; Prot_inh_kunzp-m.	
DR Pfam; PF00014; Kunitz_BPTI; 1.	
DR PRINTS; PR00759; BASICPTASE.	
DR ProDom; PD000222; Prot_inh_Kunzp-m; 1.	
DR SMART; SM00131; KU; 1.	
DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.	
DR PROSITE; PS02079; BPTI_KUNITZ_2; 1.	
DR PROSITE 83 AA; 9040 MW; CB4FE517570CF94C CRC64;	
SO SEQUENCE	

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Query Match      52.0%; Score 157; DB 2; Length 83;
Best Local Similarity 51.0%; Pred. No. 9.1e-12;
Matches 26; Conservative 6; Mismatches 19; Indels 0; Gaps 0;
```

Qy 1 CSMPQEAGPCLASIPHWYKTKICSEFIYGGQGNNNFQTEAICLVTC 51
| : | | | | : : | | | | | : | | | : | |
pb 31 CELPADTGPCRVGFPSFYNPDEKKCLEFIYGGEGNANNFTKEECSTC 81

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RESULT 32
Q6ITB6
ID Q6ITB6 PRELIMINARY; PRT; 83 AA.
AC Q6ITB6;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Scutellin-2.
OS Oxyuranus scutellatus.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC Elapidae; Acanthophiinae; Oxyuranus.
NCBI_TaxID=8668;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=venom gland;
RA Filippovich I.V., Sorokina N.I.;
RL Submitted (MAY-2004) to the EMBL/GenBank/DBJ databases.
CC -|- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.
CC EMBL; AY626929; AAT45405.1; -.
DR HSSP; F10446; 1ADZ.
DR
DR GO; GO:0004867; F:serine-type endopeptidase inhibitor activity; I:
DR InterPro; IPR004223; Prot Inh Kunz-m.

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DR pfam, PF00014; Kunitz_BPTI; 1.
DR PRINTS; P00759; BASICPTASE.
DR ProDom; PD000222; Prot_inh_kunz-m; 1.
DR SMART; SMO0131; KU; 1.
DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
DR PROSITE; PS00279; BPTI_KUNITZ_2; 1.
DR PROSITE; PS00279; BPTI_KUNITZ_2; 1.
SO SEQUENCE 83 AA; 9074 MW; 3145E51757014221 CRC64;

Query Match 52.0%; Score 157; DB 2; Length 83;
Best Local Similarity 51.0%; Pred. No. 9.1e-12;
Matches 26: Conservative 6; Mismatches 19; Indels 0; Gaps 0;

Qy	1	C	S	M	P	Q	E	A	G	P	L	A	S	I	P	H	W	Y	N	K	T	K	I	C	S	E	F	I	Y	G	C	Q	G	N	N	N	F	Q	T	E	A	I	C	L	V	T	C		51					
		:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:
Db	31	C	E	L	P	A	D	T	G	C	R	V	G	F	F	P	F	Y	N	P	D	E	K	K	C	L	E	F	I	Y	G	C	E	G	N	N	F	I	T	K	E	E	S	T	C		81							

RESULT	33
BTTA_BOOMI	
ID_BTTA_BOOMI	STANDARD; PRT; 122 AA.
AC	P83609;
DT	05-JUL-2004 (Rel. 44, Created)
DT	05-JUL-2004 (Rel. 44, Last sequence update)
DT	05-JUL-2004 (Rel. 44, Last annotation update)
DE	Kunitz-type serine protease inhibitor Bm7-A (Fragments).
OS	Boophilus microplus (Cattle tick).
OC	Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Acari;
CC	Parasitiformes; Ixodida; Ixodoidea; Ixodidae; Boophilus.
NCBI_TaxID=6941;	
ON	11
DN	11

127	SEQUENCE, AND FUNCTION.
RP	TISSUE=Larva;
RC	PubMed=10615008; DOI=10.1016/S0162-3109(99)00074-0;
RX	Tanaka A.S., Andreotti R., Gomes A., Torquato R.J.S., Sampaio M.U.,
RA	Sampaio C.A.M.;
RT	"A double headed serine proteinase inhibitor-human plasma kallikrein
RT	and elastase inhibitor-from Boophilus microplus larvae.";
RL	Immunopharmacology 45:171-177(1999).
RC	-I- FUNCTION: Inhibits bovine trypsin, bovine chymotrypsin, human
CC	plasmin, human plasma kallikrein and human neutrophil elastase,
CC	but not bovine thrombin, human factor Xa or porcine pancreatic
CC	kallikrein. May play a role in blocking blood coagulation during
CC	the larvae fixation on cattle.
CC	-I- SUBCELLULAR LOCATION: Secreted.
CC	-I- SIMILARITY: Contains 2 BPTI/Kunitz inhibitor domains.
DB	TrEMBL: I260223. Kunitz, BPTI

DR	PRINTS; PR00759; BASICPTASE.
DR	Prodom; PD000222; Prot_inh_Kunz-m; 2.
DR	SMART; SM00131; KU; 2.
DR	PROSITE; PS00280; BPTI_KUNITZ_1; 2.
DR	PROSITE; PS00379; BPTI_KUNITZ_2; 2.
KW	Direct protein sequencing; Repeat; Serine protease inhibitor.
FT	BPTI/Kunitz inhibitor 1.
FT	BPTI/Kunitz inhibitor 2.
FT	By similarity.
FT	By similarity.
FT	By similarity.
FT	By similarity.
FT	By similarity.
FT	By similarity.
FT	By similarity.
FT	Reactive bond (By similarity).
FT	Reactive bond (By similarity).
FT	Non TER
SO	SEQUENCE 122 AA; 13736 MW; 8F5B1F48B10C566F CRC64;

Query Match 52.0%; Score 157; DB 1; Length 122;
Best Local Similarity 52.9%; Pred. No. 1.3e-11;
Matches 27; Conservative 6; Mismatches 18; Indels 0; Gaps 0;

Qy 1 CSMPQEAGPCLASIPHWYNNKTKICSEFIYGGCGGNNNNFQTAEICLVTC 51
| : | | | | : | : - | | | | | | : | : | : | : | :
Dd 71 CLARPESGCLAYPMWGWDSKLGCQCFEIIYGGCDGNDNKYTTEECCLKSC 121

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RESULT 34
Q7YRQ8 PRELIMINARY; PRT; 234 AA.
ID Q7YRQ8
AC Q7YRQ8;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Tissue factor pathway inhibitor-2.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22802738; PubMed=12921785; DOI=10.1016/S0003-9861(03)00332-1;
RA Du X., Deng F.M., Chand H.S., Kiesel W.;
RT "Molecular cloning, expression, and characterization of bovine tissue
RT factor pathway inhibitor-2."
RL Arch. Biochem. Biophys. 417:96-104(2003).
RN [2]
RP SEQUENCE FROM N.A.
RA Deng F.-M., Kiesel W., Sun T.-T.;
RL Submitted (FEB-2003) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Contains 3 BPTI/Kunitz inhibitor domains.
DR EMBL; AY234861; AAO84035.1; -.
DR HSSP; P00981; 1DTK.
DR GO; GO:0004867; F:serine-type endopeptidase inhibitor activity; IEA.
DR InterPro; IPR002223; Prot_Inh_Kunz-m.
DR Pfam; PF00014; Kunitz BPTI; 3.
DR ProDom; PD000222; Prot_Inh_Kunz-m; 3.
DR SMART; SM00131; KU; 3.
DR PROSITE; PS00280; BPTI_KUNITZ_1; 3.
DR PROSITE; PS00279; BPTI_KUNITZ_2; 3.
SQ SEQUENCE 234 AA; 26675 MW; 4018EC94D589B422 CRC64;

Query Match 52.0%; Score 157; DB 2; Length 234;
Best Local Similarity 49.0%; Pred. No. 2.6e-11;
Matches 25; Conservative 10; Mismatches 16; Indels 0; Gaps 0;

QY 1 CSMPOEAGPCLASIPHHWYNNKTKICSEFIYGGCGGNNNFQTEAICLVTC 51
Db 36 CLLPPDGGPCRAIPSYDYDTQSCREPMYGCCEGNANFTEACNEAC 86

RESULT 35
Q8IT91 PRELIMINARY; PRT; 759 AA.
ID Q8IT91
AC Q8IT91;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Kunitz-like protease inhibitor precursor.
OS Ancylostoma caninum (Dog hookworm).
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Strongylida;
OC Ancylostomatidae; Ancylostomatidae; Ancylostominae; Ancylostoma.
OX NCBI_TaxID=29170;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=Baltimore;
RA Hawdon J.M., Datu B., Crowell M.;
RT "Molecular cloning of a novel multidomain Kunitz-type proteinase
RT inhibitor from the hookworm Ancylostoma caninum."
RL J. Parasitol. 89:402-407(2003).
CC -1- SIMILARITY: Contains 12 BPTI/Kunitz inhibitor domains.
DR EMBL; AF533590; AAN10061.1; -.
DR HSSP; P31713; ISHP.
DR GO; GO:0008233; F:peptidase activity; IEA.
DR GO; GO:0004867; F:serine-type endopeptidase inhibitor activity; IEA.
DR InterPro; IPR002223; Prot_Inh_Kunz-m.
DR Pfam; PF00014; Kunitz_BPTI; 12.

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PRINTS; PR00759; BASICPTASE.
DR SMART; SM00131; KU; 12.
DR PROSITE; PS00280; BPTI_KUNITZ_1; 10.
DR PROSITE; PS00279; BPTI_KUNITZ_2; 12.
KW Protease; Signal.
FT SIGNAL 1 16 Potential.
SQ SEQUENCE 759 AA; 84886 MW; C431A3C3F418F40A CRC64;

Query Match 52.0%; Score 157; DB 2; Length 759;
Best Local Similarity 51.0%; Pred. No. 8.5e-11;
Matches 26; Conservative 9; Mismatches 16; Indels 0; Gaps 0;

QY 1 CSMPOEAGPCLASIPHHWYNNKTKICSEFIYGGCGGNNNFQTEAICLVTC 51
Db 205 CSQPIKAGPCWMLKRYADNKKRCVQFIYGGCKGNKNFESMEECTRTC 255

RESULT 36
Q90WAI PRELIMINARY; PRT; 83 AA.
ID Q90WAI
AC Q90WAI;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Textilin.
OS Pseudonaja textilis textilis.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC Elapidae; Acanthophinae; Pseudonaja.
OX NCBI_TaxID=169397;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Venom gland;
RA Masci P.P., Lavin M.F., Gaffney P.J., Sorokina I.N., Flippovich I.V.;
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Venom gland;
RA Flippovich I.V., Sorokina N.I., Masci P.P., de Jersey J.,
RA Whitaker A.N., Gaffney P.J., Lavin M.F.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.
DR EMBL; AF402324; AAK95519.1; -.
DR HSSP; P25660; 1JG6.
DR GO; GO:0004867; F:serine-type endopeptidase inhibitor activity; IEA.
DR Pfam; PF00014; Kunitz BPTI; 1.
DR PRINTS; PR00759; BASICPTASE.
DR ProDom; PD000222; Prot_Inh_Kunz-m; 1.
DR SMART; SM00131; KU; 1.
DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
DR PROSITE; PS00279; BPTI_KUNITZ_2; 1.
SQ SEQUENCE 83 AA; 9173 MW; 2045E50657014221 CRC64;

Query Match 51.7%; Score 156; DB 2; Length 83;
Best Local Similarity 51.0%; Pred. No. 1.2e-11;
Matches 26; Conservative 6; Mismatches 19; Indels 0; Gaps 0;

QY 1 CSMPOEAGPCLASIPHHWYNNKTKICSEFIYGGCGGNNNFQTEAICLVTC 51
Db 31 CELPADTGPCRVRFPSFYNDPEKKCLEFIYGGCEGNANFITECESTC 81

RESULT 37
Q6AX20 PRELIMINARY; PRT; 587 AA.
ID Q6AX20
AC Q6AX20;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Atp2 A protein.
DE Name=atp2 A;
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

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OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Kidney;
RX PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heide F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bobak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettner M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grinwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Kidney;
RA Klein S., Gerhard D.S.;
RL Submitted (AUG-2004) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.
DR EMBL; BC079801; AAH79801.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0005488; F:binding; IEA.
DR GO; GO:0004867; F:serine-type endopeptidase inhibitor activity; IEA.
DR InterPro; IPR008154; A4_APP.
DR InterPro; IPR002223; Prot Inh_Kunz-m.
DR Pfam; PF02177; A4_EXTRA; 1.
DR Pfam; PF00014; Kunitz_BPTI; 1.
DR PRINTS; PR00203; AMYLOIDA4.
DR PRINTS; PR00759; BASICTPASE.
DR ProDom; PD000222; Prot Inh_Kunz-m; 1.
DR SMART; SM00006; A4_EXTRA; 1.
DR SMART; SM00131; KU; 1.
DR PROSITE; PS00320; A4_INTRA; 1.
DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
DR PROSITE; PS0279; BPTI_KUNITZ_2; 1.
KW SIGNAL.
FT SIGNAL.
FT CHAIN.
FT SEQUENCE.
SQ SEQUENCE 587 AA; 66870 MW; 7DF224C2138B94BF CRC64;

Query Match 51.7%; Score 156; DB 2; Length 587;
Best Local Similarity 49.0%; Pred. No. 8.7e-11;
Matches 25; Conservative 6; Mismatches 20; Indels 0; Gaps 0;

Qy 1 CSMPOEAGPCLASIPHHWYKTKICSEFIYGGCGGNNNFOTEICLVTC 51
Db 284 CSQEAITGPCAMRPWFNLGQKCFRIFYGGCGGNRNFESDYCMVAVC 334

RESULT 38
Q70820
ID Q70820 PRELIMINARY; PRT; 751 AA.
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AC Q70820;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Amyloid-beta-like protein A precursor.
GN Name=aplp2 A;
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RA Collin R.W.J., van Strien D., Leunissen J.A., Martens G.J.M.;
RL Submitted (NOV-2003) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.
DR EMBL; AJ608932; CAE75662.1; -.
DR HSP; Q16019; IAAp.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0005488; F:binding; IEA.
DR GO; GO:0004867; F:serine-type endopeptidase inhibitor activity; IEA.
DR InterPro; IPR008155; A4_APP.
DR InterPro; IPR002223; Prot Inh_Kunz-m.
DR Pfam; PF02177; A4_EXTRA; 1.
DR Pfam; PF00014; Kunitz_BPTI; 1.
DR PRINTS; PR00203; AMYLOIDA4.
DR PRINTS; PR00759; BASICTPASE.
DR ProDom; PD000222; Prot Inh_Kunz-m; 1.
DR SMART; SM00006; A4_EXTRA; 1.
DR SMART; SM00131; KU; 1.
DR PROSITE; PS00320; A4_INTRA; 1.
DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
DR PROSITE; PS0279; BPTI_KUNITZ_2; 1.
KW SIGNAL.
FT SIGNAL.
FT CHAIN.
FT SEQUENCE.
SQ SEQUENCE 751 AA; 85200 MW; C5E8FE7302C36B58 CRC64;

Query Match 51.7%; Score 156; DB 2; Length 751;
Best Local Similarity 49.0%; Pred. No. 1.1e-10;
Matches 25; Conservative 6; Mismatches 20; Indels 0; Gaps 0;

Qy 1 CSMPOEAGPCLASIPHHWYKTKICSEFIYGGCGGNNNFOTEICLVTC 51
Db 292 CSQEAITGPCAMRPWFNLGQKCFRIFYGGCGGNRNFESDYCMVAVC 342

RESULT 39
Q91963
ID Q91963 PRELIMINARY; PRT; 747 AA.
AC Q91963;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE AP747.
GN Name=APP747;
OS Xenopus.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;
OC Xenopodinae;
OX NCBI_TaxID=8353;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=9312927; PubMed=1282805;
RA Okado H., Okamoto H.;
RT "A Xenopus homologue of the human beta-amyloid precursor protein:
RT developmental regulation of its gene expression.";
RL Biochem. Biophys. Res. Commun. 189:1561-1568(1992).
CC -1- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.
DR EMBL; S52417; AAB24853.1; -.
DR HSP; Q16019; 1HZ3.
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DR GO:0016021; C:integral to membrane; IEA.
DR GO:0005488; F:binding; IEA.
DR GO:0004867; F:serine-type endopeptidase inhibitor activity; IEA.
DR Pfam: PF02177; A4 EXTRA; 1.
DR Pfam: PF03494; Beta-APP; 1.
DR Pfam: PF00014; Kunitz_BPTI; 1.
DR PRINTS: PR00203; AMYLOIDA4.
DR PRINTS: PR00759; BASICPTASE.
DR PRINTS: PR00204; BETANMYLOID.
DR PRODom: PD000222; Prot_Inh_Kunz-m; 1.
DR SMART: SM00131; KU; 1.
DR PROSITE: PS00319; A4_EXTRA; 1.
DR PROSITE: PS00320; A4_INTRA; 1.
DR PROSITE: PS00280; BPTI_KUNITZ_1; 1.
DR PROSITE: PS02079; BPTI_KUNITZ_2; 1.
SQ SEQUENCE 747 AA; 84893 MW; A75E81885681D948 CRC64;

Query Match 51.0%; Score 154; DB 2; Length 747;
Best Local Similarity 47.1%; Pred. No. 2e-10;
Matches 24; Conservative 8; Mismatches 19; Indels 0; Gaps 0;

QY 1 CSMPOEAGPCLASIPHHWYKTKICSEFIYGGCGNNNFOTEALCLVTC 51
DB 287 CSEQATGFCRAMISRWDYVTSKCAQFIYGGCGNNNFESDDYCMVAC 337

RESULT 40
Q6NRR1 PRELIMINARY; PRT; 749 AA.
AC Q6NRR1
DT 05-JUL-2004 (TRENBLrel. 27, Created)
DT 05-JUL-2004 (TRENBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TRENBLrel. 27, Last annotation update)
DE App protein.
GN Name=app;
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
[1]
SEQUENCE FROM N.A.
TISSUE=Kidney;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettaman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinska M.I., Skalek U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
[2]
SEQUENCE FROM N.A.
TISSUE=Kidney;
RX MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;
RA Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
RA Richardson P.;
RT "Genetic and genomic tools for Xenopus research: The NIH Xenopus
RT initiative";
RL Dev. Dyn. 225:384-391(2002).
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RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Kidney;
RA Klein S., Strausberg R.;
RL Submitted (MAY-2004) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.
DR EMBL: BC070668; AAH70668.1; -.
DR HSSP: Q16019; IEA4.
DR GO:0016021; C:integral to membrane; IEA.
DR GO:0005488; F:binding; IEA.
DR GO:0004867; F:serine-type endopeptidase inhibitor activity; IEA.
DR InterPro: IPR008155; A4_APP.
DR InterPro: IPR001255; Beta-APP.
DR InterPro: IPR002223; Prot_Inh_Kunz-m.
DR Pfam: PF02177; A4_EXTRA; 1.
DR Pfam: PF03494; Beta-APP; 1.
DR Pfam: PF00014; Kunitz_BPTI; 1.
DR PRINTS: PR00203; AMYLOIDA4.
DR PRINTS: PR00759; BASICPTASE.
DR PRINTS: PR00204; BETANMYLOID.
DR PRODom: PD000222; Prot_Inh_Kunz-m; 1.
DR SMART: SM00131; KU; 1.
DR PROSITE: PS00319; A4_EXTRA; 1.
DR PROSITE: PS00320; A4_INTRA; 1.
DR PROSITE: PS00280; BPTI_KUNITZ_1; 1.
DR PROSITE: PS02079; BPTI_KUNITZ_2; 1.
SQ SEQUENCE 749 AA; 84766 MW; 33478C6B6A8C295D CRC64;

Query Match 51.0%; Score 154; DB 2; Length 749;
Best Local Similarity 47.1%; Pred. No. 2e-10;
Matches 24; Conservative 8; Mismatches 19; Indels 0; Gaps 0;

QY 1 CSMPOEAGPCLASIPHHWYKTKICSEFIYGGCGNNNFOTEALCLVTC 51
DB 289 CSEQATGFCRAMISRWDYVTSKCAQFIYGGCGNNNFESDDYCMVAC 339

RESULT 41
Q6GQN1 PRELIMINARY; PRT; 984 AA.
AC Q6GQN1
DT 01-MAR-2001 (TRENBLrel. 16, Created)
DT 01-MAR-2001 (TRENBLrel. 16, Last sequence update)
DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)
DE Peptidylglycine alpha-amidating monooxygenase.
GN Name=PAM;
OS Calliactis parasitica (Sea anemone).
OC Eukaryota; Metazoa; Cnidaria; Anthozoa; Zoantharia; Actiniaria;
OC Nynanthaeae; Hormathiidae; Calliactis.
OX NCBI_TaxID=6114;
[1]
SEQUENCE FROM N.A.
RA Williamson M., Hauser F., Grimmelikhuijzen C.J.P.;
RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.
DR EMBL: AF221986; AAG44251.1; -.
DR HSSP: P12111; 1KNT.
DR GO:0016020; C:membrane; IEA.
DR GO:0005507; F:copper ion binding; IEA.
DR GO:0004504; F:peptidylglycine monooxygenase activity; IEA.
DR GO:0004867; F:serine-type endopeptidase inhibitor activity; IEA.
DR GO:0006518; P:peptide metabolism; IEA.
DR InterPro: IPR011044; Amine_DH_B_like.
DR InterPro: IPR000323; Cu2_monooxygenase.
DR InterPro: IPR001258; NHL.
DR InterPro: IPR000720; Pamonooxygenase.
DR InterPro: IPR008977; PHM_PNGase_F.
DR InterPro: IPR002223; Prot_Inh_Kunz-m.
DR Pfam: PF01082; Cu2_monooxygen; 1.
DR Pfam: PF03712; Cu2_monoox_C; 1.
DR Pfam: PF00014; Kunitz_BPTI; 1.
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DR Pfam; PF01436; NHL; 5.
DR PRINTS; PR00759; BASICPTASE.
DR PRINTS; PR00790; PAMONOXGNASE.
DR SMART; SM00131; KU; 1.
DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
DR PROSITE; PS02079; BPTI_KUNITZ_2; 1.
DR PROSITE; PS00084; CU2_MONOOXYGENASE_1; 1.
KW Monooxygenase.
SQ SEQUENCE 984 AA; 110265 MW; 424E4BCEB3B480D CRC64;

Query Match 51.0%; Score 154; DB 2; Length 984;
Best Local Similarity 43.1%; Pred. No. 2.6e-10;
Matches 22; Conservative 11; Mismatches 18; Indels 0; Gaps 0;

Qy 1 CSMPOEAGPCLASIPHHWYKTKICSEFIYGGCGGNNNFQTEAICLVTC 51
| : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 730 CMLEHDTGPCRAAMPRWYFDKARSCTRFIYGGCGGNNNFASKRECAK 780

RESULT 42
Q9GQN2 PRELIMINARY; PRT; 984 AA.
AC Q9GQN2;
DT 01-MAR-2001 (TremBLrel. 16, Created)
DT 01-MAR-2001 (TremBLrel. 16, Last sequence update)
DT 01-OCT-2003 (TremBLrel. 25, Last annotation update)
DE Peptidylglycine alpha-amidating monooxygenase.
GN Name=PAM;
OS Calliactis parasitica (Sea anemone).
OC Eukaryota; Metazoa; Cnidaria; Anthozoa; Zoantharia; Actiniaria;
OC Nyanthaceae; Hormathiidae; Calliactis.
OX NCBI_TaxID=6114;
RN [1]
RP SEQUENCE FROM N.A.
RA Williamson M., Hauser F., Grimelikhuijzen C.J.P.;
RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.
DR EMBL; AF221985; AAG44250.1; -.
DR HSSP; P12111; 1KNT.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005507; F:copper ion binding; IEA.
DR GO; GO:004504; F:peptidylglycine monooxygenase activity; IEA.
DR GO; GO:0004867; F:serine-type endopeptidase inhibitor activity; IEA.
DR GO; GO:0006518; P:peptide metabolism; IEA.
DR InterPro; IPR011044; Amine_DH_B-like.
DR InterPro; IPR000323; Cu2_monooxygenase.
DR InterPro; IPR001258; NHL.
DR InterPro; IPR008977; PHM_PNGase_F.
DR InterPro; IPR002223; Prot_Inh_Kunz-m.
DR Pfam; PF01082; Cu2_monooxygen; 1.
DR Pfam; PF03712; Cu2_monoox_C; 1.
DR Pfam; PF00014; Kunitz_BPTI; 1.
DR Pfam; PF01436; NHL; 5.
DR PRINTS; PR00759; BASICPTASE.
DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
DR PROSITE; PS02079; BPTI_KUNITZ_2; 1.
DR PROSITE; PS00084; CU2_MONOOXYGENASE_1; 1.
KW Monooxygenase.
SQ SEQUENCE 984 AA; 110266 MW; 7AFE2D1B74B78BEC CRC64;

Query Match 51.0%; Score 154; DB 2; Length 984;
Best Local Similarity 43.1%; Pred. No. 2.6e-10;
Matches 22; Conservative 11; Mismatches 18; Indels 0; Gaps 0;

Qy 1 CSMPOEAGPCLASIPHHWYKTKICSEFIYGGCGGNNNFQTEAICLVTC 51
| : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 730 CMLEHDTGPCRAAMPRWYFDKARSCTRFIYGGCGGNNNFASKRECAK 780

Thu Sep 22 07:16:46 2005 us-10-807-204-1_copy_77_127.std.rup Page 20
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RP SEQUENCE=Venom;
 RC MEDLINE=92077130; PubMed=1743283; DOI=10.1016/0014-5793(91)81361-B;
 RA Siddiqui A.R., Zaidi Z.H., Joernvall H.;
 RT "Purification and characterization of a Kunitz-type trypsin inhibitor
 from Leaf-nosed viper venom.";
 RL FEBS Lett. 294:141-143(1991).
 CC -!- FUNCTION: This protein inhibits trypsin and kallikrein.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- TISSUE SPECIFICITY: Expressed by the venom gland.
 CC -!- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.
 DR PIR; S19327; S19327.
 DR HSSP; P25660; LJCE.
 DR InterPro; IPR002223; Prot_Inh_Kunz-m.
 DR Pfam; PF00014; Kunitz BPTI; 1.
 DR PRINTS; PR00759; BASICTPTASE.
 DR ProDom; PD000222; Prot_Inh_Kunz-m; 1.
 DR SMART; SM00131; KU; 1.
 DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
 DR PROSITE; PS0279; BPTI_KUNITZ_2; 1.
 KW Direct protein sequencing; Serine protease inhibitor.
 FT SITE 12 13 Reactive bond (By similarity).
 FT DISULFID 2 52 By similarity.
 FT DISULFID 11 35 By similarity.
 FT DISULFID 27 48 By similarity.
 SQ SEQUENCE 62 AA; 6772 MW; 0A2ED0A2B20DF938 CRC64;
 Query Match 50.7%; Score 153; DB 1; Length 62;
 Best Local Similarity 51.0%; Pred. No. 2.1e-11;
 Matches 26; Conservative 6; Mismatches 19; Indels 0; Gaps 0;
 QY 1 CSMQAGAGCLASIPHWYNNKTKICSEFIYGGCGGNNNNFQTEAICLVTC 51
 DB 2 CYLPDDPGVCKAHPFYNNPASKNCKNFYGGCGGNNNNFETRECRHTC 52
 RESULT 45
 Q6T6S5 PRELIMINARY; PRT; 90 AA.
 AC Q6T6S5;
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE Kunitz protease inhibitor 2.
 OS Bitis gabonica (Gaboon viper).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Lepidodonta; Squamata; Scleroglossa; Serpentes; Colubroidea;
 OC Viperidae; Viperinae; Bitis.
 OX NCBI_TaxID=8694;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX PubMed=15276202; DOI=10.1016/j.gene.2004.03.024;
 RA Francischetti I.M., My-Pham V., Harrison J., Garfield M.K.,
 RA Ribeiro J.M.;
 RT "Bitis gabonica (Gaboon viper) snake venom gland: toward a catalog for
 the full-length transcripts (cdna) and proteins.";
 RL Gene 337:55-69(2004).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Francischetti I.M.B., Pham V.M., Garfield M.K., Ribeiro J.M.C.;
 RL Submitted (OCT-2003) to the EMBL/GenBank/DBJ databases.
 CC -!- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.
 DR EMBL; AY430413; AAR24535.1; -.
 DR HSSP; Q16019; IAA.
 DR GO; GO:0008233; F:peptidase activity; IEA.
 DR GO; GO:0004867; F:serine-type endopeptidase inhibitor activity; IEA.
 DR InterPro; IPR002223; Prot_Inh_Kunz-m.
 DR Pfam; PF00014; Kunitz BPTI; 1.
 DR PRINTS; PR00759; BASICTPTASE.
 DR ProDom; PD000222; Prot_Inh_Kunz-m; 1.
 DR SMART; SM00131; KU; 1.
 DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
 DR PROSITE; PS0279; BPTI_KUNITZ_2; 1.

KW Protease.
 SQ SEQUENCE 90 AA; 10006 MW; 2BEDC1D2020852AF CRC64;
 Query Match 50.7%; Score 153; DB 2; Length 90;
 Best Local Similarity 45.1%; Pred. No. 3.1e-11;
 Matches 23; Conservative 10; Mismatches 18; Indels 0; Gaps 0;
 QY 1 CSMQAGAGCLASIPHWYNNKTKICSEFIYGGCGGNNNNFQTEAICLVTC 51
 DB 31 CYLPADTGCMAFPFYDSASKCKKFTYGGCHGNANNFETRECRKCC 81
 RESULT 46
 Q7T0Z5 PRELIMINARY; PRT; 224 AA.
 AC Q7T0Z5;
 DT 01-OCT-2003 (TrEMBLrel. 25, Created)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE MGC68843 protein.
 OS Xenopus laevis (African clawed frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
 OC Xenopodinae; Xenopus.
 OX NCBI_TaxID=8355;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Embryo;
 RX MEDLINE=2338257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
 RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
 RA Jones S.J., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Embryo;
 RX MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;
 RA Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
 RA Richardson P.;
 RT "Genetic and genomic tools for Xenopus research: The NIH Xenopus
 initiative.";
 RL Dev. Dyn. 225:384-391(2002).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Embryo;
 RA Klein S., Strausberg R.;
 RL Submitted (AUG-2003) to the EMBL/GenBank/DBJ databases.
 CC -!- SIMILARITY: Contains 3 BPTI/Kunitz inhibitor domains.
 DR EMBL; BC055972; AAH55972.1; -.
 DR HSSP; P00974; IBPI.
 DR GO; GO:0004867; F:serine-type endopeptidase inhibitor activity; IEA.
 DR InterPro; IPR002223; Prot_Inh_Kunz-m.
 DR Pfam; PF00014; Kunitz BPTI; 3.
 DR ProDom; PD000222; Prot_Inh_Kunz-m; 3.
 DR SMART; SM00131; KU; 3.
 DR PROSITE; PS00280; BPTI_KUNITZ_1; 3.
 DR PROSITE; PS0279; BPTI_KUNITZ_2; 3.

SQ SEQUENCE 224 AA; 25538 MW; 11C2DLC4C789445B CRC64;
 Query Match 50.7%; Score 153; DB 2; Length 224;
 Best Local Similarity 49.0%; Pred. No. 7.7e-11;
 Matches 25; Conservative 8; Mismatches 18; Indels 0; Gaps 0;

Qy 1 CSMPOEAGPCLASIPHWYNNKTKICSEFIYGCGQGNNNNFTQAICLVTC 51
 | : | | | | | : | : | : | : | : | : | : | : | : |
 Db 30 CLPLDEGPCKALPHYVYDRYTQTCEFFYGGCDGANNFVSMECKECFC 80

RESULT 47
 IP52 ANESU STANDARD; PRT; 62 AA.
 ID _IP52 ANESU AC PI0280;
 DT 01-MAR-1989 (Rel. 10, Created)
 DT 01-FEB-1991 (Rel. 17, Last sequence update)
 DT 03-JUL-2004 (Rel. 44, Last annotation update)
 DE Protease inhibitor 5 II (SAs II).
 OS Anemonia sulcata (Snake-locks sea anemone).
 EC Eukaryota; Metazoa; Cnidaria; Anthozoa; Actiniaria;
 OC Nynanthesea; Actiniidae; Anemonia.
 OX NCBI_TaxID=6108;
 [1]
 RP SEQUENCE OF 1-59.
 RA Wunderer G., Machleidt W., Fritz H.;
 RT "The broad-specificity proteinase inhibitor 5 II from the sea anemone
 R Anemonia sulcata.";
 RL Meth. Enzymol. 80:816-820(1981).
 RN [2]
 RP SEQUENCE.
 RA Krebs H.C., Habermehl G.G.;
 RT "Isolation and structural determination of a hemolytic active peptide
 RT from the sea anemone Metridium senile.";
 RL Naturwissenschaften 74:395-396(1987).
 CC -1- FUNCTION: Inhibitor of kallikreins.
 CC -1- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.
 DR PIR; S07451; S07451.
 DR HSSP; P31713; 1SHP.
 DR InterPro; IPR002223; Prot_Inh_Kunz-m.
 DR Pfam; PF00014; Kunitz_BPTI; 1.
 DR PRINTS; PR00759; BASICPTASE.
 DR PRODOM; PD000222; Prot_Inh_kunz-m; 1.
 DR SMART; SM00131; KU; 1.
 DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
 DR PROSITE; PSS0279; BPTI_KUNITZ_2; 1.
 KW Direct protein sequencing; Serine protease inhibitor.
 FT SITE 15 16 Reactive bond (By similarity).
 FT DISULFID 5 55 By similarity.
 FT DISULFID 14 38 By similarity.
 FT DISULFID 30 51 By similarity.
 FT VARIANT 13 13 P->R.
 FT VARIANT 16 16 A->G.
 FT VARIANT 17 17 R->G.
 FT VARIANT 25 25 S->L.
 FT VARIANT 28 28 K->R.
 FT VARIANT 39 39 G->R.
 SQ SEQUENCE 62 AA; 6937 MW; 7262D028CA567BC8 CRC64;

Query Match 50.3%; Score 152; DB 1; Length 62;
 Best Local Similarity 49.0%; Pred. No. 2.8e-11;
 Matches 25; Conservative 6; Mismatches 20; Indels 0; Gaps 0;

Qy 1 CSMPOEAGPCLASIPHWYNNKTKICSEFIYGCGQGNNNNFTQAICLVTC 51
 | : | | | | | : | : | : | : | : | : | : | : | : |
 Db 5 CELPKVVGPCRARPPRYYYNSSKKRCBKFIYGGCGNANFNHTLECEKVC 55

RESULT 48
 Q90WAO PRELIMINARY; PRT; 83 AA.
 ID Q90WAO
 AC Q90WAO;
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)

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OM protein - protein search, using sw model

Run on: September 21, 2005, 14:52:13 ; Search time 31.8938 Seconds
(without alignments)
618.452 Million cell updates/sec

Title: US-10-807-204-2_COPY_52_102
Perfect score: 302
Sequence: 1 CSMPQAGFCLASIPHWYN.....GCCQGNNNFQTEAICLVTC 51

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 50 summaries

Database : A_Geneseq_16Dec04:.*
1: Geneseqp1980s:.*
2: Geneseqp1990s:.*
3: Geneseqp2000s:.*
4: Geneseqp2001s:.*
5: Geneseqp2002s:.*
6: Geneseqp2003as:.*
7: Geneseqp2003bs:.*
8: Geneseqp2004s:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	302	100.0	106	7 ADA19801	Ada19801 Mature fo
2	302	100.0	131	7 ADA19800	Ada19800 Engineere
3	302	100.0	131	7 ADA19811	Ada19811 Engineere
4	292	96.7	131	7 ADA19814	Ada19814 Human DJ1
5	224	74.2	136	7 ADA19815	Ada19815 Mouse DJ1
6	219	72.5	51	2 AAW75257	Aaw75257 Fragment
7	219	72.5	51	5 AAE27025	Aae27025 Human gen
8	219	72.5	51	5 AAE27163	Aae27163 Human gen
9	219	72.5	51	8 ADG98845	Adg98845 Human sec
10	219	72.5	58	4 AAE13084	Aae13084 Human ser
11	219	72.5	58	4 AAB60630	Aab60630 Kunitz do
12	219	72.5	58	7 ADF41997	Adf41997 Human CAB
13	219	72.5	58	8 ADL16838	Adl16838 Human Kun
14	219	72.5	58	8 ADR99980	Adr99980 Human CAB
15	219	72.5	64	4 AAE13093	Aae13093 Human ser
16	219	72.5	102	5 AAE27095	Aae27095 Human sec
17	219	72.5	102	5 AAE28009	Aae28009 Human gen
18	219	72.5	102	6 ABU65039	Abu65039 Human sec
19	219	72.5	102	8 ADG98848	Adg98848 Human sec
20	219	72.5	117	5 AAE27094	Aae27094 Human sec
21	219	72.5	117	5 AAE27165	Aae27165 Human gen
22	219	72.5	117	6 ABU65038	Abu65038 Human sec
23	219	72.5	117	8 ADG98847	Adg98847 Human sec
24	219	72.5	133	2 AAW75219	Aaw75219 Human sec
25	219	72.5	133	5 AAE26982	Aae26982 Human gen

26	219	72.5	133	5 AAE27120	Aae27120 Human gen
27	219	72.5	133	6 ABU64993	Abu64993 Human sec
28	219	72.5	133	7 ADA19812	Ada19812 Human EPP
29	219	72.5	133	8 ADG98802	Adg98802 Human pro
30	219	72.5	164	3 AAY70010	Aay70010 Human pro
31	219	72.5	179	8 ABM85103	Abm85103 Human dia
32	188	62.3	134	7 ADA19813	Ada19813 Mouse EPP
33	170	56.3	43	4 AAE13096	Aae13096 Human ear
34	169	56.0	571	7 AAE39498	Aae39498 Cloned mo
35	169	56.0	571	7 AAE39459	Aae39459 Mouse GDF
36	169	56.0	571	7 ADD93670	Add93670 Mouse GDF
37	167	55.3	58	2 AAR99146	Aar99146 Apronin
38	166	55.0	54	4 AAE13092	Aae13092 Trypsin i
39	166	55.0	86	4 AAB48380	Aab48380 I. ricinu
40	161	53.3	51	2 AAW25929	Aaw25929 Anti-tryp
41	161	53.3	55	2 AAW25931	Aaw25931 RPDF-Kuni
42	161	53.3	58	2 AAR27402	Aar27402 Human neu
43	161	53.3	58	2 AAR99160	Aar99160 Genetical
44	161	53.3	58	2 AAR99159	Aar99159 Genetical
45	161	53.3	58	2 AAR99158	Aar99158 Genetical
46	161	53.3	58	8 ADF71964	Adf71964 Kallikrei
47	161	53.3	58	8 ADF71963	Adf71963 Kallikrei
48	161	53.3	58	8 ADF71962	Adf71962 Kallikrei
49	161	53.3	124	2 AAW25933	Aaw25933 New prote
50	161	53.3	124	2 AAW25932	Aaw25932 New prote

ALIGNMENTS

RESULT 1

ADA19801
ID ADA19801 standard; protein; 106 AA.

XX AC ADA19801;

XX DT 20-NOV-2003 (first entry)

XX DE Mature form of engineered human DJ1 protein SEQ ID NO:2.

XX DJ11; Kunitz-type protease inhibitor domain; antiinflammatory;
XX anti-allergic; thrombolytic; anticoagulant; cardiac; vasotropic;
XX antibacterial; immunosuppressive; antirheumatic; antiarthritic;
XX nephrotropic; antipsoriatic; vulnery; protease inhibitor; gene therapy;
XX acute pancreatitis; pulmonary injury; allergy-induced protease release;
XX deep vein thrombosis; myocardial infarction; shock; septic shock;
XX hyperfibrinolytic haemorrhage; inflammatory disorder; emphysema;
XX idiopathic pulmonary fibrosis; rheumatoid arthritis; glomerulonephritis;
XX chronic inflammatory bowel disease; psoriasis.

XX Synthetic.
XX Homo sapiens.

Key	Location/Qualifiers
Disulfide-bond	8..36 /note = predicted disulfide bond
Disulfide-bond	15..40 /note = predicted disulfide bond
Disulfide-bond	23..35 /note = predicted disulfide bond
Disulfide-bond	29..44 /note = predicted disulfide bond
Domain	52..102 /note = Kunitz domain predicted by pfscan
Disulfide-bond	52..102 /note = predicted disulfide bond
Disulfide-bond	61..85 /note = predicted disulfide bond
Disulfide-bond	77..98 /note = predicted disulfide bond
WO2003070770-A2.	

PD	28-AUG-2003.	XX	Synthetic.
XX	18-FEB-2003; 2003WO-EP001629.	OS	Homo sapiens.
XX		XX	
PR	21-FEB-2002; 2002US-0358683P.	FT	Key
XX		FT	Misc-difference
PA	(GENE-) GENEPROT INC.	FT	Location/Qualifiers
PI	Bougueleret L, Bairoch A, Niknejad A;	FT	/note= "eppin-like precursor"
XX		FT	1. .131
XX		FT	/note= signal
XX		FT	1. .25
XX		FT	/label= signal
XX		FT	26. .131
XX		FT	/note= "mature DJ11 protein"
XX		FT	33. .61
XX		FT	/note= predicted disulfide bond
PT	New engineered human Kunitz-type protease inhibitor for diagnosing,	FT	40. .65
PT	preventing or treating conditions associated with excessive proteinase	FT	/note= predicted disulfide bond
PT	activity, e.g. inflammation, pulmonary injuries, myocardial infarction or	FT	48. .60
PT	hemorrhage.	FT	/note= predicted disulfide bond
XX		FT	54. .69
PS	Claim 5; Page 71; 87pp; English.	FT	/note= predicted disulfide bond
XX		FT	77. .127
XX	The present invention describes an isolated, purified or recombinant DJ11	FT	/note= Kunitz domain predicted by pfscan
CC	polypeptide comprising a Kunitz-type protease inhibitor domain or its	FT	77. .127
CC	biologically active portion. The polypeptide comprises at least 98 %	FT	/note= predicted disulfide bond
CC	identity to residues 77-127 of a 131 amino acid sequence (S1, see	FT	86. .110
CC	ADA19800), or to residues 52-102 of a 106 amino acid sequence (S2, see	FT	/note= predicted disulfide bond
CC	ADA19801). DJ11 has antiinflammatory, antiallergic, thrombolytic,	FT	102. .123
CC	anticoagulant, cardiant, vasotropic, antibacterial, immunosuppressive,	FT	/note= predicted disulfide bond
CC	antirheumatic, antiarthritic, nephrotropic, antipsoriatic and vulnary	FT	
CC	activities, and can be used as a protease inhibitor and in gene therapy.	FT	
CC	Composition and methods from the present invention can be used in	PN	
CC	diagnosing, preventing or treating conditions associated with excessive	XX	
CC	proteinase activity, such as acute pancreatitis, pulmonary injury,	PD	
CC	allergy-induced protease release, deep vein thrombosis, myocardial	XX	
CC	infarction, shock (including septic shock), hyperfibrinolytic	XX	
CC	haemorrhage, and especially, inflammatory disorders (e.g. emphysema,	PF	
CC	idiopathic pulmonary fibrosis, rheumatoid arthritis, glomerulonephritis,	XX	
CC	chronic inflammatory bowel disease or psoriasis). The DJ11 proteins may	PR	
CC	be used in preserving platelet function, organ preservation or in wound	XX	
CC	healing. The polynucleotide sequence encoding DJ11 may be used as	XX	
CC	hybridisation probes, in chromosome and gene mapping, in the generation	PI	
CC	of antisense RNA and DNA, and as targets for pharmaceutical intervention.	XX	
CC	The present sequence represents the mature form of an engineered human	DR	
CC	DJ11 protein from the present invention.	DR	
XX		XX	
SQ	Sequence 106 AA;	XX	
		PT	New engineered human Kunitz-type protease inhibitor for diagnosing,
		PT	preventing or treating conditions associated with excessive proteinase
		PT	activity, e.g. inflammation, pulmonary injuries, myocardial infarction or
		PT	hemorrhage.
		XX	
		PS	Claim 5; Page 69-70; 87pp; English.
		XX	
QY	1 CSMPOEAGCLASIPHHWYNNKTKICSEPIYGGCGNNNNFQTEAICLVTC 51	XX	The present invention describes an isolated, purified or recombinant DJ11
DB	52 CSMPOEAGCLASIPHHWYNNKTKICSEPIYGGCGNNNNFQTEAICLVTC 102	CC	polypeptide comprising a Kunitz-type protease inhibitor domain or its
		CC	biologically active portion. The polypeptide comprises at least 98 %
		CC	identity to residues 77-127 of a 131 amino acid sequence (S1, see
		CC	ADA19800), or to residues 52-102 of a 106 amino acid sequence (S2, see
		CC	ADA19801). DJ11 has antiinflammatory, antiallergic, thrombolytic,
		CC	anticoagulant, cardiant, vasotropic, antibacterial, immunosuppressive,
		CC	antirheumatic, antiarthritic, nephrotropic, antipsoriatic and vulnary
		CC	activities, and can be used as a protease inhibitor and in gene therapy.
		CC	Composition and methods from the present invention can be used in
		CC	diagnosing, preventing or treating conditions associated with excessive
		CC	proteinase activity, such as acute pancreatitis, pulmonary injury,
		CC	allergy-induced protease release, deep vein thrombosis, myocardial
		CC	infarction, shock (including septic shock), hyperfibrinolytic
		CC	haemorrhage, and especially, inflammatory disorders (e.g. emphysema,
		CC	idiopathic pulmonary fibrosis, rheumatoid arthritis, glomerulonephritis,
		CC	chronic inflammatory bowel disease or psoriasis). The DJ11 proteins may
		CC	be used in preserving platelet function, organ preservation or in wound
		CC	healing. The polynucleotide sequence encoding DJ11 may be used as
		CC	hybridisation probes, in chromosome and gene mapping, in the generation
		CC	of antisense RNA and DNA, and as targets for pharmaceutical intervention.
		CC	The present sequence represents the mature form of an engineered human
		CC	DJ11 protein from the present invention.
		XX	
		SQ	Sequence 106 AA;
		Query Match	100.0%; Score 302; DB 7; Length 106;
		Best Local Similarity	100.0%; Pred. NO. 3.2e-30;
		Matches	51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
		QY	1 CSMPOEAGCLASIPHHWYNNKTKICSEPIYGGCGNNNNFQTEAICLVTC 51
		DB	52 CSMPOEAGCLASIPHHWYNNKTKICSEPIYGGCGNNNNFQTEAICLVTC 102
		RESULT 2	
		ADA19800	
		ID	ADA19800 standard; protein; 131 AA.
		XX	
		AC	ADA19800;
		XX	
		XX	20-NOV-2003 (first entry)
		DT	
		XX	Engineered human DJ11 protein SEQ ID NO:1.
		DE	
		XX	
		KW	DJ11; Kunitz-type protease inhibitor domain; antiinflammatory;
		KW	antiallergic; thrombolytic; anticoagulant; cardiant; vasotropic;
		KW	antibacterial; immunosuppressive; antirheumatic; antiarthritic;
		KW	nephrotropic; antipsoriatic; vulnary; protease inhibitor; gene therapy;
		KW	acute pancreatitis; pulmonary injury; allergy-induced protease release;
		KW	deep vein thrombosis; myocardial infarction; shock; septic shock;
		KW	hyperfibrinolytic haemorrhage; inflammatory disorder; emphysema;
		KW	idiopathic pulmonary fibrosis; rheumatoid arthritis; glomerulonephritis;
		KW	chronic inflammatory bowel disease; psoriasis.

XX SQ Sequence 131 AA;
Query Match 100.0%; Score 302; DB 7; Length 131;
Best Local Similarity 100.0%; Pred. No. 4.1e-30;
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CSMPOEAGPCLASIPHHWYNNKTKICSEFIYGGCGGNNNNFQTEAICLVTC 51
|||||
DB 77 CSMPOEAGPCLASIPHHWYNNKTKICSEFIYGGCGGNNNNFQTEAICLVTC 127
|||||

RESULT 3
ADA19811
ID ADA19811 standard; protein; 131 AA.
XX
AC ADA19811;
XX
DT 20-NOV-2003 (first entry)
XX
DE Engineered human DJ11 protein SEQ ID NO:12.
XX
KW DJ11; Kunitz-type protease inhibitor domain; antiinflammatory;
KW antiallergic; thrombolytic; anticoagulant; cardiant; vasotropic;
KW antibacterial; immunosuppressive; antirheumatic; antiarthritic;
KW nephrotropic; antipsoriatic; vulnary; protease inhibitor; gene therapy;
KW acute pancreatitis; pulmonary injury; allergy-induced protease release;
KW deep vein thrombosis; myocardial infarction; shock; septic shock;
KW hyperfibrinolytic haemorrhage; inflammatory disorder; emphysema;
KW idiopathic pulmonary fibrosis; rheumatoid arthritis; glomerulonephritis;
KW chronic inflammatory bowel disease; psoriasis.
XX
OS Synthetic.
OS Homo sapiens.
XX
XX WO2003070770-A2.
XX
XX 28-AUG-2003.
XX
XX 18-FEB-2003; 2003WO-EP001629.
XX
XX 21-FEB-2002; 2002US-0358683P.
XX
XX (GENE-) GENEPROT INC.
XX
XX Bougueleret L, Bairoch A, Niknejad A;
XX
XX WPI; 2003-663849/62.
XX
XX New engineered human Kunitz-type protease inhibitor for diagnosing,
XX preventing or treating conditions associated with excessive proteinase
XX activity, e.g. inflammation, pulmonary injuries, myocardial infarction or
XX hemorrhage.
XX
XX Disclosure; Page 84; 87pp; English.
XX
XX The present invention describes an isolated, purified or recombinant DJ11
XX polypeptide comprising a Kunitz-type protease inhibitor domain or its
XX biologically active portion. The polypeptide comprises at least 98 %
XX identity to residues 77-127 of a 131 amino acid sequence (S1, see
XX ADA19800), or to residues 52-102 of a 106 amino acid sequence (S2, see
XX ADA19801). DJ11 has antiinflammatory, antiallergic, immunosuppressive,
XX anticoagulant, cardiant, vasotropic, antibacterial, immunosuppressive,
XX antirheumatic, antiarthritic, nephrotropic, antipsoriatic and vulnary
XX activities, and can be used as a protease inhibitor and in gene therapy.
XX Composition and methods from the present invention can be used in
XX diagnosing, preventing or treating conditions associated with excessive
XX allergy-induced protease release, deep vein thrombosis, myocardial
XX infarction, shock (including septic shock), hyperfibrinolytic
XX haemorrhage, and especially, inflammatory disorders (e.g. emphysema,
XX idiopathic pulmonary fibrosis, rheumatoid arthritis, glomerulonephritis,
XX chronic inflammatory bowel disease or psoriasis). The DJ11 proteins may

CC be used in preserving platelet function, organ preservation or in wound
CC healing. The polynucleotide sequence encoding DJ11 may be used as
CC hybridisation probes, in chromosome and gene mapping, in the generation
CC of antisense RNA and DNA, and as targets for pharmaceutical intervention.
CC The present sequence represents an engineered human DJ11 protein from the
CC present invention.

XX SQ Sequence 131 AA;

Query Match 100.0%; Score 302; DB 7; Length 131;
Best Local Similarity 100.0%; Pred. No. 4.1e-30;
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CSMPOEAGPCLASIPHHWYNNKTKICSEFIYGGCGGNNNNFQTEAICLVTC 51
|||||
DB 77 CSMPOEAGPCLASIPHHWYNNKTKICSEFIYGGCGGNNNNFQTEAICLVTC 127
|||||

RESULT 4
ADA19814
ID ADA19814 standard; protein; 131 AA.
XX
AC ADA19814;
XX

DT 20-NOV-2003 (first entry)

DE Human DJ11 protein SEQ ID NO:15.

XX DJ11; Kunitz-type protease inhibitor domain; antiinflammatory;
KW antiallergic; thrombolytic; anticoagulant; cardiant; vasotropic;
KW antibacterial; immunosuppressive; antirheumatic; antiarthritic;
KW nephrotropic; antipsoriatic; vulnary; protease inhibitor; gene therapy;
KW acute pancreatitis; pulmonary injury; allergy-induced protease release;
KW deep vein thrombosis; myocardial infarction; shock; septic shock;
KW hyperfibrinolytic haemorrhage; inflammatory disorder; emphysema;
KW idiopathic pulmonary fibrosis; rheumatoid arthritis; glomerulonephritis;
KW chronic inflammatory bowel disease; psoriasis.

XX OS Homo sapiens.

XX WO2003070770-A2.

XX 28-AUG-2003.

XX 18-FEB-2003; 2003WO-EP001629.

XX 21-FEB-2002; 2002US-0358683P.

XX (GENE-) GENEPROT INC.

XX Bougueleret L, Bairoch A, Niknejad A;

XX WPI; 2003-663849/62.

XX New engineered human Kunitz-type protease inhibitor for diagnosing,
PT preventing or treating conditions associated with excessive proteinase
PT activity, e.g. inflammation, pulmonary injuries, myocardial infarction or
PT hemorrhage.

XX Disclosure; Fig 1; 87pp; English.

XX The present invention describes an isolated, purified or recombinant DJ11
XX polypeptide comprising a Kunitz-type protease inhibitor domain or its
XX biologically active portion. The polypeptide comprises at least 98 %
XX identity to residues 77-127 of a 131 amino acid sequence (S1, see
XX ADA19800), or to residues 52-102 of a 106 amino acid sequence (S2, see
XX ADA19801). DJ11 has antiinflammatory, antiallergic, immunosuppressive,
XX anticoagulant, cardiant, vasotropic, antibacterial, immunosuppressive,
XX antirheumatic, antiarthritic, nephrotropic, antipsoriatic and vulnary
XX activities, and can be used as a protease inhibitor and in gene therapy.
XX Composition and methods from the present invention can be used in
XX diagnosing, preventing or treating conditions associated with excessive
XX proteinase activity, such as acute pancreatitis, pulmonary injury,

XX Isolated human poly:nucleotide(s) encoding secretory peptide(s) - used to
 PT develop products for the diagnosis and treatment of e.g. inflammation,
 PT cancers, CNS disorders or immune system disorders.

XX Disclosure; Page 24; 201pp; English.

XX This sequence represents a fragment of a secreted human protein encoded
 CC by the nucleic acid molecule designated Gene 24 (AAV34309). The gene can
 CC be used to generate fusion proteins by linking to the gene to a human
 CC immunoglobulin Fc portion (e.g. AAV34277) for increasing the stability of
 CC the fused protein as compared to the human protein only. The invention
 CC relates to 28 novel genes and their fragments (nucleic acid sequences:
 CC AAV34286-V34325; amino acid sequences AAV75196-W75235) which are useful
 CC for preventing, treating or ameliorating medical conditions e.g. by
 CC protein or gene therapy. Also, pathological conditions can be diagnosed
 CC by determining the amount of the new polypeptides in a sample or by
 CC determining the presence of mutations in the new polynucleotides.
 CC Specific uses are described for each of the 28 polynucleotides, based on
 CC which tissues they are most highly expressed in (see AAV34286 for
 CC described uses)

XX Sequence 51 AA;

Query Match 72.5%; Score 219; DB 2; Length 51;
 Best Local Similarity 68.6%; Pred. No. 4.7e-20;
 Matches 35; Conservative 5; Mismatches 11; Indels 0; Gaps 0;

QY 1 CSMQAGPCLASIPHHWYNNKTKICSEFIYGGCGNNNNFQTEAICLVTC 51

DB 1 CEMPKETGCLAYFLHWYDKDNTCSMFYGGCGNNNNFQSKANCLNTC 51

RESULT 7

AAE27025

ID AAE27025 standard; protein; 51 AA.

AC AAE27025;

DT 13-DEC-2002 (first entry)

DE Human gene 24 encoded secreted protein variant, SEQ ID NO:118.

XX Human: immunodeficiency; X-linked agammaglobulinemia; septic shock;
 KW autoimmune disorder; rheumatoid arthritis; multiple sclerosis; cancer;
 KW Grave's disease; diabetes mellitus; haematopoietic disorder; stroke;
 KW respiratory disorder; asthma; allergy; gastrointestinal disorder;
 KW inflammatory bowel disease; neurodegenerative disorder; hepatitis;
 KW Parkinson's disease; Alzheimer's disease; cardiovascular disorder;
 KW atherosclerosis; myocarditis; renal disorder; fungicide; virucide;
 KW hyperproliferative disorder; acute glomerulonephritis; tonsillitis;
 KW respiratory disorder; rhinitis; sinusitis; neurological disease;
 KW endocrine disorder; Addison's disease; reproductive system disorder;
 KW endometriosis; vasotropic; vulnary; cytostatic; nootropic; cardiant;
 KW anti-HIV; tranquiliser; gout; antiparasitic.

OS Homo sapiens.

XX US2002077287-A1.

XX 20-JUN-2002.

XX 11-MAY-2001; 2001US-00852659.

XX 11-SEP-1998; 98US-00152060.

XX (RUBE/) RUBEN S M.

XX (ROSE/) ROSEN C A.

XX (LIYI/) LI Y.

XX (ZENG/) ZENG Z.

XX (KYAW/) KYAW H.

XX (FISC/) FISCHER C L.

XX (LIH/) LI H.

PA (SOPP/) SOPPET D R.
 PA (GENT/) GENTZ R L.
 PA (WEI/) WEI Y.
 PA (MOOR/) MOORE P A.
 PA (YOUN/) YOUNG P B.
 PA (GEE/) GREENE J M.
 PA (FERR/) FERRIE A M.

XX Ruben SM, Rosen CA, Li Y, Zeng Z, Kyaw H, Fischer CL, Li H;
 PI Soppet DR, Gentz RL, Wei Y, Moore PA, Young PE, Greene JM;
 PI Ferrie AM;

XX WPI; 2002-598780/64.

XX Novel human secreted polypeptides and polynucleotides for diagnosing,
 PT preventing, treating immune, hyperproliferative, cardiovascular,
 PT neurological, reproductive disorders and identifying modulators of
 PT therapeutic use.

XX Disclosure; Page 16; 209pp; English.

XX AAD44636-AAD44676 represent cDNAs corresponding to 28 human secreted
 CC protein genes, and AAE26959-AAE26999 represent the proteins they encode.
 CC AAE27000-AAE27025 represent human secreted protein fragments or their
 CC variants. The secreted proteins and genes are useful for preventing,
 CC treating or ameliorating medical conditions, e.g., by protein or gene
 CC therapy. Specific uses are described for each of the 28 genes, based on
 CC the tissues in which they are most highly expressed and include
 CC developing products for the diagnosis or treatment of immunodeficiencies,
 CC e.g., X-linked agammaglobulinemia, B cell immunodeficiencies, severe
 CC combined immunodeficiencies, autoimmune disorders e.g., systemic lupus
 CC erythematosus, rheumatoid arthritis, multiple sclerosis, autoimmune
 CC thyroiditis, autoimmune haemolytic anaemia, Goodpasture's syndrome,
 CC Grave's disease, diabetes mellitus, dermatitis, inflammatory conditions
 CC including septic shock, sepsis, reperfusion injury, inflammatory disorders
 CC disease, Crohn's disease, haematopoietic disorders, respiratory disorders
 CC e.g., asthma and allergy, gastrointestinal disorders e.g., inflammatory
 CC bowel disease), cancers e.g., gastric, ovarian, lung, liver, bladder and
 CC breast), central nervous system (CNS) disorders e.g., ischaemic brain
 CC injury and/or stroke, neurodegenerative disorders e.g., Parkinson's
 CC disease and Alzheimer's disease, AIDS-related dementia and prion disease,
 CC cardiovascular disorders e.g., myocarditis, arrhythmias, atherosclerosis,
 CC inflammatory disorders e.g., hepatitis, gout, trauma, pancreatitis,
 CC sarcoidosis and allogenic transplant rejection, blood-related disorder
 CC (thrombosis, arterial thrombosis, atherosclerosis), hyperproliferative
 CC disorders, respiratory disorders e.g. rhinitis, sinusitis, tonsillitis,
 CC lung cancer, allergic disorders, pneumonitis, renal disorders, e.g. acute
 CC glomerulonephritis, neurological diseases, liver disorders, endocrine
 CC disorders e.g., hyperthyroidism, Addison's disease, hyperpituitarism,
 CC infectious diseases and reproductive system disorders e.g. endometriosis.
 CC The present sequence represents a human secreted protein variant of the
 CC invention

XX Sequence 51 AA;

Query Match 72.5%; Score 219; DB 5; Length 51;

Best Local Similarity 68.6%; Pred. No. 4.7e-20;

Matches 35; Conservative 5; Mismatches 11; Indels 0; Gaps 0;

QY 1 CSMQAGPCLASIPHHWYNNKTKICSEFIYGGCGNNNNFQTEAICLVTC 51

DB 1 CEMPKETGCLAYFLHWYDKDNTCSMFYGGCGNNNNFQSKANCLNTC 51

RESULT 8

AAE27163

ID AAE27163 standard; protein; 51 AA.

XX AAE27163;

XX 13-DEC-2002 (first entry)

XX Human gene 24 encoded secreted protein fragment kunitz-type domain.

XX	Human; secreted protein; autoimmune disease; hyperproliferative disorder; rheumatoid arthritis; neoplasm; cerebrovascular disorder; angiogenesis; cerebral ischaemia; cardiovascular disorder; nervous system disorder; cardiac arrest; Alzheimer's disease; ocular disorder; wound healing; infection; corneal infection; skin aging; food additive; preservative; tissue regeneration; immunosuppressive; antiproliferative; cytostatic; cardiant; vasotropic; cerebroprotective; nootropic; neuroprotective; antibacterial; virucide; fungicide; ophthalmological; gene therapy; vulnary.
XX	Homo sapiens.
OS	
XX	US2002076756-A1.
XX	20-JUN-2002.
XX	11-MAY-2001; 2001US-00853161.
XX	02-FEB-2001; 2001US-0265583P.
PR	
XX	(RUBE/) RUBEN S M.
PA	(ROSE/) ROSEN C A.
PA	(LIYY/) LI Y.
PA	(ZENG/) ZENG Z.
PA	(KYAW/) KYAW H.
PA	(FISC/) FISCHER C L.
PA	(LIHH/) LI H.
PA	(SOPP/) SOPPET D R.
PA	(GENT/) GENTZ R L.
PA	(WEIY/) WEI Y.
PA	(MOOR/) MOORE P A.
PA	(YOUN/) YOUNG P E.
PA	(GREE/) GREENE J M.
PA	(FERR/) FERRIE A M.
XX	
PI	Ruben SM, Rosen CA, Li Y, Zeng Z, Kyaw H, Fischer CL, Li H;
PI	Soppet DR, Gentz RL, Wei Y, Moore PA, Young PE, Greene JM;
PI	Ferrie AM;
XX	
DR	WPI; 2002-574454/61.
XX	
PT	New nucleic acid molecules encoding 28 human secreted proteins, useful for diagnosing, preventing, treating or ameliorating medical conditions and as food additives or preservatives.
PT	
PT	
XX	
PS	Disclosure; Page 16; 209pp; English.
XX	
CC	AA044854-AD44984 represent cDNAs corresponding to 28 human secreted protein genes, and AA027097-AA027137 represent the proteins they encode. AA027138-AA027164 represent human secreted protein fragments. The genes and their corresponding secreted proteins are useful for preventing, treating or ameliorating medical conditions, e.g., by protein or gene therapy. Secreted protein sequences of the invention are useful for the diagnosis or treatment of disorders such as autoimmune diseases (e.g. rheumatoid arthritis), hyperproliferative disorders (e.g. neoplasms of the breast or liver), cerebrovascular disorders (e.g. cerebral ischaemia, angiogenesis), cardiovascular disorders (e.g. cardiac arrest), nervous system disorders (e.g. Alzheimer's disease), infections caused by fungi, bacteria and viruses and ocular disorders (e.g. corneal infection). The polypeptides can also be used to aid wound healing and epithelial cell proliferation, to prevent skin aging due to sunburn, to maintain organs before transplantation, for supporting cell culture of primary tissues, to regenerate tissues and in chemotaxis. They can also be used as food additives or preservative to increase or decrease storage capabilities, fat content, lipid, protein, carbohydrate, vitamins, minerals, cofactors and other nutritional components. The present sequence represents a human secreted protein fragment kunitz-type domain referred to in the disclosure of the invention
CC	
CC	
XX	Sequence 51 AA;
XX	

[illegible]

PR 05-AUG-1999; 99US-00369494.
 XX (FARB) BAYER PHARM CORP.
 PA Davies C, Chen D, Roczniak S;
 XX WPI; 2004-141424/14.
 XX New isolated polynucleotide encoding BTL010 serine proteinase, useful
 PT for treating e.g. emphysema, idiopathic pulmonary fibrosis, adult
 PT respiratory distress syndrome, cystic fibrosis, rheumatoid arthritis or
 PT glomerulonephritis.
 XX
 PS Disclosure; SEQ ID NO 8; 17pp; English.
 XX
 XX The invention relates to BTL010, a human serine proteinase inhibitor of
 CC the Kunitz family and its corresponding nucleic acid sequences. The
 CC sequences of the invention are useful for treating diseases, e.g.
 CC emphysema, idiopathic pulmonary fibrosis, adult respiratory distress
 CC syndrome, cystic fibrosis, rheumatoid arthritis, organ failure,
 CC glomerulonephritis or inflammatory diseases. The BTL010 protein is also
 CC useful for preventing neutrophil and monocyte activation and formation of
 CC active oxygen species during the oxidative burst of stimulated
 CC granulocytes. It is also useful for reducing platelet activation and
 CC blood coagulation. BTL010 DNA is useful in gene therapy. The present
 CC sequence is human Kunitz domain (KD) peptide.
 XX
 XX Sequence 58 AA;
 SQ
 Query Match 72.5%; Score 219; DB 8; Length 58;
 Best Local Similarity 68.6%; Pred. NO. 5.4e-20;
 Matches 35; Conservative 5; Mismatches 11; Indels 0; Gaps 0;
 QY 1 CSMPQAGPCLASIPHHWYKTKICSEFIYGCQGNNNFQTEAICLVTC 51
 DB 5 CEMPKEGTCLAYFLHWWYDKDNTCSMFVYGCQGNNNFQSKANCLNTC 55
 RESULT 14
 ADR89980
 ID ADR89980 standard; peptide; 58 AA.
 XX
 AC ADR89980;
 XX
 DT 18-NOV-2004 (first entry)
 XX
 DE Human CAB37 protein kunitz domain peptide.
 XX
 KW Kunitz domain peptide; cystic fibrosis; cystic fibrosis related disease;
 KW hereditary angioedema; cancer; chronic obstructive pulmonary disease;
 KW asthma; bronchitis; acute respiratory syndrome; pneumonia; bleeding;
 KW cytostatic; haemostatic; CAB37 protein; human.
 XX
 OS Homo sapiens.
 XX
 XX US2004171794-A1.
 XX
 PD 02-SEP-2004.
 XX
 PF 07-FEB-2003; 2003US-00361997.
 XX
 XX 07-FEB-2003; 2003US-00361997.
 XX
 XX (LADN/) LADNER R C.
 PA (LEYA/) LEY A C.
 XX
 XX Ladner RC, Ley AC;
 PI
 XX WPI; 2004-625120/60.
 DR
 XX New kunitz domain peptide useful as human neutrophil elastase inhibitor
 PT for the treatment of e.g. cystic fibrosis and related disease.
 PT
 XX

PS Disclosure; SEQ ID NO 5; 123pp; English.
 XX
 XX The invention relates to proteins comprising kunitz domain peptide,
 CC designated DPI-14 for inhibiting human neutrophil elastase, fused to
 CC albumin. The invention is useful for treating cystic fibrosis and related
 CC diseases, hereditary angioedema, cancer and related diseases including
 CC chronic obstructive pulmonary disease, asthma, bronchitis, acute
 CC respiratory syndrome, pneumonia and bleeding. The invention acts as a
 CC cytostatic and haemostatic agent. The present sequence is the human CAB37
 CC protein (A4) kunitz domain peptide. This sequence is used in the
 CC invention.
 XX
 XX Sequence 58 AA;
 SQ
 Query Match 72.5%; Score 219; DB 8; Length 58;
 Best Local Similarity 68.6%; Pred. NO. 5.4e-20;
 Matches 35; Conservative 5; Mismatches 11; Indels 0; Gaps 0;
 QY 1 CSMPQAGPCLASIPHHWYKTKICSEFIYGCQGNNNFQTEAICLVTC 51
 DB 5 CEMPKEGTCLAYFLHWWYDKDNTCSMFVYGCQGNNNFQSKANCLNTC 55
 RESULT 15
 AAE13093
 ID AAE13093 standard; peptide; 64 AA.
 XX
 AC AAE13093;
 XX
 DT 28-JAN-2002 (first entry)
 XX
 DE Human serine proteinase inhibitor BTL009 C-terminal peptide.
 XX
 KW Human; BTL009 protein; serine proteinase inhibitor; cytostatic;
 KW nephrotic; idiopathic pulmonary fibrosis; cystic fibrosis; emphysema;
 KW rheumatoid arthritis; adult respiratory distress syndrome; angioplasty;
 KW blood coagulation; glomerulonephritis; prophylactic; platelet activation;
 KW neutrophil; monocyte; granulocyte; organ failure; inflammatory disease;
 KW elastase inhibitor; chymotrypsin inhibitor; lung injury; vascular injury;
 KW therapeutic.
 XX
 OS Homo sapiens.
 XX
 XX US6294648-B1.
 XX
 XX 25-SEP-2001.
 XX
 XX 20-JUL-1999; 99US-00358569.
 PF
 XX 20-JUL-1999; 99US-00358569.
 PR
 XX (FARB) BAYER CORP.
 PA
 XX Delaria K, Roczniak S, Davies C;
 PI
 XX WPI; 2001-662224/76.
 DR
 XX New isolated protein for inhibiting human serine protease activity in the
 PT treatment of e.g. emphysema and adult respiratory distress syndrome.
 PT
 XX Disclosure; Col 6; 16pp; English.
 PS
 XX The invention relates to human BTL009 protein, a serine proteinase
 CC inhibitor of the Kunitz family that exhibits greater potency towards
 CC neutral serine proteinases. BTL009 protein is found to inhibit leukocyte
 CC elastase, chymotrypsin-like protease and trypsin-like protease. BTL009
 CC protein is useful for treating emphysema, idiopathic pulmonary fibrosis,
 CC adult respiratory distress syndrome, cystic fibrosis, rheumatoid
 CC arthritis, organ failure, glomerulonephritis, other inflammatory diseases
 CC and diseases involving lung and vascular injury. BTL009 is also useful
 CC for preventing neutrophil and monocyte activation and formation of active
 CC oxygen species during the oxidative burst of stimulated granulocytes.
 CC BTL009 is useful for reducing platelet activation and blood coagulation

XX 02-FEB-2001; 2001US-0265583P.
 XX (RUBE/) RUBEN S M.
 XX (ROSE/) ROSEN C A.
 XX (LIYY/) LI Y.
 XX (ZENG/) ZENG Z.
 XX (KYAW/) KYAW H.
 XX (FISC/) FISCHER C L.
 XX (LIHH/) LI H.
 XX (SOPP/) SOPPET D R.
 XX (GENT/) GENTZ R L.
 XX (WEIY/) WEI Y.
 XX (MOOR/) MOORE P A.
 XX (YOUN/) YOUNG P E.
 XX (GREE/) GREENE J M.
 XX (FERR/) FERRIE A M.
 XX
 XX Ruben SM, Rosen CA, Li Y, Zeng Z, Kyaw H, Fischer CL, Li H;
 PI Soppet DR, Gentz RL, Wei Y, Moore PA, Young PE, Greene JM;
 PI Ferrie AM;
 XX
 XX WPI; 2002-574454/61.
 XX
 XX New nucleic acid molecules encoding 28 human secreted proteins, useful
 PT for diagnosing, preventing, treating or ameliorating medical conditions
 PT and as food additives or preservatives.
 XX
 XX Disclosure; Page 17; 209pp; English.
 XX
 XX AAD44854-AAD44984 represent cDNAs corresponding to 28 human secreted
 CC protein genes, and AAE27097-AAE27137 represent the proteins they encode.
 CC AAE27138-AAE27164 represent human secreted protein fragments. The genes
 CC and their corresponding secreted proteins are useful for preventing,
 CC treating or ameliorating medical conditions, e.g., by protein or gene
 CC therapy. Secreted protein sequences of the invention are useful for the
 CC diagnosis or treatment of disorders such as autoimmune diseases (e.g.
 CC rheumatoid arthritis), hyperproliferative disorders (e.g. neoplasms of
 CC the breast or liver), cerebrovascular disorders (e.g. cerebral ischaemia,
 CC angiogenesis), cardiovascular disorders (e.g. cardiac arrest), nervous
 CC system disorders (e.g. Alzheimer's disease), infections caused by fungi,
 CC bacteria and viruses and ocular disorders (e.g. corneal infection). The
 CC polypeptides can also be used to aid wound healing and epithelial cell
 CC proliferation, to prevent skin aging due to sunburn, to maintain organs
 CC before transplantation, for supporting cell culture of primary tissues,
 CC to regenerate tissues and in chemotaxis. They can also be used as food
 CC additives or preservative to increase or decrease storage capabilities,
 CC fat content, lipid, protein, carbohydrate, vitamins, minerals, cofactors
 CC and other nutritional components. The present sequence represents a human
 CC secreted protein fragment referred to in the disclosure of the invention
 XX
 XX Sequence 102 AA;
 SQ
 Query Match 72.5%; Score 219; DB 5; Length 102;
 Best Local Similarity 68.6%; Pred. No. 1e-19;
 Matches 35; Conservative 5; Mismatches 11; Indels 0; Gaps 0;
 QY 1 CSMPOAGPCLASIPHWYKTKICSEFYGGCGQNNNNFQEAICLVTC 51
 DB 46 CEMPKETGTCPLAYFLHWYDKDKNTCSMFYGGCGQNNNNFQSKANCLNTC 96
 RESULT 18
 ABU65039
 ID ABU65039 standard; peptide; 102 AA.
 XX
 XX AC ABU65039;
 XX
 XX DT 15-MAY-2003 (first entry)
 XX
 XX Human secreted protein gene 24, protein #3.
 DE
 XX Secreted protein; immunodeficiency; multiple sclerosis;
 KW severe combined immunodeficiency; autoimmune disorder; cancer;
 KW rheumatoid arthritis; diabetes mellitus; haematopoietic disorder;
 KW inflammatory condition; septic shock; inflammatory bowel disease;
 KW Crohn's disease; respiratory disorder; asthma; allergy; stroke;
 KW gastrointestinal disorder; central nervous system disorder;
 KW ischaemic brain injury; neurodegenerative disorder; Parkinson's disease;
 KW Alzheimer's disease; cardiovascular disorder; atherosclerosis;
 KW blood-related disorder; thrombosis; atherosclerosis; renal disorder;
 KW hyperproliferative disorder; acute glomerulonephritis; Addison's disease;
 KW endocrine disorder; liver disease; reproductive system disorder;
 KW endometriosis; infectious disease; pancreatic disorder; vaccine;
 KW wound repair; angiogenesis; lymphatic disorder; hair loss; body weight;
 KW body height; hair colour; human.
 XX Homo sapiens.
 OS
 XX US2002172994-A1.
 PN
 XX 21-NOV-2002.
 PD
 XX 11-MAY-2001; 2001US-00852797.
 XX
 XX 14-MAR-1997; 97US-0040710P.
 PR 14-MAR-1997; 97US-0040762P.
 PR 30-MAY-1997; 97US-0048100P.
 PR 30-MAY-1997; 97US-0048189P.
 PR 30-MAY-1997; 97US-0048357P.
 PR 30-MAY-1997; 97US-0050934P.
 PR 06-JUN-1997; 97US-0048970P.
 PR 05-SEP-1997; 97US-005776SP.
 PR 19-DEC-1997; 97US-0068368P.
 PR 12-MAR-1998; 98WO-0004858P.
 PR 11-SEP-1998; 98US-0015206O.
 PR 02-FEB-2001; 2001US-0265583P.
 XX (RUBE/) RUBEN S M.
 XX (ROSE/) ROSEN C A.
 XX (LIYY/) LI Y.
 XX (ZENG/) ZENG Z.
 XX (KYAW/) KYAW H.
 XX (FISC/) FISCHER C L.
 XX (LIHH/) LI H.
 XX (SOPP/) SOPPET D R.
 XX (GENT/) GENTZ R L.
 XX (WEIY/) WEI Y.
 XX (MOOR/) MOORE P A.
 XX (YOUN/) YOUNG P E.
 XX (GREE/) GREENE J M.
 XX (FERR/) FERRIE A M.
 XX Ruben SM, Rosen CA, Li Y, Zeng Z, Kyaw H, Fischer CL, Li H;
 PI Soppet DR, Gentz RL, Wei Y, Moore PA, Young PE, Greene JM;
 PI Ferrie AM;
 XX WPI; 2003-310989/30.
 XX
 XX New human secreted polypeptides and polynucleotides for diagnosing,
 PT prognosing, preventing and treating immune, hyperproliferative, liver,
 PT kidney, reproductive disorders and for identifying modulators of
 PT therapeutic use.
 XX
 XX Disclosure; Page 16; 209pp; English.
 XX
 XX The invention relates to an isolated polypeptide comprising an amino acid
 CC sequence at least 95% identical to sequence of 28 human secreted
 CC proteins, their fragment, polypeptide domain, epitope, secreted form,
 CC variant, allelic variant, or species homologue, or the encoded sequence
 CC included in ATCC 97921 and 97922. Also included are the encoding nucleic
 CC acids, recombinant vectors, host cells, antibodies, and genes. The
 CC proteins and nucleic acids are useful for diagnosing, preventing,
 CC treating, prognosing or ameliorating a medical condition e.g.
 CC immunodeficiencies (e.g. X-linked agammaglobulinaemia, B cell
 CC immunodeficiencies, severe combined immunodeficiencies), autoimmune

CC disorders (e.g. systemic erythematous, rheumatoid arthritis, multiple
 CC sclerosis, autoimmune thyroiditis, autoimmune haemolytic anaemia, multiple
 CC Goodpasture's syndrome, Grave's disease, diabetes mellitus, dermatitis),
 CC haematopoietic disorders, inflammatory conditions (e.g. septic shock,
 CC sepsis, reperfusion injury, inflammatory bowel disease, Crohn's disease),
 CC respiratory disorders (e.g. asthma and allergy), gastrointestinal
 CC disorders, cancers (e.g. gastric, ovarian, lung, bladder, liver and
 CC breast), central nervous system (CNS) disorders (e.g. ischaemic brain
 CC injury and/or stroke, traumatic brain injury), neurodegenerative
 CC disorders (e.g. Parkinson's disease and Alzheimer's disease, AIDS-related
 CC dementia, and prion disease), cardiovascular disorders (e.g.
 CC atherosclerosis, myocarditis, cardiovascular disease, and cardiopulmonary
 CC bypass complications), inflammation (e.g. hepatitis, gout, trauma,
 CC pancreatitis, sarcoidosis, dermatitis, allogenic transplant rejection),
 CC blood-related disorders (thrombosis, arterial thrombosis),
 CC hyperproliferative disorders, renal disorders (e.g. acute
 CC glomerulonephritis), endocrine disorders (e.g. Addison's disease,
 CC hyperthyroidism, hypopituitarism), liver diseases and disorders,
 CC reproductive system disorders (e.g. endometriosis), infectious diseases,
 CC and pancreatic disorders. Many other diseases and disorders are listed in
 CC the specification. They also useful as a vaccine adjuvant. Further they
 CC are useful to enhance or inhibit complement mediated cell lysis, for
 CC stimulating wound and tissue repair, angiogenesis, and the repair of
 CC vascular or lymphatic diseases or disorders. They are also useful to
 CC prevent hair loss, to modulate mammalian characteristics such as body
 CC height, weight, hair colour, and to increase or decrease storage
 CC capabilities, fat content, lipid, protein, carbohydrate, vitamins,
 CC minerals, cofactors or other nutritional components. The proteins are
 CC also useful for identifying binding partners. The present sequence
 CC represents a secreted protein of the invention

XX Sequence 102 AA;

Query Match 72.5%; Score 219; DB 6; Length 102;

Best Local Similarity 68.6%; Pred. No. 1e-19;

Matches 35; Conservative 5; Mismatches 11; Indels 0; Gaps 0;

QY 1 CSMPEAGCLASIPHWYKTKTCTSEFIYGGCGNNNNFQTEALCLVTC 51

DB 46 CEMPKEGTCLAYFLHWYDKDKNTCSMFYGGCGNNNNFQSKANCLNTC 96

RESULT 19

ADG89848

ID ADG89848 standard; protein; 102 AA.

XX AC

ADG89848;

DT 11-MAR-2004 (first entry)

XX DE Human secreted protein gene 24 protein #6.

XX Secreted protein; gene therapy; neural disorder; immune system disorders;
 KW muscular disorder; reproductive disorder; gastrointestinal disorder;
 KW pulmonary disorder; cardiovascular disorder; renal disorder;
 KW proliferative disorder; cancer; systemic lupus erythematous;
 KW rheumatoid arthritis; multiple sclerosis; thyroiditis; anaemia;
 KW Grave's disease; diabetes; hepatitis; asthma; allergy; nephritis;
 KW Parkinson's disease; Alzheimer's disease; atherosclerosis;
 KW myocardial infarction; AIDS; infection; human.

XX OS Homo sapiens.

XX PN US2003225009-A1.

XX PD 04-DEC-2003.

XX PF 30-JAN-2002; 2002US-00058993.

XX PR 14-MAR-1997; 97US-0040710P.

PR 14-MAR-1997; 97US-0040762P.

PR 30-MAY-1997; 97US-0048100P.

PR 30-MAY-1997; 97US-0048189P.

PR 30-MAY-1997; 97US-0048357P.
 PR 30-MAY-1997; 97US-0050934P.
 PR 06-JUN-1997; 97US-0048970P.
 PR 05-SEP-1997; 97US-0057765P.
 PR 19-DEC-1997; 97US-0068368P.
 PR 12-MAR-1998; 98WO-US004858.
 PR 11-SEP-1998; 98US-00152060.
 PR 02-FEB-2001; 2001US-0265583P.
 PR 11-MAY-2001; 2001US-0085285P.
 PR 11-MAY-2001; 2001US-00852797.
 PR 11-MAY-2001; 2001US-00853161.

XX (ROSE/) ROSEN C A.
 PA (RUBE/) RUBEN S M.
 PA (LIYY/) LI Y.
 PA (ZENG/) ZENG Z.
 PA (KYAW/) KYAW H.
 PA (FISC/) FISCHER C L.
 PA (LIHH/) LI H.
 PA (SOPP/) SOPPET D R.
 PA (GENT/) GENTZ R L.
 PA (WEIY/) WEI Y.
 PA (MOOR/) MOORE P A.
 PA (YOUN/) YOUNG P E.
 PA (GREE/) GREENE J M.
 PA (FERR/) FERRIE A M.
 PA (HAST/) HASTINGS G A.

XX Rosen CA, Ruben SM, Li Y, Zeng Z, Kyaw H, Fischer CL, Li H;
 PI Soppet DR, Gentz RL, Wei Y, Moore PA, Young PE, Greene JM;
 PI Ferrie AM, Hastings GA;

XX WPI; 2004-042167/04.

XX New polypeptides and nucleic acid molecules for diagnosing, preventing or
 PT treating diseases associated with aberrant expression or activity of the
 PT polypeptide, e.g. cancer, asthma, AIDS, Parkinson's disease or diabetes.

XX Disclosure; SEQ ID NO 121; 320pp; English.

CC The invention relates to an isolated nucleic acid molecule encoding a
 CC secreted protein that is at least 95% identical to a polynucleotide
 CC fragment of any of the nucleotide sequences listed in table 1A of the
 CC specification, which is hybridisable to the nucleotide sequences, a
 CC polynucleotide encoding a polypeptide (or a polypeptide fragment, domain
 CC or epitope of any of the amino acid sequences) listed in table 1A of the
 CC specification, a polynucleotide which is an (allelic) variant of the
 CC nucleotide sequences listed in the specification, a polynucleotide which
 CC encodes a species homologue of the above amino acid sequences, a
 CC polynucleotide capable of hybridising under stringent conditions to any
 CC of the above polynucleotides, where the polynucleotide does not hybridise
 CC under stringent conditions to a nucleic acid molecule having a nucleotide
 CC sequence of only A or T residues. Also included are a recombinant vector
 CC comprising the above nucleic acid molecule, making a recombinant host
 CC cell comprising the above nucleic acid molecule, an isolated polypeptide
 CC comprising a sequence that is at least 95% identical to the polypeptide
 CC (or its fragment, domain, epitope, secreted form, (allelic) variant or
 CC homologue) encoded by the above nucleic acid molecule, an isolated
 CC antibody that binds specifically to the above polypeptide, a recombinant
 CC host cell produced by the above method and that expresses the above
 CC polypeptide, making an isolated polypeptide, preventing, treating or
 CC ameliorating a medical condition, diagnosing a pathological condition or
 CC a susceptibility to a pathological condition in a subject, identifying a
 CC binding partner to the above polypeptide, the gene corresponding to the
 CC cDNA sequence given in the specification, and identifying an activity in
 CC a biological assay. The nucleic acid molecule and polypeptide are useful
 CC in diagnosing, preventing, prognosing or treating diseases or disorders
 CC associated with aberrant expression and/or activity of the above
 CC polypeptide, such as neural disorders, immune system disorders, muscular
 CC disorders, reproductive disorders, gastrointestinal disorders, pulmonary
 CC disorders, cardiovascular disorders, renal disorders, proliferative
 CC disorders and/or cancers. In particular, these diseases are systemic
 CC lupus erythematosus, rheumatoid arthritis, multiple sclerosis,

CC thyroiditis, anaemia, Grave's disease, diabetes, hepatitis, asthma,
CC allergies, nephritis, Parkinson's disease, Alzheimer's disease,
CC atherosclerosis, myocardial infarction, AIDS and infections. The methods
CC may be used for identifying agonists and antagonists of the
CC polynucleotide and polypeptide. The present sequence is a protein from
CC one of the 28 disclosed secreted protein genes, it is not clear whether
CC this is an alternative expressed protein or a fragment of one of the
CC claimed proteins.
XX SQ Sequence 102 AA;
Query Match 72.5%; Score 219; DB 8; Length 102;
Best Local Similarity 68.6%; Pred. No. 1e-19;
Matches 35; Conservative 5; Mismatches 11; Indels 0; Gaps 0;
QY 1 CSMPOBAGPCLASIPHHWYNNKTKICSEFIYGGCGQNNNNFQTEAICLVTC 51
DB 46 CEMPKEGTGCLAYFLHWWYDKDKNTCSMFVYGGCGQNNNNFQSKANCLNTC 96
RESULT 20
AAE27094
ID AAE27094 standard; protein; 117 AA.
XX AC AAE27094;
XX DT 13-DEC-2002 (first entry)
XX DE Human secreted protein #1.
XX KW Human; immunodeficiency; X-linked agammaglobulinaemia; septic shock;
KW autoimmune disorder; rheumatoid arthritis; multiple sclerosis; cancer;
KW Grave's disease; diabetes mellitus; haematopoietic disorder; stroke;
KW respiratory disorder; asthma; allergy; gastrointestinal disorder;
KW inflammatory bowel disease; neurodegenerative disorder; hepatitis;
KW Parkinson's disease; Alzheimer's disease; cardiovascular disorder;
KW atherosclerosis; myocarditis; renal disorder; fungicide; virucide;
KW hyperproliferative disorder; acute glomerulonephritis; tonsillitis;
KW respiratory disorder; rhinitis; sinusitis; neurological disease;
KW endocrine disorder; Addison's disease; reproductive system disorder;
KW endometriosis; vasotrophic; vulnery; cytosstatic; cardiant;
KW anti-HIV; tranquilliser; gout; antiparasitic.
XX OS Homo sapiens.
XX XN US2002077287-A1.
XX XN 20-JUN-2002.
XX XN 11-MAY-2001; 2001US-00852659.
XX XN 11-SEP-1998; 98US-00152060.
XX PA (RUBE/) RUBEN S M.
PA (ROSE/) ROSEN C A.
PA (LIYV/) LI Y.
PA (ZENG/) ZENG Z.
PA (KYAW/) KYAW H.
PA (FISC/) FISCHER C L.
PA (LIHH/) LI H.
PA (SOPP/) SOPPET D R.
PA (GENT/) GENTZ R L.
PA (WEIY/) WEI Y.
PA (MOOR/) MOORE P A.
PA (YOUN/) YOUNG P E.
PA (GREE/) GREENE J M.
PA (FERR/) FERRIE A M.
XX XN Ruben SM, Rosen CA, Li Y, Zeng Z, Kyaw H, Fischer CL, Li H;
PI Soppet DR, Gentz RL, Wei Y, Moore PA, Young PE, Greene JM;
PI Ferrie AM;
XX XN WPI; 2002-598780/64.

XX PT Novel human secreted polypeptides and polynucleotides for diagnosing,
PT preventing, treating immune, hyperproliferative, cardiovascular,
PT neurological, reproductive disorders and identifying modulators of
therapeutic use.
XX PS Disclosure; Page 16; 209pp; English.
XX XN AAD4636-AAD4676 represent cDNAs corresponding to 28 human secreted
protein genes, and AAE26959-AAE26999 represent the proteins they encode.
CC AAE27000-AAE27025 represent human secreted protein fragments or their
variants. The secreted proteins and genes are useful for preventing,
treating or ameliorating medical conditions, e.g., by protein or gene
therapy. Specific uses are described for each of the 28 genes, based on
the tissues in which they are most highly expressed and include
developing products for the diagnosis or treatment of immunodeficiencies,
e.g., X-linked agammaglobulinaemia, B cell immunodeficiencies, severe
combined immunodeficiencies, autoimmune disorders e.g., systemic lupus
erythematosus, rheumatoid arthritis, multiple sclerosis, autoimmune
thyroiditis, autoimmune haemolytic anaemia, Goodpasture's syndrome,
Grave's disease, diabetes mellitus, dermatitis, inflammatory bowel
disease, Crohn's disease, haematopoietic disorders, respiratory disorders
e.g., asthma and allergy, gastrointestinal disorders e.g., inflammatory
bowel disease), cancers e.g., gastric, ovarian, lung, liver, bladder and
breast), central nervous system (CNS) disorders e.g., ischaemic brain
injury and/or stroke, neurodegenerative disorders e.g., Parkinson's
disease and Alzheimer's disease, AIDS-related dementia and prion disease,
cardiovascular disorders e.g., myocarditis, arrhythmias, atherosclerosis,
inflammatory disorders e.g., hepatitis, gout, trauma, pancreatitis,
sarcoidosis and allogenic transplant rejection, blood-related disorder
(thrombosis, arterial thrombosis, atherosclerosis), hyperproliferative
disorders, respiratory disorders e.g. rhinitis, sinusitis, tonsillitis,
lung cancer, allergic disorders, pneumonitis, renal disorders. e.g. acute
glomerulonephritis, neurological diseases, liver disorders, endocrine
disorders e.g., hyperthyroidism, Addison's disease, hyperpituitarism,
infectious diseases and reproductive system disorders e.g. endometriosis.
XX The present sequence represents a human secreted protein of the invention
SQ Sequence 117 AA;
Query Match 72.5%; Score 219; DB 5; Length 117;
Best Local Similarity 68.6%; Pred. No. 1.2e-19;
Matches 35; Conservative 5; Mismatches 11; Indels 0; Gaps 0;
QY 1 CSMPOBAGPCLASIPHHWYNNKTKICSEFIYGGCGQNNNNFQTEAICLVTC 51
DB 61 CEMPKEGTGCLAYFLHWWYDKDKNTCSMFVYGGCGQNNNNFQSKANCLNTC 111
RESULT 21
AAE27165
ID AAE27165 standard; protein; 117 AA.
XX AC AAE27165;
XX DT 13-DEC-2002 (first entry)
XX DE Human gene 24 encoded secreted protein fragment #1.
XX KW Human; secreted protein; autoimmune disease; hyperproliferative disorder;
KW rheumatoid arthritis; neoplasm; cerebrovascular disorder; angiogenesis;
KW cerebral ischaemia; cardiovascular disorder; nervous system disorder;
KW cardiac arrest; Alzheimer's disease; ocular disorder; wound healing;
KW infection; corneal infection; skin aging; food additive; preservative;
KW tissue regeneration; immunosuppressive; antiproliferative; cytostatic;
KW cardiant; vasotrophic; cerebroprotective; nootropic; neuroprotective;
KW antibacterial; virucide; fungicide; ophthalmological; gene therapy;
vulnerary.
XX KW Homo sapiens.
XX OS Homo sapiens.
XX XN US2002076756-A1.

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XX PD 20-JUN-2002.
XX PF 11-MAY-2001; 2001US-00853161.
XX PR 02-FEB-2001; 2001US-0265583P.
XX PA (RUBE//) RUBEN S M.
XX PA (ROSE//) ROSEN C A.
XX PA (LIY//) LI Y.
XX PA (ZENG//) ZENG Z.
XX PA (KYAW//) KYAW H.
XX PA (FISC//) FISCHER C L.
XX PA (LIHH//) LI H.
XX PA (SOPP//) SOPPET D R.
XX PA (GENTZ//) GENTZ R L.
XX PA (WEI//) WEI Y.
XX PA (MOOR//) MOORE P A.
XX PA (YOUN//) YOUNG P E.
XX PA (GREE//) GREENE J M.
XX PA (FERR//) FERRIE A M.
XX PI Ruben SM, Rosen CA, Li Y, Zeng Z, Kyaw H, Fischer CL, Li H;
PI Soppet DR, Gentz RL, Wei Y, Moore PA, Young PE, Greene JM;
PI Ferrie AM;
XX WPI; 2002-574454/61.
XX DR New nucleic acid molecules encoding 28 human secreted proteins, useful
XX PT for diagnosing, preventing, treating or ameliorating medical conditions
XX PT and as food additives or preservatives.
XX PS Disclosure; Page 17; 209pp; English.
XX CC AAD44854-AAD44984 represent cDNAs corresponding to 28 human secreted
XX CC protein genes, and AAE27097-AAE27137 represent the proteins they encode.
XX CC AAE27138-AAE27164 represent human secreted protein fragments. The genes
XX CC and their corresponding secreted proteins are useful for preventing,
XX CC treating or ameliorating medical conditions, e.g., by protein or gene
XX CC therapy. Secreted protein sequences of the invention are useful for the
XX CC diagnosis or treatment of disorders such as autoimmune diseases (e.g.
XX CC rheumatoid arthritis), hyperproliferative disorders (e.g. neoplasms of
XX CC the breast or liver), cerebrovascular disorders (e.g. cerebral ischaemia,
XX CC angiotensin), cardiovascular disorders (e.g. cardiac arrest), nervous
XX CC system disorders (e.g. Alzheimer's disease), infections caused by fungi,
XX CC bacteria and viruses and ocular disorders (e.g. corneal infection). The
XX CC polypeptides can also be used to aid wound healing and epithelial cell
XX CC proliferation, to prevent skin aging due to sunburn, to maintain organs
XX CC before transplantation, for supporting cell culture of primary tissues,
XX CC to regenerate tissues and in chemotaxis. They can also be used as food
XX CC additives or preservative to increase or decrease storage capabilities,
XX CC fat content, lipid, protein, carbohydrate, vitamins, minerals, cofactors
XX CC and other nutritional components. The present sequence represents a human
XX CC secreted protein fragment referred to in the disclosure of the invention
XX SQ Sequence 117 AA;
Query Match 72.5%; Score 219; DB 5; Length 117;
Best Local Similarity 68.6%; Pred. No. 1.2e-19;
Matches 35; Conservative Indels 0; Gaps 0;
QY 1 CSMPEAGPCLASIPHHWYNNKTKTCTSEFIYGGCGNNNNFQTEAICLVTC 51
Db 61 CEMPKEGTCLAYFLHWYDKDNTCSMFVYGGCGNNNNFQSKANCLNTC 111
RESULT 22
ABU65038
ID ABU65038 standard; protein; 117 AA.
XX AC ABU65038;
XX DT 15-MAY-2003 (first entry)
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XX DE Human secreted protein gene 24, protein #4.
XX KW Secreted protein; immunodeficiency; multiple sclerosis;
KW severe combined immunodeficiency; autoimmune disorder; cancer;
KW rheumatoid arthritis; diabetes mellitus; haematopoietic disorder;
KW inflammatory condition; septic shock; inflammatory bowel disease;
KW Crohn's disease; respiratory disorder; asthma; allergy; stroke;
KW gastrointestinal disorder; central nervous system disorder;
KW Alzheimer's disease; neurodegenerative disorder; Parkinson's disease;
KW blood-related disorder; thrombosis; atherosclerosis; renal disorder;
KW hyperproliferative disorder; acute glomerulonephritis; Addison's disease;
KW endocrine disorder; liver disease; reproductive system disorder;
KW endometriosis; infectious disease; pancreatic disorder; vaccine;
KW wound repair; angiogenesis; lymphatic disorder; hair loss; body weight;
KW body height; hair colour; human.
XX OS Homo sapiens.
XX PN US2002172994-A1.
XX PD 21-NOV-2002.
XX PF 11-MAY-2001; 2001US-00852797.
XX PR 14-MAR-1997; 97US-0040710P.
XX PR 14-MAR-1997; 97US-0040762P.
XX PR 30-MAY-1997; 97US-0048100P.
XX PR 30-MAY-1997; 97US-0048189P.
XX PR 30-MAY-1997; 97US-0048357P.
XX PR 30-MAY-1997; 97US-0050934P.
XX PR 06-JUN-1997; 97US-0048970P.
XX PR 05-SEP-1997; 97US-0057765P.
XX PR 19-DEC-1997; 97US-0068368P.
XX PR 12-MAR-1998; 98MO-US004858.
XX PR 11-SEP-1998; 98US-00152060.
XX PR 02-FEB-2001; 2001US-0285583P.
XX PA (RUBE//) RUBEN S M.
XX PA (ROSE//) ROSEN C A.
XX PA (LIY//) LI Y.
XX PA (ZENG//) ZENG Z.
XX PA (KYAW//) KYAW H.
XX PA (FISC//) FISCHER C L.
XX PA (LIHH//) LI H.
XX PA (SOPP//) SOPPET D R.
XX PA (GENTZ//) GENTZ R L.
XX PA (WEI//) WEI Y.
XX PA (MOOR//) MOORE P A.
XX PA (YOUN//) YOUNG P E.
XX PA (GREE//) GREENE J M.
XX PA (FERR//) FERRIE A M.
XX PI Ruben SM, Rosen CA, Li Y, Zeng Z, Kyaw H, Fischer CL, Li H;
PI Soppet DR, Gentz RL, Wei Y, Moore PA, Young PE, Greene JM;
PI Ferrie AM;
XX WPI; 2003-310989/30.
XX DR New human secreted polypeptides and polynucleotides for diagnosing,
XX PT prognosing, preventing and treating immune, hyperproliferative, liver,
XX PT kidney, reproductive disorders and for identifying modulators of
XX PT therapeutic use.
XX PS Disclosure; Page 16; 209pp; English.
XX CC The invention relates to an isolated polypeptide comprising an amino acid
XX CC sequence at least 95% identical to sequence of 28 human secreted
XX CC proteins, their fragment, polypeptide domain, epitope, secreted form,
XX CC variant, allelic variant, or species homologue, or the encoded sequence
XX CC included in ATCC 97921 and 97922. Also included are the encoding nucleic
XX CC acids, recombinant vectors, host cells, antibodies, and genes. The
```

proteins and nucleic acids are useful for diagnosing, preventing, treating, prognosing or ameliorating a medical condition e.g. immunodeficiencies (e.g. X-linked agammaglobulinaemia, B cell immunodeficiencies, severe combined immunodeficiencies), autoimmune disorders (e.g. systemic erythematosus, rheumatoid arthritis, multiple sclerosis, autoimmune thyroiditis, autoimmune hemolytic anaemia, Goodpasture's syndrome, Grave's disease, diabetes mellitus, dermatitis), haematopoietic disorders, inflammatory conditions (e.g. septic shock, sepsis, reperfusion injury, inflammatory bowel disease, Crohn's disease), respiratory disorders (e.g. asthma and allergy), gastrointestinal disorders, cancers (e.g. gastric, ovarian, lung, bladder, liver and breast), central nervous system (CNS) disorders (e.g. ischaemic brain injury and/or stroke, traumatic brain injury), neurodegenerative disorders (e.g. Parkinson's disease and Alzheimer's disease, AIDS-related dementia, and prion disease), cardiovascular disorders (e.g. atherosclerosis, myocarditis, cardiovascular disease, and cardiopulmonary bypass complications), inflammation (e.g. hepatitis, gout, trauma, pancreatitis, sarcoidosis, dermatitis, allogeneic transplant rejection), blood-related disorders (thrombosis, arterial thrombosis), hyperproliferative disorders, renal disorders (e.g. acute glomerulonephritis), endocrine disorders (e.g. Addison's disease, hyperthyroidism, hypopituitarism), liver diseases and disorders, reproductive system disorders (e.g. endometriosis), infectious diseases, and pancreatic disorders. Many other diseases and disorders are listed in the specification. They also useful as a vaccine adjuvant. Further they are useful to enhance or inhibit complement mediated cell lysis, for stimulating wound and tissue repair, angiogenesis, and the repair of vascular or lymphatic diseases or disorders. They are also useful to prevent hair loss, to modulate mammalian characteristics such as body height, weight, hair colour, and to increase or decrease storage capabilities, fat content, lipid, protein, carbohydrate, vitamins, minerals, cofactors or other nutritional components. The proteins are also useful for identifying binding partners. The present sequence represents a secreted protein of the invention

Sequence 117 AA;

Query Match 72.5%; Score 219; DB 6; Length 117;

Best Local Similarity 68.6%; Pred. No. 1.2e-19;

Matches 35; Conservative 5; Mismatches 11; Indels 0; Gaps 0;

QY 1 CSMQAGPCLASIPHWYNNKTKICSEFIYGCQGNNNFQTEALCLVTC 51

Db 61 CEMPKETGCLAYFLHWYDKDNTCSMFYIGCGQNNNNFQSKANCLNTC 111

RESULT 23

ID ADG89847

AC ADG89847 standard; protein; 117 AA.

XX

DT 11-MAR-2004 (first entry)

XX Human secreted protein gene 24 protein #5.

XX Secreted protein; gene therapy; neural disorder; immune system disorders; muscular disorder; reproductive disorder; gastrointestinal disorder; pulmonary disorder; cardiovascular disorder; renal disorder; proliferative disorder; cancer; systemic lupus erythematosus; rheumatoid arthritis; multiple sclerosis; thyroiditis; anaemia; Grave's disease; diabetes; hepatitis; asthma; allergy; nephritis; Parkinson's disease; Alzheimer's disease; atherosclerosis; myocardial infarction; AIDS; infection; human.

XX Homo sapiens.

XX US2003225009-A1.

XX 04-DEC-2003.

XX 30-JAN-2002; 2002US-00058993.

XX

PR 14-MAR-1997; 97US-0040710P.
PR 14-MAR-1997; 97US-0040762P.
PR 30-MAY-1997; 97US-0048100P.
PR 30-MAY-1997; 97US-0048189P.
PR 30-MAY-1997; 97US-0048357P.
PR 30-MAY-1997; 97US-0050934P.
PR 06-JUN-1997; 97US-0048970P.
PR 05-SEP-1997; 97US-0057765P.
PR 12-DEC-1997; 97US-0068368P.
PR 19-MAR-1998; 98WO-US004858.
PR 01-SEP-1998; 98US-0015206P.
PR 02-FEB-2001; 2001US-0265583P.
PR 11-MAY-2001; 2001US-0085265P.
PR 11-MAY-2001; 2001US-0085277P.
PR 11-MAY-2001; 2001US-0085316P.

XX (ROSE/) ROSEN C A.
PA (RUBE/) RUBEN S M.
PA (LIYY/) LI Y.
PA (ZENG/) ZENG Z.
PA (KYAM/) KYAM H.
PA (FISC/) FISCHER C L.
PA (LIHF/) LI H.
PA (SOPP/) SOPPET D R.
PA (GENT/) GENTZ R L.
PA (WEIY/) WEI Y.
PA (MOOR/) MOORE P A.
PA (YOUN/) YOUNG P E.
PA (GREE/) GREENE J M.
PA (FERR/) FERRIE A M.
PA (HAST/) HASTINGS G A.

XX Rosen CA, Ruben SM, Li Y, Zeng Z, Kyaw H, Fischer CL, Li H;
PI Soppet DR, Gentz RL, Wei Y, Moore PA, Young PE, Greene JM;
PI Ferrie AM, Hastings GA;

XX WPI; 2004-042167/04.

XX New polypeptides and nucleic acid molecules for diagnosing, preventing or treating diseases associated with aberrant expression or activity of the polypeptide, e.g. cancer, asthma, AIDS, Parkinson's disease or diabetes.

PS Disclosure; SEQ ID NO 120; 320pp; English.

XX The invention relates to an isolated nucleic acid molecule encoding a secreted protein that is at least 95% identical to a polynucleotide fragment of any of the nucleotide sequences listed in table 1A of the specification, which is hybridisable to the nucleotide sequences, a polynucleotide encoding a polypeptide (or a polypeptide fragment, domain or epitope of any of the amino acid sequences) listed in table 1A of the specification, a polynucleotide which is an (allelic) variant of the nucleotide sequences listed in the specification, a polynucleotide which encodes a species homologue of the above amino acid sequences, a polynucleotide capable of hybridising under stringent conditions to any of the above polynucleotides, where the polynucleotide does not hybridise under stringent conditions to a nucleic acid molecule having a nucleotide sequence of only A or T residues. Also included are a recombinant vector comprising the above nucleic acid molecule, making a recombinant host cell comprising the above nucleic acid molecule, an isolated polypeptide comprising a sequence that is at least 95% identical to the polypeptide (or its fragment, domain, epitope, secreted form, (allelic) variant or homologue) encoded by the above nucleic acid molecule, an isolated antibody that binds specifically to the above polypeptide, a recombinant host cell produced by the above method and that expresses the above polypeptide, making an isolated polypeptide, preventing, treating or ameliorating a medical condition, diagnosing a pathological condition or a susceptibility to a pathological condition in a subject, identifying a binding partner to the above polypeptide, the gene corresponding to the cDNA sequence given in the specification, and identifying an activity in a biological assay. The nucleic acid molecule and polypeptide are useful in diagnosing, preventing, prognosing or treating diseases or disorders associated with aberrant expression and/or activity of the above polypeptide, such as neural disorders, immune system disorders, muscular

CC disorders, reproductive disorders, gastrointestinal disorders, pulmonary
CC disorders, cardiovascular disorders, renal disorders, proliferative
CC disorders and/or cancers. In particular, these diseases are systemic
CC lupus erythematosus, rheumatoid arthritis, multiple sclerosis,
CC thyroiditis, anaemia, Grave's disease, diabetes, hepatitis, asthma,
CC allergies, nephritis, Parkinson's disease, Alzheimer's disease,
CC atherosclerosis, myocardial infarction, AIDS and infections. The methods
CC may be used for identifying agonists and antagonists of the
CC polynucleotide and polypeptide. The present sequence is a protein from
CC one of the 28 disclosed secreted protein genes, it is not clear whether
CC this is an alternative expressed protein or a fragment of one of the
CC claimed proteins.

XX
SQ Sequence 117 AA;

Query Match 72.5%; Score 219; DB 8; Length 117;
Best Local Similarity 68.6%; Pred. No. 1.2e-19;
Matches 35; Conservative 5; Mismatches 11; Indels 0; Gaps 0;

QY 1 CSMPOEAGPCLASIPHHWYKTKICSEFIYGGCGGNNNFQTEAICLVTC 51
DB 61 CEMPKEGTGCLAYFLHWYDKDNTCSMFVYGGCGGNNNFQSKANCLNTC 111

RESULT 24
AAW75219
ID AAW75219 standard; protein; 133 AA.
XX
AC AAW75219;
XX
DT 29-JAN-1999 (first entry)
XX
DE Human secreted protein encoded by gene 24 clone HTEBY11.
XX
KW Human; secreted protein; fusion protein; gene therapy; protein therapy;
KW diagnosis; tissue; cancer; tumour; neurodegenerative disorder; leukaemia;
KW developmental abnormality; foetal deficiency; blood; allergy; renal;
KW immune system; asthma; lymphocytic disease; brain; hepatic; lymphoma;
KW inflammation; ischaemic shock; Alzheimer's disease; restenosis; AIDS;
KW cognitive disorder; schizophrenia; prostate; obesity; osteoclast; thymus;
KW osteoporosis; arthritis; testis; lung; thyroiditis; thyroid; digestion;
KW endocrine; metabolism; regulation; malabsorption; gastritis; neoplasm.
XX
OS Homo sapiens.
XX
PN WO9840483-A2.
XX
PD 17-SEP-1998.
XX
PF 12-MAR-1998; 98WO-US004858.
XX
PR 14-MAR-1997; 97US-0040710P.
PR 14-MAR-1997; 97US-0040762P.
PR 30-MAY-1997; 97US-0048100P.
PR 30-MAY-1997; 97US-0048189P.
PR 30-MAY-1997; 97US-0048357P.
PR 30-MAY-1997; 97US-0050934P.
PR 06-JUN-1997; 97US-0048970P.
PR 05-SEP-1997; 97US-0057765P.
PR 19-DEC-1997; 97US-0068368P.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Ruben SM, Rosen CA, Li Y, Zeng Z, Kyaw H, Fischer CL, Li H;
PI Soppet DR, Gentz RL, Wei YF, Moore PA, Young PE, Greene JM;
PI Ferrie AM;
XX
XX WPI: 1998-520811/44.
DR N-PSDB; AAV34309.
XX
PT Isolated human polynucleotide(s) encoding secretory peptide(s) - used to
PT develop products for the diagnosis and treatment of e.g. inflammation,
PT cancers, CNS disorders or immune system disorders.

XX
PS Claim 1; Page 167-168; 201pp; English.
XX
CC This sequence represents a secreted human protein encoded by the gene
CC clone detailed in the descriptor line. The gene can be used to generate
CC fusion proteins by linking to the gene to a human immunoglobulin Fc
CC portion (e.g. AAV34277) for increasing the stability of the fused protein
CC as compared to the human protein only. The invention relates to 28 novel
CC genes and their fragments (nucleic acid sequences: AAV34286-V34325; amino
CC acid sequences AAW75196-W75235) which are useful for preventing, treating
CC or ameliorating medical conditions e.g. by protein or gene therapy. Also,
CC pathological conditions can be diagnosed by determining the amount of the
CC new polypeptides in a sample or by determining the presence of mutations
CC in the new polynucleotides. Specific uses are described for each of the
CC 28 polynucleotides, based on which tissues they are most highly expressed
CC in (see AAV34286 for described uses)

XX
SQ Sequence 133 AA;

Query Match 72.5%; Score 219; DB 2; Length 133;
Best Local Similarity 68.6%; Pred. No. 1.3e-19;
Matches 35; Conservative 5; Mismatches 11; Indels 0; Gaps 0;

QY 1 CSMPOEAGPCLASIPHHWYKTKICSEFIYGGCGGNNNFQTEAICLVTC 51
DB 77 CEMPKEGTGCLAYFLHWYDKDNTCSMFVYGGCGGNNNFQSKANCLNTC 127

RESULT 25
AAE26982
ID AAE26982 standard; protein; 133 AA.
XX
AC AAE26982;
XX
DT 13-DEC-2002 (first entry)
XX
DE Human gene 24 encoded secreted protein HTEBY11, SEQ ID NO:34.
XX
KW Human; immunodeficiency; X-linked agammaglobulinaemia; septic shock;
KW autoimmune disorder; rheumatoid arthritis; multiple sclerosis; cancer;
KW Grave's disease; diabetes mellitus; haematopoietic disorder; stroke;
KW respiratory disorder; asthma; allergy; gastrointestinal disorder;
KW inflammatory bowel disease; neurodegenerative disorder; hepatitis;
KW Parkinson's disease; Alzheimer's disease; cardiovascular disorder;
KW atherosclerosis; myocarditis; renal disorder; fungicide; virucide;
KW hyperproliferative disorder; acute glomerulonephritis; tonsillitis;
KW respiratory disorder; rhinitis; sinusitis; neurological disease;
KW endocrine disorder; Addison's disease; reproductive system disorder;
KW endometriosis; vasotropic; vulnery; cytostatic; nootropic; cardiant;
KW anti-HIV; tranquilliser; gout; antiparasitic.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Peptide 1..21 /label= Signal_peptide
FT Protein 22..133 /note= "Human mature secreted protein"
XX
PN US2002077287-A1.
XX
PD 20-JUN-2002.
XX
PF 11-MAY-2001; 2001US-00852659.
XX
PR 11-SEP-1998; 98US-00152060.
XX
PA (RUBE/) RUBEN S M.
PA (ROSE/) ROSEN C A.
PA (LIYY/) LI Y.
PA (ZENG/) ZENG Z.
PA (KYAW/) KYAW H.
PA (FISC/) FISCHER C L.

XX (INCY-) INCYTE CORP.
 XX Schmidt JP, Wright RJ, Bruns CM, Marianovic MM, Shen F;
 PI Harchshorne TA, Suchorski MT, Altus CM, Pitts SJ, Elder LV;
 PI Mooney EM, Deleage AM, Panesar IS, Banville SC, Reddy TP;
 PI Stevens KA, Blanchard JL, Panzer SR, Wang X, Au AP, Gerstin EH;
 PI Peralta CH, Anderson SB, Rioux P, Shen EJ, Wu MC, Stuve LL;
 PI Lagace RE, Spiro PA, Stewart EA, Wingrove J, Vitt UA, Kirton ES;
 PI Xu Y, Kwong M, Pollick JL, Hurwitz BL, Ma Y, Jackson JL, Gietzen D;
 PI Patry S, Shi X, Suarez CJ;
 XX WPI; 2004-329368/30.
 DR N-PSDB; ACN43755.
 XX New diagnostic and therapeutic polynucleotides and polypeptides, useful
 PT in diagnosing a condition, disease or disorder associated with human
 PT molecules, e.g. autoimmune or inflammatory disorders, in gene therapy or
 PT in gene mapping.
 XX Claim 27; Page; 190pp; English.
 PS
 XX The invention relates to novel diagnostic and therapeutic polynucleotides
 CC selected from one of the 2722 sequences defined in the specification. A
 CC polynucleotide of the invention may have a use in gene therapy. The human
 CC polynucleotide and therapeutic polynucleotides (dithp) or polypeptides may be
 CC used to diagnose a particular condition, disease or disorder associated
 CC with human molecules, e.g. cell proliferative disorders,
 CC autoimmune/inflammatory disorder, developmental disorder, endocrine
 CC disorder, neurological disorders, gastrointestinal disorders, or
 CC infections caused by virus, bacteria, fungi or parasite. The dithp
 CC molecules may also be used in genetic mapping, in identifying individuals
 CC from minute biological samples, in detecting single nucleotide
 CC polymorphisms, as molecular weight markers, and for somatic or germline
 CC gene therapy. The present sequence represents a dithp protein of the
 CC invention. Note: The sequence data for this patent is not represented in
 CC the printed specification, but was obtained in electronic format directly
 CC from WIPO at www.wipo.int/pct/en/sequences/listing.htm
 XX Sequence 179 AA;
 SQ
 Query Match 72.5%; Score 219; DB 8; Length 179;
 Best Local Similarity 68.6%; Pred. No. 1.8e-19;
 Matches 35; Conservative 5; Mismatches 11; Indels 0; Gaps 0;
 QY 1 CSMPOAGPCLASIPHHWYNNKTKICSEFIYGGCGGNNNNFQTEAICLVTC 51
 DB 77 CEMPKETGPCLAYFLHWYDKDNTCSMFYGGCGGNNNNFOSKANCLWTC 127
 RESULT 32
 ADAL19813
 ID ADAL19813 standard; protein; 134 AA.
 XX ADAL19813;
 AC
 XX 20-NOV-2003 (first entry)
 DT
 XX Mouse EPPIN protein SEQ ID NO:14.
 DE
 XX DJ11; Kunitz-type protease inhibitor domain; antiinflammatory;
 KW antiatherogenic; antithrombotic; antidiabetic; antihypertensive;
 KW antibacterial; immunosuppressive; antirheumatic; antiarthritic;
 KW nephrotropic; antipsoriatic; vulnary; protease inhibitor; gene therapy;
 KW acute pancreatitis; pulmonary injury; allergy-induced protease release;
 KW deep vein thrombosis; myocardial infarction; shock; septic shock;
 KW hyperfibrinolytic haemorrhage; inflammatory disorder; emphysema;
 KW idiopathic pulmonary fibrosis; rheumatoid arthritis; glomerulonephritis;
 KW chronic inflammatory bowel disease; psoriasis; EPPIN.
 XX Mus musculus.
 OS
 XX WO2003070770-A2.
 PN

XX 28-AUG-2003.
 PD
 XX 18-FEB-2003; 2003WO-EP001629.
 PF
 XX 21-FEB-2002; 2002US-0358683P.
 PR
 XX (GENE-) GENEPROT INC.
 PA
 XX Bougueleret L, Bairoch A, Niknejad A;
 PI WPI; 2003-663849/62.
 DR
 XX New engineered human Kunitz-type protease inhibitor for diagnosing,
 PT preventing or treating conditions associated with excessive proteinase
 PT activity, e.g. inflammation, pulmonary injuries, myocardial infarction or
 PT hemorrhage.
 PT
 XX Disclosure; Fig 1; 87pp; English.
 PS
 XX The present invention describes an isolated, purified or recombinant DJ11
 CC polypeptide comprising a Kunitz-type protease inhibitor domain or its
 CC biologically active portion. The polypeptide comprises at least 98 %
 CC identity to residues 77-127 of a 131 amino acid sequence (S1, see
 CC ADA19800), or to residues 52-102 of a 106 amino acid sequence (S2, see
 CC ADA19801). DJ11 has antiinflammatory, antibacterial, immunosuppressive,
 CC anticoagulant, cardiant, vasotropic, antidiabetic, antihypertensive,
 CC antirheumatic, antiarthritic, nephrotropic, antipsoriatic and vulnary
 CC activities, and can be used as a protease inhibitor and in gene therapy.
 CC Composition and methods from the present invention can be used in
 CC diagnosing, preventing or treating conditions associated with excessive
 CC proteinase activity, such as acute pancreatitis, pulmonary injury,
 CC allergy-induced protease release, deep vein thrombosis, myocardial
 CC infarction, shock (including septic shock), hyperfibrinolytic
 CC haemorrhage, and especially, inflammatory disorders (e.g. emphysema,
 CC idiopathic pulmonary fibrosis, rheumatoid arthritis, glomerulonephritis,
 CC chronic inflammatory bowel disease or psoriasis). The DJ11 proteins may
 CC be used in preserving platelet function, organ preservation or in wound
 CC healing. The polynucleotide sequence encoding DJ11 may be used as
 CC hybridisation probes, in chromosome and gene mapping, in the generation
 CC of antisense RNA and DNA, and as targets for pharmaceutical intervention.
 CC The present sequence represents a mouse EPPIN protein given in comparison
 CC with DJ11 proteins in the exemplification of the present invention.
 XX Sequence 134 AA;
 SQ
 Query Match 62.3%; Score 188; DB 7; Length 134;
 Best Local Similarity 54.9%; Pred. No. 1.1e-15;
 Matches 28; Conservative 10; Mismatches 13; Indels 0; Gaps 0;
 QY 1 CSMPOAGPCLASIPHHWYNNKTKICSEFIYGGCGGNNNNFQTEAICLVTC 51
 DB 77 CSLPKDSGYCMAYFRWWFKENSTQVFIYGGCGGNNNNFOSQICQAC 127
 RESULT 33
 AAE13096
 ID AAE13096 standard; peptide; 43 AA.
 XX AAE13096;
 AC
 XX 28-JAN-2002 (first entry)
 DT
 XX Human serine proteinase inhibitor BTL.009 peptide fragment #2.
 DE
 XX Human; BTL.009 protein; serine proteinase inhibitor; cytostatic;
 KW nephrotropic; idiopathic pulmonary fibrosis; cystic fibrosis; emphysema;
 KW rheumatoid arthritis; adult respiratory distress syndrome; angioplasty;
 KW blood coagulation; glomerulonephritis; prophylactic; platelet activation;
 KW neutrophil; monocyte; granulocyte; organ failure; inflammatory disease;
 KW elastase inhibitor; chymotrypsin inhibitor; lung injury; vascular injury;
 KW therapeutic.
 XX

[illegible]

```
PF 06-JUN-2000; 2000WO-BE000061.
XX
XX
XX 09-JUN-1999; 99GB-00013425.
XX
XX (HENO-) HENOGEN SA.
XX
XX Godfroid E, Bollen A, Leboullie G;
PI
XX WPI; 2001-080687/09.
XX
XX DR N-PSDB; AAC84925.
XX
XX Characterization of genes induced in tick salivary glands during slow
XX feeding phase of blood meal by cloning genes by forming subtractive
XX PT library containing selectively induced mRNA during tick feeding phase.
XX
XX Claim 19; Page 42-43; 77pp; English.
XX
XX The invention relates to producing a library of cDNAs which are induced
XX in the salivary gland of Ixodes ricinus arthropod tick. The method
XX involves selectively cloning mRNAs induced during the tick feeding phase
XX to obtain a corresponding cDNA library and cloning full-length cDNAs
XX corresponding to at least one incomplete cDNA sequence identified in the
XX library obtained. The method is useful for identifying genes induced
XX during feeding. A therapeutic agent having anticoagulant or
XX immunomodulatory properties comprising a salivary gland polypeptide can
XX be used alone or in combination with an anti-tick vaccine to prevent the
XX transmission of pathogens carried by the ticks. The polypeptides encoded
XX by the isolated cDNAs are useful in the manufacture of medicinal agents
XX for use in hematology, transplantation, rheumatology and for general
XX treatment. The salivary gland polypeptides, or its epitope bearing
XX fragments, analogs, outer membrane vesicles or cells (attenuated or
XX otherwise) are useful for inducing an immunological response in a mammal
XX adequate to produce antibody and/or T cell immune response to protect the
XX animal from bacteria and viruses which could be transmitted during the
XX blood meal of I. ricinus and other related species. The vectors
XX comprising the cDNAs are also useful for inducing immunological response
XX in a mammal by expressing the polypeptides in vivo in order induce an
XX antibody response to protect the animal from diseases such as Lyme
XX disease, tick encephalitis virus disease etc. The polynucleotides and
XX polypeptides may be employed as research reagents and materials for
XX discovery of treatments and diagnostics to animal and human disease. The
XX present sequence represents a tick salivary gland polypeptide similar to
XX a human tissue factor pathway inhibitor PI-2
XX
XX Sequence 86 AA;
SQ
Query Match 55.0%; Score 166; DB 4; Length 86;
Best Local Similarity 49.0%; Pred. No. 4.2e-13;
Matches 25; Conservative 10; Mismatches 16; Indels 0; Gaps 0;
QY 1 CSMQPEAGPCLASIPHHWYNNKTKICSEFIYGGCGGNNNNFOTEALCLVTC 51
DB 31 CKLPDDGDCRARIPISYFDKTKTCKEFYMGCGEGNNENNFNITTCQEC 81
RESULT 40
AAW25929
ID AAW25929 standard; peptide; 51 AA.
XX
XX AAW25929;
XX
XX 11-NOV-1997 (first entry)
XX
XX Anti-trypsin inhibitor UTI Kunitz domain 1.
XX
XX Trypsin inhibitor; Kunitz domain; protease; active site; elastase;
XX neutrophil; disease; modification; site directed mutagenesis.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
XX Disulfide-bond 1. .51
XX Disulfide-bond 10. .34
PF
FT
```

```
FT Modified-site 20
FT Disulfide-bond 26. .47
XX
XX JP09124700-A.
XX
XX 13-MAY-1997.
XX
XX 07-NOV-1995; 95JP-00288527.
XX
XX 07-NOV-1995; 95JP-00288527.
XX (GREC ) GREEN CROSS CORP.
XX
XX WPI; 1997-316576/29.
XX N-PSDB; AAT79077.
XX
XX New protease inhibitor - useful for treating diseases involving elastase.
XX
XX Claim 1; Page 2; 37pp; Japanese.
XX
XX This is the amino acid sequence of the anti-trypsin inhibitor UTI Kunitz
XX domain 1. The encoding nucleotide sequence was used to construct a novel
XX protease inhibitor by replacing the active site of the Kunitz domain 1
XX (see AAT79080, AAT79081 and AAT79083). The modified protease inhibitors
XX are targeted to the protease elastase, especially from neutrophils and
XX can be used to treat diseases associated with elastase. Modifications of
XX the active site were done by site directed mutagenesis
XX
XX Sequence 51 AA;
SQ
Query Match 53.3%; Score 161; DB 2; Length 51;
Best Local Similarity 51.0%; Pred. No. 1e-12;
Matches 26; Conservative 6; Mismatches 19; Indels 0; Gaps 0;
QY 1 CSMQPEAGPCLASIPHHWYNNKTKICSEFIYGGCGGNNNNFOTEALCLVTC 51
DB 1 COLGYSAGPCTAFFPRYPYNGTSMACQTFVYGGCMGNGNNFVTEKCLQTC 51
RESULT 41
AAW25931
ID AAW25931 standard; peptide; 55 AA.
XX
XX AAW25931;
XX
XX 11-NOV-1997 (first entry)
XX
XX RPDF-Kunitz domain 1.
XX
XX Trypsin inhibitor; Kunitz domain; protease; active site; elastase;
XX neutrophil; disease; modification; site directed mutagenesis.
XX
XX Synthetic.
XX
XX Key Location/Qualifiers
XX Disulfide-bond 5. .55
XX Disulfide-bond 14. .38
XX Modified-site 24
XX Disulfide-bond 30. .51
XX
XX JP09124700-A.
XX
XX 13-MAY-1997.
XX
XX 07-NOV-1995; 95JP-00288527.
XX
XX 07-NOV-1995; 95JP-00288527.
XX (GREC ) GREEN CROSS CORP.
XX
XX WPI; 1997-316576/29.
XX
```

DR N-PSDB; AAT79079.

XX New protease inhibitor - useful for treating diseases involving elastase.

XX Claim 2; Page 2; 37pp; Japanese.

XX This is the amino acid sequence of a construct comprising the anti-trypsin inhibitor UTI Kunitz domain 1 (AAT79077) linked at the N-terminus to the peptide Arg-Pro-Asp-Phe. The recombinant sequence is used in the construction of a novel protease inhibitor where the active site residues of the Kunitz domain 1 (see AAT79080, AAT79081 and AAT79083) are substituted. The modified protease inhibitors are targeted to the protease elastase, especially from neutrophils and can be used to treat diseases associated with elastase. Modifications of the active site were done by site directed mutagenesis

XX Sequence 55 AA;

Query Match 53.3%; Score 161; DB 2; Length 55;
 Best Local Similarity 51.0%; Pred. No. 1.1e-12;
 Matches 26; Conservative 6; Mismatches 19; Indels 0; Gaps 0;

OY 1 CSMPOEAGPCLASIPHWYNNKTKICSEFIYGGCGNNNNFQTEAICLVTC 51
 Db 5 COLGYSAGPCIAFFRYFYNGTSMACQTFVYGGCMGNGNFFVTEKCLQTC 55

RESULT 42

AAR27402

ID AAR27402 standard; peptide; 58 AA.

XX AAR27402;

XX 07-OCT-2004 (revised)

DT 25-MAR-2003 (revised)

DT 20-MAY-1998 (first entry)

XX Human neutrophil elastase inhibitor MUTQE.

XX Kunitz Domain serine protease inhibitor; mutant;

KW Bovine pancreatic trypsin inhibitor.

XX Synthetic.

XX Key Location/Qualifiers

FT Region 1..4

FT /note= "mutated from ITI-D1 (KEDS) -> (RPDF) "

FT Region 15..19

FT /note= "mutated from ITI-D1 (MGMTS) -> (VAMFP) "

FT Region 34

FT /note= "mutated from ITI-D1 (Q) -> (V) "

XX WO215605-A2.

XX 17-SEP-1992.

XX 28-FEB-1992; 92WO-US001501.

XX 01-MAR-1991; 91US-00664989.

XX 17-JUN-1991; 91US-00715834.

XX (PROT-) PROTEIN ENG CORP.

XX Ley AC, Ladner RC, Guterman SK, Roberts BL, Markland W, Kent RB;

XX WPI; 1992-331666/40.

XX New peptide inhibitors of elastase or cathepsin G - are e.g. mutants of Kunitz Domain serine protease inhibitors, useful for treating and preventing conditions caused by excessive neutrophil elastase or cathepsin G.

XX Example; Page 103; 126pp; English.

XX The sequence is that of a mutant of inter-alpha trypsin inhibitor-D1 (ITI -D1) MUTQE which is an inhibitor with very strong (Kd< 10-11) specific binding activity for human neutrophil elastase (hNE). It can be used for the treatment or prophylaxis of a condition caused by excessive hNE activity, e.g. inflammation, emphysema, cystic fibrosis, adult respiratory distress syndrome or rheumatoid arthritis. It may also be used to purify hNE. See also AAR27373-R27403 and AAR27443. (Updated on 25 -MAR-2003 to correct PN field.)

XX Revised record issued on 07-OCT-2004 : Correction to FT field

XX Sequence 58 AA;

Query Match 53.3%; Score 161; DB 2; Length 58;
 Best Local Similarity 51.0%; Pred. No. 1.2e-12;
 Matches 26; Conservative 6; Mismatches 19; Indels 0; Gaps 0;

OY 1 CSMPOEAGPCLASIPHWYNNKTKICSEFIYGGCGNNNNFQTEAICLVTC 51
 Db 5 COLGYSAGPCVAMPFRFYNGTSMACETFYVGGCMGNGNFFVTEKDLQTC 55

RESULT 43

AAR99160

ID AAR99160 standard; protein; 58 AA.

XX AAR99160;

XX 12-FEB-1997 (first entry)

XX Genetically engineered aprotinin-like Kunitz domain (MUTQE).

XX Aprotinin; Kunitz domain; human neutrophil elastase; hNE;
 KW connective tissue; alpha 1 protease inhibitor; API; neutrophil;
 KW alaphal antitrypsin; respiratory disorder; cystic fibrosis;
 KW smokers emphysema.

XX Synthetic.

XX WO9620278-A2.

XX 04-JUL-1996.

XX 15-DEC-1995; 95WO-US016349.

XX 16-DEC-1994; 94US-00358160.

XX (PROT-) PROTEIN ENG CORP.

XX Ley AC, Ladner RC, Guterman SK, Roberts BL, Markland W, Kent RB;

XX WPI; 1996-321851/32.

XX New engineered inhibitors of human neutrophil elastase - contg. aprotinin-like Kunitz domain for treating, e.g. cystic fibrosis or other respiratory disorders.

XX Claim 1; Page 48; 105pp; English.

XX Genetically engineered human derived Kunitz domains can be used to inhibit human neutrophil elastase, an enzyme involved in the elimination of pathogens and the restructuring of connective tissue. In cases of reduction of the circulating alpha-1-protease inhibitor (API or alpha antitrypsin), or the inactivation of API by oxidation (smokers emphysema), extensive destruction of the lung tissue may result from uncontrolled elastolytic activity of human neutrophil elastase. Other respiratory disorders such as cystic fibrosis are thought to be caused by human neutrophil elastase release by neutrophils. The genetically engineered human derived Kunitz domains can be used to treat such respiratory disorders. See AAR99146-R99211

XX Sequence 58 AA;

Query Match 53.3%; Score 161; DB 2; Length 58;
Best Local Similarity 51.0%; Pred. No. 1.2e-12;
Matches 26; Conservative 6; Mismatches 19; Indels 0; Gaps 0;

QY 1 CSMPQAGPCLASIPHWYNNKTKICSEFIYGGCGQNNNFQTEAICLVTC 51
| : ||| :
DB 5 CQLGYSAGPCVAMPFRFYNGTSMACQTFVYGGCMGNGNPFVTEKDLQTC 55

RESULT 44
AAR99159
ID AAR99159 standard; protein; 58 AA.

AC AAR99159;
DT 12-FEB-1997 (first entry)

Genetically engineered aprotinin-like Kunitz domain (MUTT26A).

XX Aprotinin; Kunitz domain; human neutrophil elastase; hNE;
KW connective tissue; alpha 1 protease inhibitor; API; neutrophil;
KW alpha 1 antitrypsin; respiratory disorder; cystic fibrosis;
KW smokers emphysema.

XX Synthetic.

XX WO9620278-A2.

XX 04-JUL-1996.

XX 15-DEC-1995; 95WO-US016349.

XX 16-DEC-1994; 94US-00358160.

XX (PROT-) PROTEIN ENG CORP.

XX Ley AC, Ladner RC, Guterman SK, Roberts BL, Markland W, Kent RB;

XX WPI; 1996-321851/32.

XX New engineered inhibitors of human neutrophil elastase - contg. aprotinin
PT -like Kunitz domain for treating, e.g. cystic fibrosis or other
PT respiratory disorders.

XX Claim 1; Page 48; 105pp; English.

XX Genetically engineered human derived Kunitz domains can be used to
CC inhibit human neutrophil elastase, an enzyme involved in the elimination
CC of pathogens and the restructuring of connective tissue. In cases of
CC reduction of the circulating alpha-1-protease inhibitor (API or alpha
CC antitrypsin), or the inactivation of API by oxidation (smokers
CC emphysema), extensive destruction of the lung tissue may result from
CC uncontrolled elastolytic activity of human neutrophil elastase. Other
CC respiratory disorders such as cystic fibrosis are thought to be caused by
CC human neutrophil elastase release by neutrophils. The genetically
CC engineered human derived Kunitz domains can be used to treat such
CC respiratory disorders. See AAR99146-R99211

XX Sequence 58 AA;

Query Match 53.3%; Score 161; DB 2; Length 58;
Best Local Similarity 51.0%; Pred. No. 1.2e-12;
Matches 26; Conservative 6; Mismatches 19; Indels 0; Gaps 0;

QY 1 CSMPQAGPCLASIPHWYNNKTKICSEFIYGGCGQNNNFQTEAICLVTC 51
| : ||| :
DB 5 CQLGYSAGPCVAMPFRFYNGTSMACQTFVYGGCMGNGNPFVTEKDLQTC 55

RESULT 45
AAR99158
ID AAR99158 standard; protein; 58 AA.

XX AAR99158;
AC 12-FEB-1997 (first entry)
DT Genetically engineered aprotinin-like Kunitz domain (BITI-E7-141).
DE Aprotinin; Kunitz domain; human neutrophil elastase; hNE;
KW connective tissue; alpha 1 protease inhibitor; API; neutrophil;
KW alpha 1 antitrypsin; respiratory disorder; cystic fibrosis;
KW smokers emphysema.

XX Synthetic.

XX WO9620278-A2.

XX 04-JUL-1996.

XX 15-DEC-1995; 95WO-US016349.

XX 16-DEC-1994; 94US-00358160.

XX (PROT-) PROTEIN ENG CORP.

XX Ley AC, Ladner RC, Guterman SK, Roberts BL, Markland W, Kent RB;

XX WPI; 1996-321851/32.

XX New engineered inhibitors of human neutrophil elastase - contg. aprotinin
PT -like Kunitz domain for treating, e.g. cystic fibrosis or other
PT respiratory disorders.

XX Claim 1; Page 48; 105pp; English.

XX Genetically engineered human derived Kunitz domains can be used to
CC inhibit human neutrophil elastase, an enzyme involved in the elimination
CC of pathogens and the restructuring of connective tissue. In cases of
CC reduction of the circulating alpha-1-protease inhibitor (API or alpha
CC antitrypsin), or the inactivation of API by oxidation (smokers
CC emphysema), extensive destruction of the lung tissue may result from
CC uncontrolled elastolytic activity of human neutrophil elastase. Other
CC respiratory disorders such as cystic fibrosis are thought to be caused by
CC human neutrophil elastase release by neutrophils. The genetically
CC engineered human derived Kunitz domains can be used to treat such
CC respiratory disorders. See AAR99146-R99211

XX Sequence 58 AA;

Query Match 53.3%; Score 161; DB 2; Length 58;
Best Local Similarity 51.0%; Pred. No. 1.2e-12;
Matches 26; Conservative 6; Mismatches 19; Indels 0; Gaps 0;

QY 1 CSMPQAGPCLASIPHWYNNKTKICSEFIYGGCGQNNNFQTEAICLVTC 51
| : ||| :
DB 5 CQLGYSAGPCVAMPFRFYNGTSMACQTFVYGGCMGNGNPFVTEKDLQTC 55

RESULT 46
ADF71964
ID ADF71964 standard; protein; 58 AA.

XX ADF71964;

XX 11-MAR-2004 (first entry)

XX Kallikrein inhibitor related amino acid sequence SEQ ID NO:44.
DE ischaemia; vasotropic; kallikrein inhibitor; blood loss;
KW systemic inflammatory response.

XX Homo sapiens.

XX WO2003103475-A2.

```
XX PD 18-DEC-2003.
XX PF 06-JUN-2003; 2003WO-US017665.
XX PR 07-JUN-2002; 2002US-0387239P.
XX PR 28-AUG-2002; 2002US-0407003P.
XX PA (DYAX-) DYAX CORP.
XX PI Ladner RC, Ley AC, Hirani S, Williams A;
XX DR WPI; 2004-062190/06.
XX PT Preventing or reducing ischemia in patient involves administering to
XX PT patient composition comprising a kallikrein inhibitory polypeptide.
XX PS Disclosure; SEQ ID NO 44; 46pp; English.
XX CC The present invention describes a method (M1) for preventing or reducing
XX CC ischaemia in a patient. M1 involves administering to the patient a
XX CC composition comprising a polypeptide (I) having an amino acid sequence of
XX CC ADF71962 and inhibiting kallikrein. (I) has vasotrophic activity, and can
XX CC be used as a kallikrein inhibitor. (M1) is useful for preventing or
XX CC reducing ischaemia in a patient such as perioperative blood loss due to a
XX CC surgical procedure which is cardiothoracic surgery (e.g. cardiopulmonary
XX CC bypass or coronary artery bypass grafting) performed on the patient. (M1)
XX CC is also useful for preventing or reducing the onset of systemic
XX CC inflammatory response associated with a surgical procedure in a patient
XX CC which involves administering (I) to a patient. The present sequence is
XX CC used in the exemplification of the present invention.
XX CC Sequence 58 AA;
XX CC Query Match 53.3%; Score 161; DB 8; Length 58;
XX CC Best Local Similarity 51.0%; Pred. No. 1.2e-12;
XX CC Matches 26; Conservative 6; Mismatches 19; Indels 0; Gaps 0;
XX QY 1 CSMQPEGPCLASIPHHWYNNKTKICSEFTYGGCGGNNNNFOTEAICLVTC 51
XX DB 5 CQLGYSAGPCVAMFPRFYNGTSMACETFYGGCGGNNNNFVTEKDCQLTC 55
XX
XX RESULT 47
XX ADF71963
XX ID ADF71963 standard; protein; 58 AA.
XX AC ADF71963;
XX DT 11-MAR-2004 (first entry)
XX DE Kallikrein inhibitor related amino acid sequence SEQ ID NO:43.
XX KW ischaemia; vasotrophic; kallikrein inhibitor; blood loss;
XX KW systemic inflammatory response.
XX OS Homo sapiens.
XX PN WO2003103475-A2.
XX PD 18-DEC-2003.
XX PF 06-JUN-2003; 2003WO-US017665.
XX PR 07-JUN-2002; 2002US-0387239P.
XX PR 28-AUG-2002; 2002US-0407003P.
XX PA (DYAX-) DYAX CORP.
XX PI Ladner RC, Ley AC, Hirani S, Williams A;
XX PI WPI; 2004-062190/06.
XX DR 18-DEC-2003.
XX PT Preventing or reducing ischemia in patient involves administering to
XX PT patient composition comprising a kallikrein inhibitory polypeptide.
XX PS Disclosure; SEQ ID NO 43; 46pp; English.
XX CC The present invention describes a method (M1) for preventing or reducing
XX CC ischaemia in a patient. M1 involves administering to the patient a
XX CC composition comprising a polypeptide (I) having an amino acid sequence of
XX CC ADF71962 and inhibiting kallikrein. (I) has vasotrophic activity, and can
XX CC be used as a kallikrein inhibitor. (M1) is useful for preventing or
XX CC reducing ischaemia in a patient such as perioperative blood loss due to a
XX CC surgical procedure which is cardiothoracic surgery (e.g. cardiopulmonary
XX CC bypass or coronary artery bypass grafting) performed on the patient. (M1)
XX CC is also useful for preventing or reducing the onset of systemic
XX CC inflammatory response associated with a surgical procedure in a patient
XX CC which involves administering (I) to a patient. The present sequence is
XX CC used in the exemplification of the present invention.
XX CC Sequence 58 AA;
XX CC Query Match 53.3%; Score 161; DB 8; Length 58;
XX CC Best Local Similarity 51.0%; Pred. No. 1.2e-12;
XX CC Matches 26; Conservative 6; Mismatches 19; Indels 0; Gaps 0;
XX QY 1 CSMQPEGPCLASIPHHWYNNKTKICSEFTYGGCGGNNNNFOTEAICLVTC 51
XX DB 5 CQLGYSAGPCVAMFPRFYNGTSMACETFYGGCGGNNNNFVTEKDCQLTC 55
XX
XX RESULT 48
XX ADF71962
XX ID ADF71962 standard; protein; 58 AA.
XX AC ADF71962;
XX DT 11-MAR-2004 (first entry)
XX DE Kallikrein inhibitor related amino acid sequence SEQ ID NO:42.
XX KW ischaemia; vasotrophic; kallikrein inhibitor; blood loss;
XX KW systemic inflammatory response.
XX OS Homo sapiens.
XX PN WO2003103475-A2.
XX PD 18-DEC-2003.
XX PF 06-JUN-2003; 2003WO-US017665.
XX PR 07-JUN-2002; 2002US-0387239P.
XX PR 28-AUG-2002; 2002US-0407003P.
XX PA (DYAX-) DYAX CORP.
XX PI Ladner RC, Ley AC, Hirani S, Williams A;
XX PI WPI; 2004-062190/06.
XX DR 18-DEC-2003.
XX PT Preventing or reducing ischemia in patient involves administering to
XX PT patient composition comprising a kallikrein inhibitory polypeptide.
XX PS Disclosure; SEQ ID NO 42; 46pp; English.
XX CC The present invention describes a method (M1) for preventing or reducing
XX CC ischaemia in a patient. M1 involves administering to the patient a
XX CC composition comprising a polypeptide (I) having an amino acid sequence of
XX CC ADF71926 and inhibiting kallikrein. (I) has vasotrophic activity, and can
XX CC be used as a kallikrein inhibitor. (M1) is useful for preventing or
XX CC reducing ischaemia in a patient such as perioperative blood loss due to a
XX CC surgical procedure which is cardiothoracic surgery (e.g. cardiopulmonary
XX CC bypass or coronary artery bypass grafting) performed on the patient. (M1)
XX CC is also useful for preventing or reducing the onset of systemic
```


CC inflammatory response associated with a surgical procedure in a patient
CC which involves administering (i) to a patient. The present sequence is
CC used in the exemplification of the present invention.

XX Sequence 58 AA;

SQ Query Match 53.3%; Score 161; DB 8; Length 58;

Best Local Similarity 51.0%; Pred. No. 1.2e-12;

Matches 26; Conservative 6; Mismatches 19; Indels 0; Gaps 0;

QY 1 CSMPOEAGPCLASIPHHWYKTKICSEFIYGGCGGNNNNFOTEAICLVTC 51

DB 5 COLGYSAGPCVAMFPFYPYNGTSMACQTFYGGCMGNGNNFVTEKCLQTC 55

RESULT 49

AAW25933

ID AAW25933 standard; protein; 124 AA.

XX AC AAW25933;

XX 11-NOV-1997 (first entry)

XX DE New protease inhibitor Ep7-d21-RPDF-52-55.

XX KW Trypsin inhibitor; Kunitz domain; protease; active site; elastase;
XX KW neutrophil; disease; modification; site directed mutagenesis.

XX OS Synthetic.

XX FH Key Location/Qualifiers

FT Domain 5..56

FT /note= "Kunitz domain 1"

FT Disulfide-bond 5..55

FT Disulfide-bond 14..38

FT Misc-difference 15..19

FT /note= "mutated region; amino acids substituted for wild
FT type amino acid sequence MGMTS; this includes the active
FT site residue of domain 1 (aa 36 of the wild type sequence
FT AAW25928)"

FT Disulfide-bond 30..51

FT Misc-difference 31

FT /note= "mutated amino acid; replaces amino acid Glu in
FT wild type sequence"

FT Misc-difference 34

FT /note= "mutated amino acid; replaces amino acid Gln in
FT wild type sequence"

FT Domain 57..126

FT /note= "Kunitz domain 2"

FT Disulfide-bond 61..111

FT Disulfide-bond 70..94

FT Active-site 71

FT /note= "active site residue"

FT Disulfide-bond 86..107

XX JP09124700-A.

XX 13-MAY-1997.

XX 07-NOV-1995; 95JP-00288527.

XX 07-NOV-1995; 95JP-00288527.

XX (GREC) GREEN CROSS CORP.

XX WPI; 1997-316576/29.

XX N-PSDB; AAT79081.

XX New protease inhibitor - useful for treating diseases involving elastase.
XX Claim 6; Page 3; 37pp; Japanese.
XX This is the amino acid sequence of a novel protease inhibitor based on

CC the sequence of the anti-trypsin inhibitor UTI. The protein comprises
CC Kunitz domains 1 and 2 of UTI, but lacks amino acids 1-21. Of the
CC remaining amino acids, residues 1-4 (22-26 of the native sequence) are
CC replaced by the peptide Arg-Pro-Asp-Phe. The construct also has the
CC sequence encoding the active site residue and the adjacent amino acids
CC (amino acids 36-40 of the wild type sequence) and amino acids 52 and 55
CC substituted. The modified protease inhibitors are targeted to the
CC protease elastase, especially from neutrophils and can be used to treat
CC diseases associated with elastase. Modifications of the active site were
CC done by site directed mutagenesis

XX Sequence 124 AA;

SQ Query Match 53.3%; Score 161; DB 2; Length 124;

Best Local Similarity 51.0%; Pred. No. 2.7e-12;

Matches 26; Conservative 6; Mismatches 19; Indels 0; Gaps 0;

QY 1 CSMPOEAGPCLASIPHHWYKTKICSEFIYGGCGGNNNNFOTEAICLVTC 51

DB 5 COLGYSAGPCVAMFPFYPYNGTSMACQTFYGGCMGNGNNFVTEKCLQTC 55

RESULT 50

AAW25932

ID AAW25932 standard; protein; 124 AA.

XX AC AAW25932;

XX 11-NOV-1997 (first entry)

XX DE New protease inhibitor Ep1-d21-RPDF-52-55.

XX KW Trypsin inhibitor; Kunitz domain; protease; active site; elastase;
XX KW neutrophil; disease; modification; site directed mutagenesis.

XX OS Synthetic.

XX FH Key Location/Qualifiers

FT Domain 5..56

FT /note= "Kunitz domain 1"

FT Disulfide-bond 5..55

FT Disulfide-bond 14..38

FT Misc-difference 15..19

FT /note= "mutated region; amino acids substituted for wild
FT type amino acid sequence MGMTS; this includes the active
FT site residue of domain 1 (aa 36 of the wild type sequence
FT AAW25928)"

FT Disulfide-bond 30..51

FT Misc-difference 31

FT /note= "mutated amino acid; replaces amino acid Glu in
FT wild type sequence"

FT Misc-difference 34

FT /note= "mutated amino acid; replaces amino acid Gln in
FT wild type sequence"

FT Domain 57..126

FT /note= "Kunitz domain 2"

FT Disulfide-bond 61..111

FT Disulfide-bond 70..94

FT Active-site 71

FT /note= "active site residue"

FT Disulfide-bond 86..107

XX JP09124700-A.

XX 13-MAY-1997.

XX 07-NOV-1995; 95JP-00288527.

XX 07-NOV-1995; 95JP-00288527.

XX (GREC) GREEN CROSS CORP.

XX WPI; 1997-316576/29.

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 21, 2005, 16:27:13 ; Search time 9.32743 Seconds
(without alignments)
408.162 Million cell updates/sec

Title: US-10-807-204-2_COPY_52_102
Perfect score: 302
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Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 50 summaries

Database : Issued Patents AA:*

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- 2: /cgn2_6/prodata/1/aaa/5B-COMB.pep:*
- 3: /cgn2_6/prodata/1/aaa/6A-COMB.pep:*
- 4: /cgn2_6/prodata/1/aaa/6B-COMB.pep:*
- 5: /cgn2_6/prodata/1/aaa/PCUS-COMB.pep:*
- 6: /cgn2_6/prodata/1/aaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	219	72.5	54	US-09-358-569D-8	Sequence 8, Appli
2	219	72.5	55	US-09-358-569D-1	Sequence 1, Appli
3	219	72.5	58	US-09-369-494-8	Sequence 8, Appli
4	219	72.5	58	US-09-569-670-8	Sequence 10, Appli
5	219	72.5	64	US-09-358-569D-10	Sequence 75, Appli
6	219	72.5	133	US-09-152-060-75	Sequence 13, Appli
7	170	56.3	43	US-09-358-569D-13	Sequence 113, Appli
8	170	56.3	66	US-08-358-160-113	Patent No. 5466783
9	170	56.3	79	5466783-7	Patent No. 5466783
10	170	56.3	79	5466783-7	Sequence 71, Appli
11	167	55.3	54	US-08-358-160-71	Sequence 9, Appli
12	166	55.0	54	US-09-358-569D-9	Sequence 123, Appli
13	166	55.0	67	US-08-358-160-123	Sequence 8, Appli
14	166	55.0	86	US-09-910-430-8	Sequence 17, Appli
15	161	53.3	58	US-08-358-160-17	Sequence 18, Appli
16	161	53.3	58	US-08-358-160-18	Patent No. 5466783
17	160	53.0	77	5466783-4	Patent No. 5466783
18	160	53.0	77	5466783-4	Sequence 211, Appli
19	157	52.0	61	US-08-829-876-211	Sequence 214, Appli
20	157	52.0	61	US-08-829-876-214	Sequence 211, Appli
21	157	52.0	61	US-09-234-874A-211	Sequence 214, Appli
22	157	52.0	61	US-09-234-874A-214	Sequence 211, Appli
23	157	52.0	61	US-09-234-873A-211	Sequence 214, Appli
24	157	52.0	61	US-09-234-873A-214	Sequence 48, Appli
25	156	51.7	58	US-07-664-989B-48	Sequence 51, Appli
26	156	51.7	58	US-07-664-989B-51	Sequence 1, Appli
27	156	51.7	58	US-08-358-160-1	

28	156	51.7	58	1	US-08-358-160-26	Sequence 26, Appli
29	156	51.7	58	1	US-08-463-155A-56	Sequence 56, Appli
30	156	51.7	58	1	US-08-463-432B-56	Sequence 56, Appli
31	156	51.7	61	2	US-08-829-876-180	Sequence 180, Appli
32	156	51.7	61	2	US-08-829-876-218	Sequence 218, Appli
33	156	51.7	61	3	US-09-234-874A-180	Sequence 180, Appli
34	156	51.7	61	3	US-09-234-874A-218	Sequence 218, Appli
35	156	51.7	61	4	US-09-234-873A-180	Sequence 180, Appli
36	156	51.7	61	4	US-09-234-873A-218	Sequence 218, Appli
37	156	51.7	62	1	US-08-358-160-27	Sequence 27, Appli
38	155	51.3	58	1	US-07-664-989B-49	Sequence 49, Appli
39	155	51.3	58	1	US-08-358-160-9	Sequence 9, Appli
40	155	51.3	58	1	US-08-358-160-10	Sequence 10, Appli
41	155	51.3	58	1	US-08-358-160-11	Sequence 11, Appli
42	155	51.3	58	1	US-08-358-160-13	Sequence 15, Appli
43	155	51.3	58	1	US-08-358-160-16	Sequence 16, Appli
44	155	51.3	58	1	US-08-358-160-24	Sequence 24, Appli
45	155	51.3	61	2	US-08-829-876-129	Sequence 129, Appli
46	155	51.3	61	2	US-08-829-876-139	Sequence 139, Appli
47	155	51.3	61	2	US-08-829-876-208	Sequence 208, Appli
48	155	51.3	61	2	US-08-829-876-217	Sequence 217, Appli
49	155	51.3	61	2	US-08-829-876-222	Sequence 222, Appli
50	155	51.3	61	3	US-09-234-874A-129	Sequence 129, Appli

ALIGNMENTS

RESULT 1
US-09-358-569D-8
; Sequence 8, Application US/09358569D
; Patent No. 6294648
; GENERAL INFORMATION:
; APPLICANT: Delaria, Kathy
; APPLICANT: Rocznia, Steve
; APPLICANT: Davies, Christopher
; TITLE OF INVENTION: Protein Having Proteinase Inhibitor Activity
; FILE REFERENCE: MSB-7259
; CURRENT APPLICATION NUMBER: US/09/358,569D
; CURRENT FILING DATE: 1999-07-20
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 8
; LENGTH: 54
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: derived from
; OTHER INFORMATION: EST sequence database

US-09-358-569D-8
Query Match 72.5%; Score 219; DB 3; Length 54;
Best Local Similarity 68.6%; Pred. No. 3.1e-21;
Matches 35; Conservative 5; Mismatches 11; Indels 0; Gaps 0;

QY 1 CSMPOEAGPCLASIPHHWYNKTKTCSEFIYCGCGNNNNFQTEAICLVTC 51
DB 3 CEMPKEGTCLAYFLHWYDKDNTCSMFVYCGCGNNNNFQSKANCLNTC 53

RESULT 2
US-09-358-569D-1
; Sequence 1, Application US/09358569D
; Patent No. 6294648
; GENERAL INFORMATION:
; APPLICANT: Delaria, Kathy
; APPLICANT: Rocznia, Steve
; APPLICANT: Davies, Christopher
; TITLE OF INVENTION: Protein Having Proteinase Inhibitor Activity
; FILE REFERENCE: MSB-7259
; CURRENT APPLICATION NUMBER: US/09/358,569D
; CURRENT FILING DATE: 1999-07-20
; NUMBER OF SEQ ID NOS: 15

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; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 55
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:derived from
; OTHER INFORMATION: EST sequence database
US-09-358-569D-1

Query Match      72.5%; Score 219; DB 3; Length 55;
Best Local Similarity 68.6%; Pred. No. 3.2e-21;
Matches 35; Conservative 5; Mismatches 11; Indels 0; Gaps 0;

QY 1 CSMPOEAGPCLASIPHHWYNNKTKICSEFIYGGCGGNNNNFQTEAICLVTC 51
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Db 5 CEMPKEGTGCLAYFLHWYDKDNTCSMFVYGGCGGNNNNFQSKANCLNTC 55

RESULT 3
US-09-369-494-8
; Sequence 8, Application US/09369494
; Patent No. 6180607
; GENERAL INFORMATION:
; APPLICANT: Davies, Christopher
; APPLICANT: Chen, Dadong
; APPLICANT: Rocznia, Steve
; TITLE OF INVENTION: Protein Having Proteinase Inhibitor Activity
; FILE REFERENCE: MSB-7260
; CURRENT APPLICATION NUMBER: US/09/369,494
; CURRENT FILING DATE: 1999-08-05
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 8
; LENGTH: 58
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:fragment from
; OTHER INFORMATION: computer database
US-09-369-494-8

Query Match      72.5%; Score 219; DB 3; Length 58;
Best Local Similarity 68.6%; Pred. No. 3.4e-21;
Matches 35; Conservative 5; Mismatches 11; Indels 0; Gaps 0;

QY 1 CSMPOEAGPCLASIPHHWYNNKTKICSEFIYGGCGGNNNNFQTEAICLVTC 51
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Db 5 CEMPKEGTGCLAYFLHWYDKDNTCSMFVYGGCGGNNNNFQSKANCLNTC 55

RESULT 4
US-09-569-670-8
; Sequence 8, Application US/09569670
; Patent No. 6689582
; GENERAL INFORMATION:
; APPLICANT: Davies, Christopher
; APPLICANT: Chen, Dadong
; APPLICANT: Rocznia, Steve
; TITLE OF INVENTION: Protein Having Proteinase Inhibitor Activity
; FILE REFERENCE: MSB-7260
; CURRENT APPLICATION NUMBER: US/09/569,670
; CURRENT FILING DATE: 2000-05-12
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 8
; LENGTH: 58
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:fragment from
; OTHER INFORMATION: computer database
US-09-569-670-8
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Query Match      72.5%; Score 219; DB 4; Length 58;
Best Local Similarity 68.6%; Pred. No. 3.4e-21;
Matches 35; Conservative 5; Mismatches 11; Indels 0; Gaps 0;

QY 1 CSMPOEAGPCLASIPHHWYNNKTKICSEFIYGGCGGNNNNFQTEAICLVTC 51
    |||:||||| |||:||| |||:||||| |||:||||| |||:||||| |||:|||||
Db 5 CEMPKEGTGCLAYFLHWYDKDNTCSMFVYGGCGGNNNNFQSKANCLNTC 55

RESULT 5
US-09-358-569D-10
; Sequence 10, Application US/09358569D
; Patent No. 6294648
; GENERAL INFORMATION:
; APPLICANT: Delaria, Kathy
; APPLICANT: Rocznia, Steve
; APPLICANT: Davies, Christopher
; TITLE OF INVENTION: Protein Having Proteinase Inhibitor Activity
; FILE REFERENCE: MSB-7259
; CURRENT APPLICATION NUMBER: US/09/358,569D
; CURRENT FILING DATE: 1999-07-20
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 10
; LENGTH: 64
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Extension of
; OTHER INFORMATION: Seq Id 1
US-09-358-569D-10

Query Match      72.5%; Score 219; DB 3; Length 64;
Best Local Similarity 68.6%; Pred. No. 3.7e-21;
Matches 35; Conservative 5; Mismatches 11; Indels 0; Gaps 0;

QY 1 CSMPOEAGPCLASIPHHWYNNKTKICSEFIYGGCGGNNNNFQTEAICLVTC 51
    |||:||||| |||:||| |||:||||| |||:||||| |||:||||| |||:|||||
Db 7 CEMPKEGTGCLAYFLHWYDKDNTCSMFVYGGCGGNNNNFQSKANCLNTC 57

RESULT 6
US-09-152-060-75
; Sequence 75, Application US/09152060
; Patent No. 6448230
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 28 Human Secreted Proteins
; FILE REFERENCE: P2003P1.US
; CURRENT APPLICATION NUMBER: US/09/152,060
; CURRENT FILING DATE: 1998-09-11
; EARLIER APPLICATION NUMBER: PCT/US98/04858
; EARLIER FILING DATE: 1998-03-12
; EARLIER APPLICATION NUMBER: 60/040,762
; EARLIER FILING DATE: 1997-03-14
; EARLIER APPLICATION NUMBER: 60/040,710
; EARLIER FILING DATE: 1997-03-14
; EARLIER APPLICATION NUMBER: 60/050,934
; EARLIER FILING DATE: 1997-05-30
; EARLIER APPLICATION NUMBER: 60/048,100
; EARLIER FILING DATE: 1997-05-30
; EARLIER APPLICATION NUMBER: 60/048,357
; EARLIER FILING DATE: 1997-05-30
; EARLIER APPLICATION NUMBER: 60/048,189
; EARLIER FILING DATE: 1997-05-30
; EARLIER APPLICATION NUMBER: 60/057,765
; EARLIER FILING DATE: 1997-09-05
; EARLIER APPLICATION NUMBER: 60/048,970
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/068,368
; EARLIER FILING DATE: 1997-12-19
; NUMBER OF SEQ ID NOS: 118
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; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 75
; LENGTH: 133
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-152-060-75

Query Match      72.5%; Score 219; DB 4; Length 133;
Best Local Similarity 68.6%; Pred. No. 8.2e-21;
Matches 35; Conservative 5; Mismatches 11; Indels 0; Gaps 0;

QY 1 CSMPOAGPCLASIPHWYNNKTKICSEFIYGGCGGNNNNFQTEAICLVTC 51
Db 77 CEMPKEGTCLAYFLHWYDKDNTCSMFYGGCGGNNNNFQSKANCLNTC 127

RESULT 7
US-09-358-569D-13
; Sequence 13, Application US/09358569D
; Patent No. 6294648
; GENERAL INFORMATION:
; APPLICANT: Delaria, Kathy
; APPLICANT: Rocznia, Steve
; APPLICANT: Davies, Christopher
; TITLE OF INVENTION: Protein Having Proteinase Inhibitor Activity
; FILE REFERENCE: MSB-7259
; CURRENT APPLICATION NUMBER: US/09/358,569D
; CURRENT FILING DATE: 1999-07-20
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 13
; LENGTH: 43
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Artificial
; OTHER INFORMATION: sequence derived from EST database
US-09-358-569D-13

Query Match      56.3%; Score 170; DB 3; Length 43;
Best Local Similarity 68.3%; Pred. No. 5.3e-15;
Matches 28; Conservative 4; Mismatches 9; Indels 0; Gaps 0;

QY 11 LASIPHWYNNKTKICSEFIYGGCGGNNNNFQTEAICLVTC 51
Db 1 LAYFLHWYDKDNTCSMFYGGCGGNNNNFQSKANCLNTC 41

RESULT 8
US-08-358-160-113
; Sequence 113, Application US/08358160
; Patent No. 5663143
; GENERAL INFORMATION:
; APPLICANT: LEY, Arthur C.
; APPLICANT: LADNER, Robert C.
; APPLICANT: GUTERMAN, Sonia K.
; APPLICANT: ROBERTS, Bruce L.
; APPLICANT: MARKLAND, William
; APPLICANT: KENT, Rachel B.
; TITLE OF INVENTION: ENGINEERED HUMAN-DERIVED KUNITZ
; TITLE OF INVENTION: DOMAINS THAT INHIBIT HUMAN NEUTROPHIL ELASTASE
; NUMBER OF SEQUENCES: 234
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W. Suite 300
; CITY: Washington
; STATE: District of Columbia
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/358,160
; FILING DATE: 16-DEC-1994
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/133,031
; FILING DATE: 13-OCT-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/009,319
; FILING DATE: 26-JAN-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/664,989
; FILING DATE: 01-MAR-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/487,063
; FILING DATE: 02-MAR-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/240,160
; FILING DATE: 02-SEP-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Cooper, Iver P.
; REGISTRATION NUMBER: 28,005
; REFERENCE/DOCKET NUMBER: LEY-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; TELEX: 248633
; INFORMATION FOR SEQ ID NO: 113:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 66 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-358-160-113

Query Match      56.3%; Score 170; DB 1; Length 66;
Best Local Similarity 51.0%; Pred. No. 8.4e-15;
Matches 26; Conservative 10; Mismatches 15; Indels 0; Gaps 0;

QY 1 CSMPOAGPCLASIPHWYNNKTKICSEFIYGGCGGNNNNFQTEAICLVTC 51
Db 8 CRLPPEQGPKGRIPRYFYNPASRMCSFIYGGCKGNKNNFKTKAECVRAC 58

RESULT 9
5466783-7
; Patent No. 5466783
; APPLICANT: Wun, Tze-Chen, Kretzmer, Kuniko K.; Broze,
; George J. Jr.
; TITLE OF INVENTION: HUMAN TISSUE FACTOR INHIBITOR
; NUMBER OF SEQUENCES: 26
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/93,285
; FILING DATE: 15-JUL-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 566,280
; FILING DATE: 13-AUG-1990
; APPLICATION NUMBER: 123,753
; FILING DATE: 23-NOV-1987
; APPLICATION NUMBER: 77,366
; FILING DATE: 23-JUL-1987
; SEQ ID NO: 7
; LENGTH: 79
5466783-7

Query Match      56.3%; Score 170; DB 6; Length 79;
Best Local Similarity 51.0%; Pred. No. 1e-14;
Matches 26; Conservative 10; Mismatches 15; Indels 0; Gaps 0;

QY 1 CSMPOAGPCLASIPHWYNNKTKICSEFIYGGCGGNNNNFQTEAICLVTC 51
```


APPLICANT: KENT, Rachel B.
TITLE OF INVENTION: ENGINEERED HUMAN-DERIVED KUNITZ
TITLE OF INVENTION: DOMAINS THAT INHIBIT HUMAN NEUTROPHIL ELASTASE
NUMBER OF SEQUENCES: 234
CORRESPONDENCE ADDRESS:
ADDRESSES: BROWDY AND NEIMARK
STREET: 419 Seventh Street, N.W. Suite 300
CITY: Washington
STATE: District of Columbia
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/358,160
FILING DATE: 16-DEC-1994
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/133,031
FILING DATE: 13-OCT-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/009,319
FILING DATE: 26-JAN-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/664,989
FILING DATE: 01-MAR-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/487,063
FILING DATE: 02-MAR-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/240,160
FILING DATE: 02-SEP-1988
ATTORNEY/AGENT INFORMATION:
NAME: Cooper, Iver P.
REGISTRATION NUMBER: 28,005
REFERENCE/DOCKET NUMBER: LEY=1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
TELEX: 248633
INFORMATION FOR SEQ ID NO: 123:
SEQUENCE CHARACTERISTICS:
LENGTH: 67 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-358-160-123
Query Match 55.0%; Score 166; DB 1; Length 67;
Best Local Similarity 51.0%; Pred. No. 2.8e-14;
Matches 26; Conservative 8; Mismatches 17; Indels 0; Gaps 0;
QY 1 CSMPOEAGPCLASIPHHWYNNKTKICSEFYGGCGGNNNFQTEAICLVTC 51
DB 8 COLPQARGPKAALLRYFNSTSNACEPFTYGGCGGNNNFETEMCLRIC 58
RESULT 14
US-09-910-430-8
Sequence 8, Application US/09910430
Patent No. 6794166
GENERAL INFORMATION:
APPLICANT: Godfroi, Edmond
APPLICANT: Bollen, Alex
APPLICANT: Lebouille, Gerard
TITLE OF INVENTION: IDENTIFICATION AND MOLECULAR CHARACTERIZATION OF
TITLE OF INVENTION: PROTEINS, EXPRESSED IN THE IXODES RICINUS SALIVARY
TITLE OF INVENTION: GLANDS
FILE REFERENCE: VANM229.001CP1

CURRENT APPLICATION NUMBER: US/09/910,430
CURRENT FILING DATE: 2001-07-19
PRIOR APPLICATION NUMBER: PCT/BE00/00061
PRIOR FILING DATE: 2000-06-06
PRIOR APPLICATION NUMBER: GB 913425.6
PRIOR FILING DATE: 1999-06-09
NUMBER OF SEQ ID NOS: 34
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 8
LENGTH: 86
TYPE: PRT
ORGANISM: Ixodes ricinus
US-09-910-430-8
Query Match 55.0%; Score 166; DB 4; Length 86;
Best Local Similarity 49.0%; Pred. No. 3.7e-14;
Matches 25; Conservative 10; Mismatches 16; Indels 0; Gaps 0;
QY 1 CSMPOEAGPCLASIPHHWYNNKTKICSEFYGGCGGNNNFQTEAICLVTC 51
DB 31 CKLPDPDGPFCRARIPIYSYFDRKTKCKEPMYGGCEGNNNFENITTCQEEC 81
RESULT 15
US-08-358-160-17
Sequence 17, Application US/08358160
Patent No. 5663143
GENERAL INFORMATION:
APPLICANT: LEY, Arthur C.
APPLICANT: LADNER, Robert C.
APPLICANT: GUTERMAN, Sonia K.
APPLICANT: ROBERTS, Bruce L.
APPLICANT: MARKLAND, William
APPLICANT: KENT, Rachel B.
TITLE OF INVENTION: ENGINEERED HUMAN-DERIVED KUNITZ
TITLE OF INVENTION: DOMAINS THAT INHIBIT HUMAN NEUTROPHIL ELASTASE
NUMBER OF SEQUENCES: 234
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEIMARK
STREET: 419 Seventh Street, N.W. Suite 300
CITY: Washington
STATE: District of Columbia
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/358,160
FILING DATE: 16-DEC-1994
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/133,031
FILING DATE: 13-OCT-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/009,319
FILING DATE: 26-JAN-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/664,989
FILING DATE: 01-MAR-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/487,063
FILING DATE: 02-MAR-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/240,160
FILING DATE: 02-SEP-1988
ATTORNEY/AGENT INFORMATION:
NAME: Cooper, Iver P.
REGISTRATION NUMBER: 28,005
REFERENCE/DOCKET NUMBER: LEY=1
TELECOMMUNICATION INFORMATION:

```
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; TELEX: 248633
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 58 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-358-160-17

Query Match 53.3%; Score 161; DB 1; Length 58;
Best Local Similarity 51.0%; Pred. No. 1.1e-13;
Matches 26; Conservative 6; Mismatches 19; Indels 0; Gaps 0;

Qy 1 CSMQAEAGPCLASIPHHWYNNKTKICSEFIYGGCGGNNNNFQTEAICLVTC 51
Db 5 COLGYSAGPCVAMPFRIFYNGTSMACETFYVGGCGNGNMFVTEKDCLOTC 55

RESULT 16
US-08-358-160-18
; Patent No. 5663143
; Application US/08358160
; GENERAL INFORMATION:
; APPLICANT: LEY, Arthur C.
; APPLICANT: LADNER, Robert C.
; APPLICANT: GUTERMAN, Sonia K.
; APPLICANT: ROBERTS, Bruce L.
; APPLICANT: MARKLAND, William
; APPLICANT: KENT, Rachel B.
; TITLE OF INVENTION: ENGINEERED HUMAN-DERIVED KUNITZ
; TITLE OF INVENTION: DOMAINS THAT INHIBIT HUMAN NEUTROPHIL ELASTASE
; NUMBER OF SEQUENCES: 234
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W. Suite 300
; CITY: Washington
; STATE: District of Columbia
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/358,160
; FILING DATE: 16-DEC-1994
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/133,031
; FILING DATE: 13-OCT-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/009,319
; FILING DATE: 26-JAN-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/664,989
; FILING DATE: 01-MAR-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/487,063
; FILING DATE: 02-MAR-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/240,160
; FILING DATE: 02-SEP-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Cooper, Iver P.
; REGISTRATION NUMBER: 28,005
; REFERENCE/DOCKET NUMBER: LEY=1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
```

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; TELEX: 248633
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 58 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-358-160-18

Query Match 53.3%; Score 161; DB 1; Length 58;
Best Local Similarity 51.0%; Pred. No. 1.1e-13;
Matches 26; Conservative 6; Mismatches 19; Indels 0; Gaps 0;

Qy 1 CSMQAEAGPCLASIPHHWYNNKTKICSEFIYGGCGGNNNNFQTEAICLVTC 51
Db 5 COLGYSAGPCVAMPFRIFYNGTSMACQTFVYGGCGNGNMFVTEKDCLOTC 55

RESULT 17
5466783-4
; Patent No. 5466783
; APPLICANT: Wun, Tze-Chain.;Kretzmer, Kuniko K.;Broze,
;George J. Jr.
; TITLE OF INVENTION: HUMAN TISSUE FACTOR INHIBITOR
; NUMBER OF SEQUENCES: 26
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/93,285
; FILING DATE: 15-JUL-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 566,280
; FILING DATE: 13-AUG-1990
; APPLICATION NUMBER: 123,753
; FILING DATE: 23-NOV-1987
; APPLICATION NUMBER: 77,366
; FILING DATE: 23-JUL-1987
; SEQ ID NO:4:
; LENGTH: 77
5466783-4

Query Match 53.0%; Score 160; DB 6; Length 77;
Best Local Similarity 47.1%; Pred. No. 1.9e-13;
Matches 24; Conservative 10; Mismatches 17; Indels 0; Gaps 0;

Qy 1 CSMQAEAGPCLASIPHHWYNNKTKICSEFIYGGCGGNNNNFQTEAICLVTC 51
Db 8 COLPQARGPCKALLRYFBSTSNACEPFTYGGCGGNNBNFETTEMCLRIC 58

RESULT 18
5466783-4
; Patent No. 5466783
; APPLICANT: Wun, Tze-Chain.;Kretzmer, Kuniko K.;Broze,
;George J. Jr.
; TITLE OF INVENTION: HUMAN TISSUE FACTOR INHIBITOR
; NUMBER OF SEQUENCES: 26
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/93,285
; FILING DATE: 15-JUL-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 566,280
; FILING DATE: 13-AUG-1990
; APPLICATION NUMBER: 123,753
; FILING DATE: 23-NOV-1987
; APPLICATION NUMBER: 77,366
; FILING DATE: 23-JUL-1987
; SEQ ID NO:4:
; LENGTH: 77
5466783-4

Query Match 53.0%; Score 160; DB 6; Length 77;
Best Local Similarity 47.1%; Pred. No. 1.9e-13;
Matches 24; Conservative 10; Mismatches 17; Indels 0; Gaps 0;
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;
; FILING DATE: 11-Jun-2001
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/436,555
; FILING DATE: 08-MAY-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Bent, Stephen
; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 056324/0106
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 211:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 61 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 211:
US-09-234-874A-211

Query Match 52.0%; Score 157; DB 3; Length 61;
Best Local Similarity 49.0%; Pred. No. 3.7e-13;
Matches 25; Conservative 6; Mismatches 20; Indels 0; Gaps 0;

QY 1 CSMPOEAGPCIASIPHHWYKTKICSEFIYGGCGGNNNFQTEAICLVTC 51
||| | | | | | | | | | | | | | | | | | | | | | | | | |
Db 7 CSEQAETGPCRAAIQHWFYDVTGKCAPFFYGGCGGNNNFDTTEYCMVAVC 57

RESULT 22
US-09-234-874A-214
; Sequence 214, Application US/09234874A
; Patent No. 6376648
; GENERAL INFORMATION:
; APPLICANT: White, Tyler R.
; Damm, Deborah
; Lesikar, David D.
; McFadden, Kathleen
; Garrick, Brett L.
; TITLE OF INVENTION: PROTEASE INHIBITOR PEPTIDES
; NUMBER OF SEQUENCES: 228
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/234,873A
; FILING DATE: 21-Jan-1999
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/829,876
; FILING DATE: 02-APR-1997
; APPLICATION NUMBER: 08/436,555
; FILING DATE: 08-MAY-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Bent, Stephen
; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 056324/0116
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 211:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 61 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; INFORMATION FOR SEQ ID NO: 211:
US-09-234-873A-211

Query Match 52.0%; Score 157; DB 4; Length 61;
Best Local Similarity 49.0%; Pred. No. 3.7e-13;
Matches 25; Conservative 6; Mismatches 20; Indels 0; Gaps 0;

QY 1 CSMPOEAGPCIASIPHHWYKTKICSEFIYGGCGGNNNFQTEAICLVTC 51
||| | | | | | | | | | | | | | | | | | | | | | | | | |
Db 7 CSEQAETGPCRAAIQHWFYDVTGKCAPFFYGGCGGNNNFDTTEYCMVAVC 57

;
; FILING DATE: 11-Jun-2001
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/436,555
; FILING DATE: 08-MAY-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Bent, Stephen
; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 056324/0106
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 211:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 61 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 211:
US-09-234-874A-211

Query Match 52.0%; Score 157; DB 3; Length 61;
Best Local Similarity 49.0%; Pred. No. 3.7e-13;
Matches 25; Conservative 6; Mismatches 20; Indels 0; Gaps 0;

QY 1 CSMPOEAGPCIASIPHHWYKTKICSEFIYGGCGGNNNFQTEAICLVTC 51
||| | | | | | | | | | | | | | | | | | | | | | | | | |
Db 7 CSEQAETGPCRAAIQHWFYDVTGKCAPFFYGGCGGNNNFDTTEYCMVAVC 57

RESULT 22
US-09-234-874A-214
; Sequence 214, Application US/09234874A
; Patent No. 6376648
; GENERAL INFORMATION:
; APPLICANT: White, Tyler R.
; Damm, Deborah
; Lesikar, David D.
; McFadden, Kathleen
; Garrick, Brett L.
; TITLE OF INVENTION: PROTEASE INHIBITOR PEPTIDES
; NUMBER OF SEQUENCES: 228
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/234,874A
; FILING DATE: 11-Jun-2001
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/436,555
; FILING DATE: 08-MAY-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Bent, Stephen
; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 056324/0106
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 214:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 61 amino acids
; TYPE: amino acid
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RESULT 24
US-09-234-873A-214
; Sequence 214, Application US/09234873A
; Patent No. 6613890
; GENERAL INFORMATION:
; APPLICANT: White, Tyler R.
;      Damn, Deborah
;      Lesikar, David D.
;      McFadden, Kathleen
;      Garrick, Brett L.
; TITLE OF INVENTION: PROTEASE INHIBITOR PEPTIDES
; NUMBER OF SEQUENCES: 228
; CORRESPONDENCE ADDRESS:
;      ADDRESSEE: Foley & Lardner
;      STREET: 3000 K Street, N.W., Suite 500
;      CITY: Washington
;      STATE: D.C.
;      COUNTRY: USA
;      ZIP: 20007-5109
; COMPUTER READABLE FORM:
;      MEDIUM TYPE: Floppy disk
;      COMPUTER: IBM PC compatible
;      OPERATING SYSTEM: PC-DOS/MS-DOS
;      SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
;      APPLICATION NUMBER: US/09/234,873A
;      FILING DATE: 21-Jan-1999
; PRIOR APPLICATION DATA:
;      APPLICATION NUMBER: 08/829,876
;      FILING DATE: 02-APR-1997
;      APPLICATION NUMBER: 08/436,555
;      FILING DATE: 08-MAY-1995
; ATTORNEY/AGENT INFORMATION:
;      NAME: Bent, Stephen
;      REGISTRATION NUMBER: 29,768
;      REFERENCE/DOCKET NUMBER: 056324/0116
; TELECOMMUNICATION INFORMATION:
;      TELEPHONE: (202)672-5300
;      TELEFAX: (202)672-5399
;      TELEX: 904136
; INFORMATION FOR SEQ ID NO: 214:
;      SEQUENCE CHARACTERISTICS:
;          LENGTH: 61 amino acids
;          TYPE: amino acid
;          STRANDEDNESS: single
;          TOPOLOGY: linear
;      MOLECULE TYPE: protein
;      SEQUENCE DESCRIPTION: SEQ ID NO: 214:
US-09-234-873A-214

Query Match      52.0%; Score 157; DB 4; Length 61;
Best Local Similarity 49.0%; Pred.No.3.7e-13;
Matches 25; Conservative 6; Mismatches 20; Indels 0; Gaps 0;

Qy      1  CSMPEAGPCLASIPHWYNNKTKICSEFTYGGCGGNNNPQTEAICLVTC 51
      |||||
Db      7  CSEQAEFGPCRALIPRYFDVTEKGCAFFYGGCGRNNPDTIEYCMAVC 57
      |||||

RESULT 25
US-07-664-989B-48
; Sequence 48, Application US/07664989B
; Patent No. 5223409
; GENERAL INFORMATION:
; APPLICANT: Ladner, Robert Charles
; APPLICANT: Guterman, Sonia Kosow
; APPLICANT: Roberts, Bruce Lindsey
; APPLICANT: Markland, William
; APPLICANT: Ley, Arthur Charles
; APPLICANT: Kent, Rachel Barbault
; TITLE OF INVENTION: Directed Evolution of No. 5223409el
; TITLE OF INVENTION: Binding Proteins

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; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WORDPERFECT 4.2
; CURRENT APPLICATION DATA: US/07/664,989B
; APPLICATION NUMBER: US/07/664,989B
; FILING DATE: 19910301
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA: PCT/US89/03731
; APPLICATION NUMBER: PCT/US89/03731
; FILING DATE: 01-SEP-1989
; PRIOR APPLICATION DATA: 07/487,063
; APPLICATION NUMBER: 07/487,063
; FILING DATE: 02-MAR-1990
; PRIOR APPLICATION DATA: 07/240,160
; APPLICATION NUMBER: 07/240,160
; FILING DATE: 02-SEP-1988
; ATTORNEY/AGENT INFORMATION: NAME: Cooper, Iver P.
; REGISTRATION NUMBER: 28005
; REFERENCE/DOCKET NUMBER: LADNER 7
; TELECOMMUNICATION INFORMATION: TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; INFORMATION FOR SEQ ID NO: 51:
; SEQUENCE CHARACTERISTICS: LENGTH: 58 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-07-664-989B-51
Query Match 51.7%; Score 156; DB 1; Length 58;
Best Local Similarity 47.1%; Pred. No. 4.7e-13;
Matches 24; Conservative 8; Mismatches 19; Indels 0; Gaps 0;

QY 1 CSMPEAGPCLASIPHWYNKTKICSEFYGGCGGNNNNFQTEAICLVTC 51
DB 5 CLEPPYTGCIAFFPRFYNAKAGLCQTFFVYGCMGNGNFKSABDCMRTC 55

RESULT 27
US-08-358-160-1
; Sequence 1, Application US/08358160
; Patent No. 5663143
; GENERAL INFORMATION:
; APPLICANT: LEY, Arthur C.
; APPLICANT: LADNER, Robert C.
; APPLICANT: GUTERMAN, Sonia K.
; APPLICANT: ROBERTS, Bruce L.
; APPLICANT: MARKLAND, William
; APPLICANT: KENT, Rachel B.
; TITLE OF INVENTION: ENGINEERED HUMAN-DERIVED KUNITZ
; NUMBER OF SEQUENCES: 234
; CORRESPONDENCE ADDRESS: ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W. Suite 300
; CITY: Washington
; STATE: District of Columbia
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/358,160
; FILING DATE: 16-DEC-1994
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA: APPLICATION NUMBER: US 08/133,031
; FILING DATE: 13-OCT-1993

;
; APPLICATION NUMBER: US 08/133,031
; FILING DATE: 13-OCT-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/009,319
; FILING DATE: 26-JAN-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/664,989
; FILING DATE: 01-MAR-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/487,063
; FILING DATE: 02-MAR-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/240,160
; FILING DATE: 02-SEP-1988
; ATTORNEY/AGENT INFORMATION: NAME: Cooper, Iver P.
; REGISTRATION NUMBER: 28,005
; REFERENCE/DOCKET NUMBER: LEY=1
; TELECOMMUNICATION INFORMATION: TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; TELEX: 248633
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS: LENGTH: 58 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-358-160-1
Query Match 51.7%; Score 156; DB 1; Length 58;
Best Local Similarity 47.1%; Pred. No. 4.7e-13;
Matches 24; Conservative 8; Mismatches 19; Indels 0; Gaps 0;

QY 1 CSMPEAGPCLASIPHWYNKTKICSEFYGGCGGNNNNFQTEAICLVTC 51
DB 5 CLEPPYTGCIVAMFPFRFYNAKAGLCQTFFVYGCMGNGNFKSABDCMRTC 55

RESULT 28
US-08-358-160-26
; Sequence 26, Application US/08358160
; Patent No. 5663143
; GENERAL INFORMATION:
; APPLICANT: LEY, Arthur C.
; APPLICANT: LADNER, Robert C.
; APPLICANT: GUTERMAN, Sonia K.
; APPLICANT: ROBERTS, Bruce L.
; APPLICANT: MARKLAND, William
; APPLICANT: KENT, Rachel B.
; TITLE OF INVENTION: ENGINEERED HUMAN-DERIVED KUNITZ
; NUMBER OF SEQUENCES: 234
; CORRESPONDENCE ADDRESS: ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W. Suite 300
; CITY: Washington
; STATE: District of Columbia
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/358,160
; FILING DATE: 16-DEC-1994
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA: APPLICATION NUMBER: US 08/133,031
; FILING DATE: 13-OCT-1993

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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/009,319
FILING DATE: 26-JAN-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/664,989
FILING DATE: 01-MAR-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/487,063
FILING DATE: 02-MAR-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/240,160
FILING DATE: 02-SEP-1988
ATTORNEY/AGENT INFORMATION:
NAME: Cooper, Iver P.
REGISTRATION NUMBER: 28,005
REFERENCE/DOCKET NUMBER: LEV=1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
TELEX: 248633
INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
LENGTH: 58 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-358-160-26

Query Match 51.7%; Score 156; DB 1; Length 58;
Best Local Similarity 47.1%; Pred. No. 4.7e-13;
Matches 24; Conservative 8; Mismatches 19; Indels 0; Gaps 0;

QY 1 CSMPEAGPCLASIPHWYNNKTKICSEFIYGGCGGNNNNFQTEAICLVTC 51
DB 5 CLEPPYTGPCIAFPFYFNKAGLCQTFYVGGCMGNNFKSAEDCMRTC 55

RESULT 29
US-08-463-155A-56
Sequence 56, Application US/08463155A
Patent No. 5780265
GENERAL INFORMATION:
APPLICANT: Dennis, Mark S.
APPLICANT: Lazarus, Robert A.
TITLE OF INVENTION: KUNITZ TYPE PLASMA KALLIKREIN INHIBITORS
NUMBER OF SEQUENCES: 72
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/463,155A
FILING DATE: 05-Jun-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Kubinec, Jeffrey S.
REGISTRATION NUMBER: 36,575
REFERENCE/DOCKET NUMBER: P0944
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-8228
TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 56:
SEQUENCE CHARACTERISTICS:

LENGTH: 58 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
US-08-463-155A-56

Query Match 51.7%; Score 156; DB 1; Length 58;
Best Local Similarity 51.0%; Pred. No. 4.7e-13;
Matches 26; Conservative 5; Mismatches 20; Indels 0; Gaps 0;

QY 1 CSMPEAGPCLASIPHWYNNKTKICSEFIYGGCGGNNNNFQTEAICLVTC 51
DB 5 CSEQAEDGPCRAAIPRWYFDVTGKCAPFIYGGCGGNNRNNFDTTEYCAAVC 55

RESULT 30
US-08-463-432B-56
Sequence 56, Application US/08463432B
Patent No. 5786328
GENERAL INFORMATION:
APPLICANT: Dennis, Mark S.
APPLICANT: Lazarus, Robert A.
TITLE OF INVENTION: KUNITZ TYPE PLASMA KALLIKREIN INHIBITORS
NUMBER OF SEQUENCES: 72
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/463,432B
FILING DATE: 05-Jun-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Kubinec, Jeffrey S.
REGISTRATION NUMBER: 36,575
REFERENCE/DOCKET NUMBER: P0944-2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-8228
TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 56:
SEQUENCE CHARACTERISTICS:
LENGTH: 58 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
US-08-463-432B-56

Query Match 51.7%; Score 156; DB 1; Length 58;
Best Local Similarity 51.0%; Pred. No. 4.7e-13;
Matches 26; Conservative 5; Mismatches 20; Indels 0; Gaps 0;

QY 1 CSMPEAGPCLASIPHWYNNKTKICSEFIYGGCGGNNNNFQTEAICLVTC 51
DB 5 CSEQAEDGPCRAAIPRWYFDVTGKCAPFIYGGCGGNNRNNFDTTEYCAAVC 55

RESULT 31
US-08-829-876-180
Sequence 180, Application US/08829876
Patent No. 5962266
GENERAL INFORMATION:
APPLICANT: White, Tyler R.
APPLICANT: Damm, Deborah
APPLICANT: Lesikar, David D.
APPLICANT: McFadden, Kathleen
APPLICANT: Garrick, Brett L.

```

; TITLE OF INVENTION: PROTEASE INHIBITOR PEPTIDES
; NUMBER OF SEQUENCES: 228
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/829,876
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/436,555
; FILING DATE: 08-MAY-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Pelto, Don J.
; REGISTRATION NUMBER: 33,754
; REFERENCE/DOCKET NUMBER: 56324/106/SCNO
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 180:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 61 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-829-876-180

Query Match 51.7%; Score 156; DB 2; Length 61;
Best Local Similarity 49.0%; Pred. No. 5e-13;
Matches 25; Conservative 5; Mismatches 21; Indels 0; Gaps 0;

Qy 1 CSMPOEAGPCLASIPHWYNNKTKICSEFIYGGCGNNNNFQTEAICLVTC 51
Db 7 CSEAETGCRAGIPRWYFDVTEGKCAPFFYGGCGNNRNFDTTEYCMAVC 57

RESULT 32
US-08-829-876-218
; Sequence 218, Application US/08829876
; Patent No. 5962286
; GENERAL INFORMATION:
; APPLICANT: White, Tyler R.
; APPLICANT: Damm, Deborah
; APPLICANT: Lesikar, David D.
; APPLICANT: McFadden, Kathleen
; APPLICANT: Garrick, Brett L.
; APPLICANT: McFadden, Kathleen
; TITLE OF INVENTION: PROTEASE INHIBITOR PEPTIDES
; NUMBER OF SEQUENCES: 228
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/829,876
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/436,555
; FILING DATE: 08-MAY-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Bent, Stephen
; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 056324/0106
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 180:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 61 amino acids
; TYPE: amino acid
; US-08-829-876-218
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; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/436,555
; FILING DATE: 08-MAY-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Pelto, Don J.
; REGISTRATION NUMBER: 33,754
; REFERENCE/DOCKET NUMBER: 56324/106/SCNO
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 218:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 61 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-829-876-218

Query Match 51.7%; Score 156; DB 2; Length 61;
Best Local Similarity 49.0%; Pred. No. 5e-13;
Matches 25; Conservative 7; Mismatches 19; Indels 0; Gaps 0;

Qy 1 CSMPOEAGPCLASIPHWYNNKTKICSEFIYGGCGNNNNFQTEAICLVTC 51
Db 7 CSEAESGPCRAIYHWYFDVTEGKCAPFFYGGCGNNRNFDTTEYCMAVC 57

RESULT 33
US-09-234-874A-180
; Sequence 180, Application US/09234874A
; Patent No. 6376648
; GENERAL INFORMATION:
; APPLICANT: White, Tyler R.
; APPLICANT: Damm, Deborah
; APPLICANT: Lesikar, David D.
; APPLICANT: McFadden, Kathleen
; APPLICANT: Garrick, Brett L.
; TITLE OF INVENTION: PROTEASE INHIBITOR PEPTIDES
; NUMBER OF SEQUENCES: 228
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/234,874A
; FILING DATE: 11-Jun-2001
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/436,555
; FILING DATE: 08-MAY-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Bent, Stephen
; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 056324/0106
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 180:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 61 amino acids
; TYPE: amino acid
; US-09-234-874A-180
```

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; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 180:
US-09-234-874A-180
Query Match 51.7%; Score 156; DB 3; Length 61;
Best Local Similarity 49.0%; Pred. No. 5e-13;
Matches 25; Conservative 5; Mismatches 21; Indels 0; Gaps 0;

QY 1 CSMPOEAGPCLASIPHHWYNNKTKICSEFIYGGCGNNNNFOTEALCLVTC 51
Db 7 CSEQAETGCRAGIPRWYFDVTEGKCAPFFYGGCGNNRNNFDTTEYCMVAVC 57

RESULT 34
US-09-234-874A-218
; Sequence 218, Application US/09234874A
; Patent No. 6376648
; GENERAL INFORMATION:
; APPLICANT: White, Tyler R.
; Damm, Deborah
; Lesikar, David D.
; McFadden, Kathleen
; Garrick, Brett L.
; TITLE OF INVENTION: PROTEASE INHIBITOR PEPTIDES
; NUMBER OF SEQUENCES: 228
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/234,874A
; FILING DATE: 11-Jun-2001
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: 08/436,555
; FILING DATE: 08-MAY-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Bent, Stephen
; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 056324/0106
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 218:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 61 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 218:
US-09-234-874A-218
Query Match 51.7%; Score 156; DB 3; Length 61;
Best Local Similarity 49.0%; Pred. No. 5e-13;
Matches 25; Conservative 7; Mismatches 19; Indels 0; Gaps 0;

QY 1 CSMPOEAGPCLASIPHHWYNNKTKICSEFIYGGCGNNNNFOTEALCLVTC 51
Db 7 CSEQAESGPCRAAIYHWYFDVTEGKCAPFFYGGCGNNRNNFDTTEYCMVAVC 57

RESULT 35
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US-09-234-873A-180
; Sequence 180, Application US/09234873A
; Patent No. 6613890
; GENERAL INFORMATION:
; APPLICANT: White, Tyler R.
; Damm, Deborah
; Lesikar, David D.
; McFadden, Kathleen
; Garrick, Brett L.
; TITLE OF INVENTION: PROTEASE INHIBITOR PEPTIDES
; NUMBER OF SEQUENCES: 228
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/234,873A
; FILING DATE: 21-Jan-1999
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: 08/829,876
; FILING DATE: 02-APR-1997
; APPLICATION NUMBER: 08/436,555
; FILING DATE: 08-MAY-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Bent, Stephen
; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 056324/0116
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 180:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 61 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 180:
US-09-234-873A-180
Query Match 51.7%; Score 156; DB 4; Length 61;
Best Local Similarity 49.0%; Pred. No. 5e-13;
Matches 25; Conservative 5; Mismatches 21; Indels 0; Gaps 0;

QY 1 CSMPOEAGPCLASIPHHWYNNKTKICSEFIYGGCGNNNNFOTEALCLVTC 51
Db 7 CSEQAETGCRAGIPRWYFDVTEGKCAPFFYGGCGNNRNNFDTTEYCMVAVC 57

RESULT 36
US-09-234-873A-218
; Sequence 218, Application US/09234873A
; Patent No. 6613890
; GENERAL INFORMATION:
; APPLICANT: White, Tyler R.
; Damm, Deborah
; Lesikar, David D.
; McFadden, Kathleen
; Garrick, Brett L.
; TITLE OF INVENTION: PROTEASE INHIBITOR PEPTIDES
; NUMBER OF SEQUENCES: 228
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
```


PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US89/03731
FILING DATE: 01-SEP-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/487,063
FILING DATE: 02-MAR-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/240,160
FILING DATE: 02-SEP-1988
ATTORNEY/AGENT INFORMATION:
NAME: Cooper, Iver P.
REGISTRATION NUMBER: 28005
REFERENCE/DOCKET NUMBER: LADNER 7
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
INFORMATION FOR SEQ ID NO: 49:
SEQUENCE CHARACTERISTICS:
LENGTH: 58 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear
MOLECULE TYPE: protein
US-07-664-989B-49

Query Match 51.3%; Score 155; DB 1; Length 58;
Best Local Similarity 47.1%; Pred. No. 6.4e-13;
Matches 24; Conservative 8; Mismatches 19; Indels 0; Gaps 0;

QY 1 CSMQAGAGCLASIPHHWYKTKICSEFIYGGCGGNNNNFQTEAICLVTC 51
DB 5 CLEPPYTGPCVAIFPRFYNAKGLCQTFYGGCGMGNGNFKSABDCMRTC 55

RESULT 39
US-08-358-160-9
Sequence 9, Application US/08358160
Patent No. 5663143

GENERAL INFORMATION:
APPLICANT: LEY, Arthur C.
APPLICANT: LADNER, Robert C.
APPLICANT: GUTERMAN, Sonia K.
APPLICANT: ROBERTS, Bruce L.
APPLICANT: MARKLAND, William
APPLICANT: KENT, Rachel B.
TITLE OF INVENTION: ENGINEERED HUMAN-DERIVED KUNITZ
NUMBER OF SEQUENCES: 234
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEIMARK
STREET: 419 Seventh Street, N.W. Suite 300
CITY: Washington
STATE: District of Columbia
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/358,160
FILING DATE: 16-DEC-1994
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/133,031
FILING DATE: 13-OCT-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/009,319
FILING DATE: 26-JAN-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/664,989
FILING DATE: 01-MAR-1991
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/487,063
FILING DATE: 02-MAR-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/240,160
FILING DATE: 02-SEP-1988
ATTORNEY/AGENT INFORMATION:
NAME: Cooper, Iver P.
REGISTRATION NUMBER: 28,005
REFERENCE/DOCKET NUMBER: LEY=1
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
TELEX: 248633

INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 58 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-358-160-9

Query Match 51.3%; Score 155; DB 1; Length 58;
Best Local Similarity 51.0%; Pred. No. 6.4e-13;
Matches 26; Conservative 5; Mismatches 20; Indels 0; Gaps 0;

QY 1 CSMQAGAGCLASIPHHWYKTKICSEFIYGGCGGNNNNFQTEAICLVTC 51
DB 5 CQLGYSAGPCVAMPFRFYNGTSMACETFOYGGCMGNGNFTVKDCLQTC 55

RESULT 40

US-08-358-160-10
Sequence 10, Application US/08358160
Patent No. 5663143

GENERAL INFORMATION:
APPLICANT: LEY, Arthur C.
APPLICANT: LADNER, Robert C.
APPLICANT: GUTERMAN, Sonia K.
APPLICANT: ROBERTS, Bruce L.
APPLICANT: MARKLAND, William
APPLICANT: KENT, Rachel B.
TITLE OF INVENTION: ENGINEERED HUMAN-DERIVED KUNITZ
NUMBER OF SEQUENCES: 234
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEIMARK
STREET: 419 Seventh Street, N.W. Suite 300
CITY: Washington
STATE: District of Columbia
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/358,160
FILING DATE: 16-DEC-1994
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/133,031
FILING DATE: 13-OCT-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/009,319
FILING DATE: 26-JAN-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/664,989
FILING DATE: 01-MAR-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/487,063
FILING DATE: 02-MAR-1990

```
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/240,160
; FILING DATE: 02-SEP-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Cooper, Iver P.
; REGISTRATION NUMBER: 28,005
; REFERENCE/DOCKET NUMBER: LEY=1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; TELEX: 248633
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 58 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-358-160-11

Query Match 51.3%; Score 155; DB 1; Length 58;
Best Local Similarity 51.0%; Pred. No. 6.4e-13;
Matches 26; Conservative 5; Mismatches 20; Indels 0; Gaps 0;

Qy 1 CSMQEGAPCLASIPHHWYKTKICSEFYGGCGNNNNFQTEAICLVTC 51
   : ||||| : ||| : ||||| : ||||| : ||||| : ||||| : |||||
Db 5 COLGYSAGPCVAMPFRFYNGTSMACETFQYGGCMGNGNMFVTEKDCIQTC 55

RESULT 41
US-08-358-160-11
; Sequence 11, Application US/08358160
; Patent No. 5663143
; GENERAL INFORMATION:
; APPLICANT: LEY, Arthur C.
; APPLICANT: LADNER, Robert C.
; APPLICANT: GUTERMAN, Sonia K.
; APPLICANT: ROBERTS, Bruce L.
; APPLICANT: MARKLAND, William
; APPLICANT: KENT, Rachel B.
; TITLE OF INVENTION: ENGINEERED HUMAN-DERIVED KUNITZ
; NUMBER OF SEQUENCES: 234
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W. Suite 300
; CITY: Washington
; STATE: District of Columbia
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/358,160
; FILING DATE: 16-DEC-1994
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/133,031
; FILING DATE: 13-OCT-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/009,319
; FILING DATE: 26-JAN-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/664,989
; FILING DATE: 01-MAR-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/487,063
; FILING DATE: 02-MAR-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/240,160
; FILING DATE: 02-SEP-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Cooper, Iver P.
; REGISTRATION NUMBER: 28,005
; REFERENCE/DOCKET NUMBER: LEY=1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; TELEX: 248633
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 58 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-358-160-11

Query Match 51.3%; Score 155; DB 1; Length 58;
Best Local Similarity 51.0%; Pred. No. 6.4e-13;
Matches 26; Conservative 5; Mismatches 20; Indels 0; Gaps 0;

Qy 1 CSMQEGAPCLASIPHHWYKTKICSEFYGGCGNNNNFQTEAICLVTC 51
   : ||||| : ||| : ||||| : ||||| : ||||| : ||||| : |||||
Db 5 COLGYSAGPCVAMPFRFYNGTSMACETFQYGGCMGNGNMFVTEKDCIQTC 55

RESULT 42
US-08-358-160-15
; Sequence 15, Application US/08358160
; Patent No. 5663143
; GENERAL INFORMATION:
; APPLICANT: LEY, Arthur C.
; APPLICANT: LADNER, Robert C.
; APPLICANT: GUTERMAN, Sonia K.
; APPLICANT: ROBERTS, Bruce L.
; APPLICANT: MARKLAND, William
; APPLICANT: KENT, Rachel B.
; TITLE OF INVENTION: ENGINEERED HUMAN-DERIVED KUNITZ
; NUMBER OF SEQUENCES: 234
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W. Suite 300
; CITY: Washington
; STATE: District of Columbia
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/358,160
; FILING DATE: 16-DEC-1994
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/133,031
; FILING DATE: 13-OCT-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/009,319
; FILING DATE: 26-JAN-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/664,989
; FILING DATE: 01-MAR-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/487,063
; FILING DATE: 02-MAR-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/240,160
; FILING DATE: 02-SEP-1988
; ATTORNEY/AGENT INFORMATION:
```

NAME: Cooper, Iver P.
REGISTRATION NUMBER: 28,005
REFERENCE/DOCKET NUMBER: LEY=1
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
TELEX: 248633
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 58 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-358-160-15

Query Match 51.3%; Score 155; DB 1; Length 58;
Best Local Similarity 51.0%; Pred. No. 6.4e-13;
Matches 26; Conservative 5; Mismatches 20; Indels 0; Gaps 0;

QY 1 CSMPOEAGPCLASIPHHWYNNKTKICSEFIYGGCGGNNNNFOTEALCLVTC 51
Db 5 CQLGYSAGFCVAMFFRYFYNGTSMACETFYGGCGMGNGNNFVTEKDCIQT 55

RESULT 43

US-08-358-160-16
Sequence 16, Application US/08358160
Patent No. 563143

GENERAL INFORMATION:

APPLICANT: LEY, Arthur C.
APPLICANT: LADNER, Robert C.
APPLICANT: GUTERMAN, Sonia K.
APPLICANT: ROBERTS, Bruce L.
APPLICANT: MARKLAND, William
APPLICANT: KENT, Rachel B.

TITLE OF INVENTION: ENGINEERED HUMAN-DERIVED KUNITZ

TITLE OF INVENTION: DOMAINS THAT INHIBIT HUMAN NEUTROPHIL ELASTASE

NUMBER OF SEQUENCES: 234

CORRESPONDENCE ADDRESS:

ADDRESSEE: BROWDY AND NEIMARK
STREET: 419 Seventh Street, N.W. Suite 300

CITY: Washington

STATE: District of Columbia

COUNTRY: USA

ZIP: 20004

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent In Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/358,160

FILING DATE: 16-DEC-1994

CLASSIFICATION: 514

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/133,031

FILING DATE: 13-OCT-1993

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/009,319

FILING DATE: 26-JAN-1993

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/664,989

FILING DATE: 01-MAR-1991

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/487,063

FILING DATE: 02-MAR-1990

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/240,160

FILING DATE: 02-SEP-1988

ATTORNEY/AGENT INFORMATION:

NAME: Cooper, Iver P.

REGISTRATION NUMBER: 28,005

REFERENCE/DOCKET NUMBER: LEY=1

TELECOMMUNICATION INFORMATION:

REFERENCE/DOCKET NUMBER: LEY=1
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
TELEX: 248633

INFORMATION FOR SEQ ID NO: 16:

SEQUENCE CHARACTERISTICS:

LENGTH: 58 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-358-160-16

Query Match 51.3%; Score 155; DB 1; Length 58;

Best Local Similarity 51.0%; Pred. No. 6.4e-13;

Matches 26; Conservative 5; Mismatches 20; Indels 0; Gaps 0;

QY 1 CSMPOEAGPCLASIPHHWYNNKTKICSEFIYGGCGGNNNNFOTEALCLVTC 51

Db 5 CQLGYSAGFCVAMFFRYFYNGTSMACETFYGGCGMGNGNNFVTEKDCIQT 55

RESULT 44

US-08-358-160-24

Sequence 24, Application US/08358160

Patent No. 563143

GENERAL INFORMATION:

APPLICANT: LEY, Arthur C.

APPLICANT: LADNER, Robert C.

APPLICANT: GUTERMAN, Sonia K.

APPLICANT: ROBERTS, Bruce L.

APPLICANT: MARKLAND, William

APPLICANT: KENT, Rachel B.

TITLE OF INVENTION: ENGINEERED HUMAN-DERIVED KUNITZ

TITLE OF INVENTION: DOMAINS THAT INHIBIT HUMAN NEUTROPHIL ELASTASE

NUMBER OF SEQUENCES: 234

CORRESPONDENCE ADDRESS:

ADDRESSEE: BROWDY AND NEIMARK

STREET: 419 Seventh Street, N.W. Suite 300

CITY: Washington

STATE: District of Columbia

COUNTRY: USA

ZIP: 20004

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent In Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/358,160

FILING DATE: 16-DEC-1994

CLASSIFICATION: 514

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/133,031

FILING DATE: 13-OCT-1993

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/009,319

FILING DATE: 26-JAN-1993

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/664,989

FILING DATE: 01-MAR-1991

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/487,063

FILING DATE: 02-MAR-1990

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/240,160

FILING DATE: 02-SEP-1988

ATTORNEY/AGENT INFORMATION:

NAME: Cooper, Iver P.

REGISTRATION NUMBER: 28,005

REFERENCE/DOCKET NUMBER: LEY=1

TELECOMMUNICATION INFORMATION:

TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
TELEX: 248633
; INFORMATION FOR SEQ ID NO: 24:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 58 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-358-160-24

Query Match 51.3%; Score 155; DB 1; Length 58;
Best Local Similarity 47.1%; Pred. No. 6.4e-13;
Matches 24; Conservative 8; Mismatches 19; Indels 0; Gaps 0;

QY 1 CSMPOEAGPCLASIPHHWYNNKTKICSEFYGGCGGNNNNFQTEAICLVTC 51
DB 5 CLEPPYTGPCVAIPFRYFYNKAGLCQTFVYGGCGGNNNNFKSAEDCMRTC 55

RESULT 45
US-08-829-876-129
; Sequence 129, Application US/08829876
; Patent No. 5962266

GENERAL INFORMATION:
; APPLICANT: White, Tyler R.
; APPLICANT: Damm, Deborah
; APPLICANT: Lesikar, David D.
; APPLICANT: McFadden, Kathleen
; APPLICANT: Garrick, Brett L.
; TITLE OF INVENTION: PROTEASE INHIBITOR PEPTIDES
; NUMBER OF SEQUENCES: 228
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/829,876
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/436,555
; FILING DATE: 08-MAY-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Pelto, Don J.
; REGISTRATION NUMBER: 33,754
; REFERENCE/DOCKET NUMBER: 56324/106/SCNO
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 129:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 61 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-829-876-129

Query Match 51.3%; Score 155; DB 2; Length 61;
Best Local Similarity 49.0%; Pred. No. 6.7e-13;
Matches 25; Conservative 5; Mismatches 21; Indels 0; Gaps 0;

QY 1 CSMPOEAGPCLASIPHHWYNNKTKICSEFYGGCGGNNNNFQTEAICLVTC 51
DB 7 CSEQAETGPCRAMISHWYFDVTEGKCAPFFYGGCGGNNNNFDTBEYCNMVC 57

RESULT 46

US-08-829-876-139
; Sequence 139, Application US/08829876
; Patent No. 5962266
; GENERAL INFORMATION:
; APPLICANT: White, Tyler R.
; APPLICANT: Damm, Deborah
; APPLICANT: Lesikar, David D.
; APPLICANT: McFadden, Kathleen
; APPLICANT: Garrick, Brett L.
; TITLE OF INVENTION: PROTEASE INHIBITOR PEPTIDES
; NUMBER OF SEQUENCES: 228
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/829,876
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/436,555
; FILING DATE: 08-MAY-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Pelto, Don J.
; REGISTRATION NUMBER: 33,754
; REFERENCE/DOCKET NUMBER: 56324/106/SCNO
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 139:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 61 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-829-876-139

Query Match 51.3%; Score 155; DB 2; Length 61;
Best Local Similarity 49.0%; Pred. No. 6.7e-13;
Matches 25; Conservative 5; Mismatches 21; Indels 0; Gaps 0;

QY 1 CSMPOEAGPCLASIPHHWYNNKTKICSEFYGGCGGNNNNFQTEAICLVTC 51
DB 7 CSEQAETGPCRAMISHWYFDVTEGKCAPFFYGGCGGNNNNFDTBEYCNMVC 57

RESULT 47

US-08-829-876-208
; Sequence 208, Application US/08829876
; Patent No. 5962266
; GENERAL INFORMATION:
; APPLICANT: White, Tyler R.
; APPLICANT: Damm, Deborah
; APPLICANT: Lesikar, David D.
; APPLICANT: McFadden, Kathleen
; APPLICANT: Garrick, Brett L.
; TITLE OF INVENTION: PROTEASE INHIBITOR PEPTIDES

```

; NUMBER OF SEQUENCES: 228
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/829,876
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/436,555
; FILING DATE: 08-MAY-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Pelto, Don J.
; REGISTRATION NUMBER: 33,754
; REFERENCE/DOCKET NUMBER: 563224/106/SCNO
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 208:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 61 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-829-876-208

Query Match 51.3%; Score 155; DB 2; L
Best Local Similarity 49.0%; Pred. No. 6.7e-13;
Matches 25; Conservative 6; Mismatches 20;

Oy 1 CSMQAGAGCLASIPHWYNNKTKICSEFIYGGCGGNNN
||| :||| :||| :||| :||| :||| :||| :|||
Db 7 CSQAEATGPCRAIYHWYFDVTGKCAPFYGGCGGNRNN

RESULT 48
US-08-829-876-217
; Sequence 217, Application US/08829876
; Patent No. 5962266
; GENERAL INFORMATION:
; APPLICANT: White, Tyler R.
; APPLICANT: Damm, Deborah
; APPLICANT: Lesikar, David D.
; APPLICANT: McFadden, Kathleen
; APPLICANT: Garrick, Brett L.
; TITLE OF INVENTION: PROTEASE INHIBITOR PEPTIDES
; NUMBER OF SEQUENCES: 228
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/829,876
; FILING DATE:

```

```

; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/436,555
; FILING DATE: 08-MAY-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Peltó, Don J.
; REGISTRATION NUMBER: 33,754
; REFERENCE/DOCKET NUMBER: 56324/106/SCNO
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 217:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 61 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-829-876-217

Query Match 51.3%; Score 155; DB 2; Length 61;
Best Local Similarity 49.0%; Pred. NO. 6.7e-13;
Matches 25; Conservative 6; Mismatches 20; Indels 0;

Qy 1 CSMQAGCLASIPHWNTKTKTCSRFYGGCGGNNNFOTEAICLVTC 51
   |||||:||||:||||:|||||:|||||:|||||:|||||:
Db 7 CSQAEVGPRAAIYHVFDTVGKCAPFFYGGCGGNNNFOTEEYCMAVC 51

RESULT 49
US-08-829-876-222
; Sequence 222, Application US/08829876
; Patent No. 5962266
; GENERAL INFORMATION:
; APPLICANT: White, Tyler R.
; APPLICANT: Damm, Deborah
; APPLICANT: Lesikar, David D.
; APPLICANT: McFadden, Kathleen
; APPLICANT: Garrick, Brett L.
; TITLE OF INVENTION: PROTEASE INHIBITOR PEPTIDES
; NUMBER OF SEQUENCES: 228
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/829,876
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/436,555
; FILING DATE: 08-MAY-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Peltó, Don J.
; REGISTRATION NUMBER: 33,754
; REFERENCE/DOCKET NUMBER: 56324/106/SCNO
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 222:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 61 amino acids
; TYPE: amino acid

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; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-829-876-222

Query Match      51.3%; Score 155; DB 2; Length 61;
Best Local Similarity 49.0%; Pred. No. 6.7e-13;
Matches 25; Conservative 5; Mismatches 21; Indels 0; Gaps 0;

QY 1 CSMPOEAGPCLASIPHHWYKTKICSEFIYGGCGGNNNFQTEAICLVTC 51
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Db 7 CSEQAETGFCRGIIRHWYFDVTEGKCAPFFYGGCGGNRRNFDTEYCNMAVC 57

RESULT 50
US-09-234-874A-129
; Sequence 129, Application US/09234874A
; Patent No. 6376648
; GENERAL INFORMATION:
; APPLICANT: White, Tyler R.
; Damm, Deborah
; Lesikar, David D.
; McFadden, Kathleen
; Garrick, Brett L.
;
; TITLE OF INVENTION: PROTEASE INHIBITOR PEPTIDES
; NUMBER OF SEQUENCES: 228
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/234,874A
; FILING DATE: 11-Jun-2001
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/436,555
; FILING DATE: 08-MAY-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Bent, Stephen
; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 056324/0106
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 129:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 61 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 129:
US-09-234-874A-129

Query Match      51.3%; Score 155; DB 3; Length 61;
Best Local Similarity 49.0%; Pred. No. 6.7e-13;
Matches 25; Conservative 5; Mismatches 21; Indels 0; Gaps 0;

QY 1 CSMPOEAGPCLASIPHHWYKTKICSEFIYGGCGGNNNFQTEAICLVTC 51
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Db 7 CSEQAETGFCRAMIPRWTFDVTGKCAPFFYGGCGGNRRNFDTEYCNMAVC 57

Search completed: September 21, 2005, 16:42:18
Job time : 9.32743 secs
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OM protein - protein search, using sw model

Run on: September 21, 2005, 16:33:14 ; Search time 31.8938 Seconds
(without alignments)
650.835 Million cell updates/sec

Title: US-10-807-204-2_COPY_52_102

Perfect score: 302

Sequence: 1 CSMPOEAGPCLASIPHWYN.....GCCQGNNNFQTEAICLVTC 51

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1826521 seqs, 407012169 residues

Total number of hits satisfying chosen parameters: 1826521

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 50 summaries

Database : Published Applications AA.*

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22: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	302	100.0	106	16	US-10-807-204-2
2	302	100.0	131	16	US-10-807-204-1
3	302	100.0	131	16	US-10-807-204-12
4	292	96.7	131	16	US-10-807-204-15
5	224	74.2	136	16	US-10-807-204-16
6	219	72.5	51	15	US-10-058-993-118
7	219	72.5	58	16	US-10-361-997-5
8	219	72.5	58	17	US-10-931-153-21
9	219	72.5	102	9	US-09-852-659A-120
10	219	72.5	102	15	US-10-058-993-121
11	219	72.5	117	9	US-09-852-659A-119
					Sequence 2, Appli
					Sequence 1, Appli
					Sequence 12, Appl
					Sequence 15, Appl
					Sequence 16, Appl
					Sequence 118, App
					Sequence 5, Appli
					Sequence 21, Appl
					Sequence 120, App
					Sequence 121, App
					Sequence 119, App

12	219	72.5	117	15	US-10-058-993-120	Sequence 120, App
13	219	72.5	133	9	US-09-853-181-75	Sequence 75, Appl
14	219	72.5	133	9	US-09-852-659A-75	Sequence 75, Appl
15	219	72.5	133	9	US-09-852-797-75	Sequence 75, Appl
16	219	72.5	133	15	US-10-058-993-75	Sequence 75, Appl
17	219	72.5	133	16	US-10-807-204-13	Sequence 13, Appl
18	188	62.3	134	16	US-10-807-204-14	Sequence 14, Appl
19	169	58.0	571	14	US-10-369-736-3	Sequence 3, Appli
20	169	58.0	571	14	US-10-369-736-49	Sequence 49, Appl
21	169	58.0	571	14	US-10-369-738-3	Sequence 3, Appli
22	169	58.0	571	14	US-10-369-738-49	Sequence 49, Appl
23	169	58.0	571	19	US-11-028-058-3	Sequence 3, Appli
24	169	58.0	571	19	US-11-028-058-49	Sequence 49, Appl
25	168	55.6	64	10	US-09-896-095-160	Sequence 160, App
26	168	55.6	64	14	US-10-038-722-103	Sequence 103, App
27	168	55.6	64	15	US-10-115-134-17	Sequence 17, Appl
28	167	55.3	58	14	US-10-038-722-5	Sequence 5, Appli
29	166	55.0	67	10	US-09-896-095-147	Sequence 147, App
30	166	55.0	67	14	US-10-038-722-90	Sequence 90, Appl
31	166	55.0	67	15	US-10-115-134-4	Sequence 4, Appli
32	166	55.0	86	9	US-09-910-430-8	Sequence 8, Appli
33	166	55.0	86	14	US-10-165-605A-8	Sequence 8, Appli
34	161	53.3	58	14	US-10-038-722-17	Sequence 17, Appl
35	161	53.3	58	14	US-10-038-722-18	Sequence 18, Appl
36	161	53.3	58	14	US-10-038-722-19	Sequence 19, Appl
37	161	53.3	58	15	US-10-115-134-88	Sequence 88, Appl
38	161	53.3	58	15	US-10-115-134-89	Sequence 89, Appl
39	161	53.3	58	15	US-10-115-134-90	Sequence 90, Appl
40	161	53.3	58	15	US-10-456-986A-42	Sequence 42, Appl
41	161	53.3	58	15	US-10-456-986A-43	Sequence 43, Appl
42	161	53.3	58	15	US-10-456-986A-44	Sequence 44, Appl
43	161	53.3	58	18	US-10-953-902A-42	Sequence 42, Appl
44	161	53.3	58	18	US-10-953-902A-43	Sequence 43, Appl
45	161	53.3	58	18	US-10-953-902A-44	Sequence 44, Appl
46	160	53.0	503	14	US-10-007-280A-233	Sequence 233, App
47	160	53.0	576	9	US-09-794-589-2	Sequence 2, Appli
48	160	53.0	576	14	US-10-315-380-2	Sequence 2, Appli
49	160	53.0	576	14	US-10-369-736-7	Sequence 7, Appli
50	160	53.0	576	14	US-10-369-738-7	Sequence 7, Appli

ALIGNMENTS

RESULT 1
US-10-807-204-2
; Sequence 2, Application US/10807204
; Publication No. US20040229312A1
; GENERAL INFORMATION:
; APPLICANT: Bougueleret, Lydie
; APPLICANT: Bairoch, Amos
; APPLICANT: Niknejad, Anne
; TITLE OF INVENTION: Engineered Human Kunitz-Type Protease
; TITLE OF INVENTION: Inhibitor
; FILE REFERENCE: 54720-8015.US00
; CURRENT APPLICATION NUMBER: US/10/807,204
; PRIOR FILING DATE: 2004-03-22
; PRIOR APPLICATION NUMBER: PCT/EP03/01629
; PRIOR FILING DATE: 2003-02-18
; PRIOR APPLICATION NUMBER: US 60/358,683
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 106
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (1)...(106)
; OTHER INFORMATION: mature form
; FEATURE:
; NAME/KEY: DOMAIN

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; LOCATION: (52)...(102)
; OTHER INFORMATION: Kunitz domain predicted by pfscan
; FEATURE:
; NAME/KEY: DISULFID
; LOCATION: (8)...(36)
; OTHER INFORMATION: predicted disulfide bond
; FEATURE:
; NAME/KEY: DISULFID
; LOCATION: (15)...(40)
; OTHER INFORMATION: predicted disulfide bond
; FEATURE:
; NAME/KEY: DISULFID
; LOCATION: (23)...(35)
; OTHER INFORMATION: predicted disulfide bond
; FEATURE:
; NAME/KEY: DISULFID
; LOCATION: (29)...(44)
; OTHER INFORMATION: predicted disulfide bond
; FEATURE:
; NAME/KEY: DISULFID
; LOCATION: (52)...(102)
; OTHER INFORMATION: predicted disulfide bond
; FEATURE:
; NAME/KEY: DISULFID
; LOCATION: (61)...(85)
; OTHER INFORMATION: predicted disulfide bond
; FEATURE:
; NAME/KEY: DISULFID
; LOCATION: (77)...(98)
; OTHER INFORMATION: predicted disulfide bond
US-10-807-204-2
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Query Match 100.0%; Score 302; DB 16; Length 106;
Best Local Similarity 100.0%; Pred. No. 3.1e-29;
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 52 CSMQEAGPCLASIPHHWYNNKTKICSEFIYGGCGNNNFQTEAICLVTC 102
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RESULT 2
US-10-807-204-1
; Sequence 1, Application US/10807204
; Publication No. US20040229312A1
; GENERAL INFORMATION:
; APPLICANT: Bougueleret, Lydie
; APPLICANT: Bairoch, Amos
; APPLICANT: Niknejad, Anne
; TITLE OF INVENTION: Engineered Human Kunitz-Type Protease
; TITLE OF INVENTION: Inhibitor
; FILE REFERENCE: 54720-8015.US00
; CURRENT APPLICATION NUMBER: US/10/807,204
; PRIOR FILING DATE: 2004-03-22
; PRIOR APPLICATION NUMBER: PCT/EP03/01629
; PRIOR FILING DATE: 2003-02-18
; PRIOR APPLICATION NUMBER: US 60/358,683
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 131
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (1)...(131)
; OTHER INFORMATION: eppin-like precursor
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: (1)...(25)
; OTHER INFORMATION: predicted by SignalP 2.0
; FEATURE:
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; NAME/KEY: PEPTIDE
; LOCATION: (26)...(131)
; OTHER INFORMATION: mature peptide
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (77)...(127)
; OTHER INFORMATION: Kunitz domain predicted by pfscan
; FEATURE:
; NAME/KEY: DISULFID
; LOCATION: (33)...(61)
; OTHER INFORMATION: predicted disulfide bond
; FEATURE:
; NAME/KEY: DISULFID
; LOCATION: (40)...(65)
; OTHER INFORMATION: predicted disulfide bond
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; LOCATION: (48)...(60)
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; OTHER INFORMATION: predicted disulfide bond
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; NAME/KEY: DISULFID
; LOCATION: (77)...(127)
; OTHER INFORMATION: predicted disulfide bond
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; NAME/KEY: DISULFID
; LOCATION: (86)...(110)
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; OTHER INFORMATION: predicted disulfide bond
US-10-807-204-1
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Best Local Similarity 100.0%; Pred. No. 3.8e-29;
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 77 CSMQEAGPCLASIPHHWYNNKTKICSEFIYGGCGNNNFQTEAICLVTC 127
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RESULT 3
US-10-807-204-12
; Sequence 12, Application US/10807204
; Publication No. US20040229312A1
; GENERAL INFORMATION:
; APPLICANT: Bougueleret, Lydie
; APPLICANT: Bairoch, Amos
; APPLICANT: Niknejad, Anne
; TITLE OF INVENTION: Engineered Human Kunitz-Type Protease
; TITLE OF INVENTION: Inhibitor
; FILE REFERENCE: 54720-8015.US00
; CURRENT APPLICATION NUMBER: US/10/807,204
; CURRENT FILING DATE: 2004-03-22
; PRIOR APPLICATION NUMBER: PCT/EP03/01629
; PRIOR FILING DATE: 2003-02-18
; PRIOR APPLICATION NUMBER: US 60/358,683
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12
; LENGTH: 131
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-807-204-12
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Best Local Similarity 100.0%; Pred. No. 3.8e-29;
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Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 4
 US-10-807-204-15
 ; Sequence 15, Application US/10807204
 ; Publication No. US20040229312A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Bougueleret, Lydie
 ; APPLICANT: Bairoch, Amos
 ; APPLICANT: Niknejad, Anne
 ; TITLE OF INVENTION: Engineered Human Kunitz-Type Protease
 ; TITLE OF INVENTION: Inhibitor
 ; FILE REFERENCE: 54720-8015:US00
 ; CURRENT APPLICATION NUMBER: US/10/807,204
 ; CURRENT FILING DATE: 2004-03-22
 ; PRIOR APPLICATION NUMBER: PCT/EP03/01629
 ; PRIOR FILING DATE: 2003-02-18
 ; PRIOR APPLICATION NUMBER: US 60/358,683
 ; PRIOR FILING DATE: 2002-02-21
 ; NUMBER OF SEQ ID NOS: 16
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 15
 ; LENGTH: 131
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens

US-10-807-204-15
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 Db 77 CSMQAEAGPCLASIPHWYNNKTKICSEFIYGGCGQNNNNFQTEAICLVTC 127

RESULT 5
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 ; Sequence 16, Application US/10807204
 ; Publication No. US20040229312A1
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 ; APPLICANT: Bougueleret, Lydie
 ; APPLICANT: Bairoch, Amos
 ; APPLICANT: Niknejad, Anne
 ; TITLE OF INVENTION: Engineered Human Kunitz-Type Protease
 ; TITLE OF INVENTION: Inhibitor
 ; FILE REFERENCE: 54720-8015:US00
 ; CURRENT APPLICATION NUMBER: US/10/807,204
 ; CURRENT FILING DATE: 2004-03-22
 ; PRIOR APPLICATION NUMBER: PCT/EP03/01629
 ; PRIOR FILING DATE: 2003-02-18
 ; PRIOR APPLICATION NUMBER: US 60/358,683
 ; PRIOR FILING DATE: 2002-02-21
 ; NUMBER OF SEQ ID NOS: 16
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 16
 ; LENGTH: 136
 ; TYPE: PRT
 ; ORGANISM: Mus musculus

US-10-807-204-16
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 Best Local Similarity 66.7%; Pred. No. 1.5e-19;
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RESULT 6
 US-10-058-993-118
 ; Sequence 118, Application US/10058993
 ; Publication No. US20030225009A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Rosen et al.
 ; TITLE OF INVENTION: 28 Human Secreted Proteins
 ; FILE REFERENCE: PZ003P5
 ; CURRENT APPLICATION NUMBER: US/10/058,993
 ; CURRENT FILING DATE: 2002-01-30
 ; PRIOR APPLICATION NUMBER: 09/852,659
 ; PRIOR FILING DATE: 2001-05-11
 ; PRIOR APPLICATION NUMBER: 09/852,797
 ; PRIOR FILING DATE: 2001-05-11
 ; PRIOR APPLICATION NUMBER: 09/853,161
 ; PRIOR FILING DATE: 2001-05-11
 ; PRIOR APPLICATION NUMBER: 60/265,583
 ; PRIOR FILING DATE: 2001-02-02
 ; PRIOR APPLICATION NUMBER: 09/152,060
 ; PRIOR FILING DATE: 1998-09-11
 ; PRIOR APPLICATION NUMBER: PCT/US98/04858
 ; PRIOR FILING DATE: 1998-03-12
 ; PRIOR APPLICATION NUMBER: 60/068,368
 ; PRIOR FILING DATE: 1997-12-19
 ; PRIOR APPLICATION NUMBER: 60/057,765
 ; PRIOR FILING DATE: 1997-09-05
 ; PRIOR APPLICATION NUMBER: 60/048,970
 ; PRIOR FILING DATE: 1997-06-05
 ; PRIOR APPLICATION NUMBER: 60/050,934
 ; PRIOR FILING DATE: 1997-05-30
 ; PRIOR APPLICATION NUMBER: 60/048,100
 ; PRIOR FILING DATE: 1997-05-30
 ; PRIOR APPLICATION NUMBER: 60/048,189
 ; PRIOR FILING DATE: 1997-05-30
 ; PRIOR APPLICATION NUMBER: 60/048,357
 ; PRIOR FILING DATE: 1997-05-30
 ; PRIOR APPLICATION NUMBER: 60/040,710
 ; PRIOR FILING DATE: 1997-03-14
 ; PRIOR APPLICATION NUMBER: 60/040,762
 ; PRIOR FILING DATE: 1997-03-14
 ; NUMBER OF SEQ ID NOS: 122
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 118
 ; LENGTH: 51
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens

US-10-058-993-118
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 Best Local Similarity 68.6%; Pred. No. 2.5e-19;
 Matches 35; Conservative 5; Mismatches 11; Indels 0; Gaps 0;
 QY 1 CSMQAEAGPCLASIPHWYNNKTKICSEFIYGGCGQNNNNFQTEAICLVTC 51
 Db 1 CEMPKEGPGCLAYFLHWYNNQETDLCTEFTYGGCGQNNNNFQSKANCLNTC 51

RESULT 7
 US-10-361-997-5
 ; Sequence 5, Application US/10361997
 ; Publication No. US20040171794A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Ladner, Robert Charles
 ; APPLICANT: Ley, Arthur C.
 ; TITLE OF INVENTION: KUNITZ DOMAIN PEPTIDES
 ; FILE REFERENCE: 3421.1015-000
 ; CURRENT APPLICATION NUMBER: US/10/361,997
 ; CURRENT FILING DATE: 2003-02-07
 ; PRIOR APPLICATION NUMBER: US 60/355,547
 ; PRIOR FILING DATE: 2002-02-07
 ; NUMBER OF SEQ ID NOS: 84

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; SOFTWARE: FaestSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 58
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-361-997-5

Query Match          72.5%; Score 219; DB 16; Length 58;
Best Local Similarity 68.6%; Pred. No. 2.8e-19;
Matches 35; Conservative 5; Mismatches 11; Indels 0; Gaps 0;

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Db 5 CEMPKEGTGCLAYFLHWWYDKDNTCSMFVYGGCGGNNNNFQSKANCLNTC 55

RESULT 8
US-10-931-153-21
; Sequence 21, Application US/10931153
; Publication No. US20050089515A1
; GENERAL INFORMATION:
; APPLICANT: Ley, Arthur C.
; APPLICANT: Sadner, Robert C.
; APPLICANT: Ladner, Robert C.
; APPLICANT: Stochl, Mark
; TITLE OF INVENTION: POLY-BEGLYATED PROTEASE INHIBITORS
; FILE REFERENCE: 10280-119001
; CURRENT APPLICATION NUMBER: US/10/931,153
; CURRENT FILING DATE: 2004-08-30
; PRIOR APPLICATION NUMBER: US 60/498,845
; PRIOR FILING DATE: 2003-08-29
; PRIOR APPLICATION NUMBER: US 60/598,967
; PRIOR FILING DATE: 2004-08-04
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: FaestSeq for Windows Version 4.0
; SEQ ID NO 21
; LENGTH: 58
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-931-153-21

Query Match          72.5%; Score 219; DB 17; Length 58;
Best Local Similarity 68.6%; Pred. No. 2.8e-19;
Matches 35; Conservative 5; Mismatches 11; Indels 0; Gaps 0;

Qy 1 CSMPOEAGPCLASIPHHWYNNKTKICSEFIYGGCGGNNNNFQTEAICLVTC 51
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 5 CEMPKEGTGCLAYFLHWWYDKDNTCSMFVYGGCGGNNNNFQSKANCLNTC 55

RESULT 9
US-09-852-659A-120
; Sequence 120, Application US/09852659A
; Patent No. US2002007287A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 28 Human Secreted Proteins
; FILE REFERENCE: P2003P4
; CURRENT APPLICATION NUMBER: US/09/852,659A
; CURRENT FILING DATE: 2001-05-11
; PRIOR APPLICATION NUMBER: 60/265,583
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: 09/152,060
; PRIOR FILING DATE: 1998-09-11
; PRIOR APPLICATION NUMBER: PCT/US98/04858
; PRIOR FILING DATE: 1998-03-12
; PRIOR APPLICATION NUMBER: 60/040,762
; PRIOR FILING DATE: 1997-03-14
; PRIOR APPLICATION NUMBER: 60/040,710
; PRIOR FILING DATE: 1997-03-14
; PRIOR APPLICATION NUMBER: 60/050,934
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/048,100
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/048,189
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/048,357
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/040,710
; PRIOR FILING DATE: 1997-03-14
; PRIOR APPLICATION NUMBER: 60/040,762
; PRIOR FILING DATE: 1997-03-14
; NUMBER OF SEQ ID NOS: 122
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 121
; LENGTH: 102
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-852-659A-120

Query Match          72.5%; Score 219; DB 9; Length 102;
Best Local Similarity 68.6%; Pred. No. 4.8e-19;
Matches 35; Conservative 5; Mismatches 11; Indels 0; Gaps 0;

Qy 1 CSMPOEAGPCLASIPHHWYNNKTKICSEFIYGGCGGNNNNFQTEAICLVTC 51
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 46 CEMPKEGTGCLAYFLHWWYDKDNTCSMFVYGGCGGNNNNFQSKANCLNTC 96

RESULT 10
US-10-058-993-121
; Sequence 121, Application US/10058993
; Publication No. US20030225009A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 28 Human Secreted Proteins
; FILE REFERENCE: P2003P5
; CURRENT APPLICATION NUMBER: US/10/058,993
; CURRENT FILING DATE: 2002-01-30
; PRIOR APPLICATION NUMBER: 09/852,659
; PRIOR FILING DATE: 2001-05-11
; PRIOR APPLICATION NUMBER: 09/852,797
; PRIOR FILING DATE: 2001-05-11
; PRIOR APPLICATION NUMBER: 09/853,161
; PRIOR FILING DATE: 2001-05-11
; PRIOR APPLICATION NUMBER: 60/265,583
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: 09/152,060
; PRIOR FILING DATE: 1998-09-11
; PRIOR APPLICATION NUMBER: PCT/US98/04858
; PRIOR FILING DATE: 1998-03-12
; PRIOR APPLICATION NUMBER: 60/068,368
; PRIOR FILING DATE: 1997-12-19
; PRIOR APPLICATION NUMBER: 60/057,765
; PRIOR FILING DATE: 1997-09-05
; PRIOR APPLICATION NUMBER: 60/048,970
; PRIOR FILING DATE: 1997-06-05
; PRIOR APPLICATION NUMBER: 60/050,934
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/048,100
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/048,189
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/048,357
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/040,710
; PRIOR FILING DATE: 1997-03-14
; PRIOR APPLICATION NUMBER: 60/040,762
; PRIOR FILING DATE: 1997-03-14
; NUMBER OF SEQ ID NOS: 122
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 121
; LENGTH: 102
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-852-659A-120
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; ORGANISM: Homo sapiens
US-10-058-993-121

Query Match          72.5%; Score 219; DB 15; Length 102;
Best Local Similarity 68.6%; Pred. No. 4.8e-19;
Matches 35; Conservative 5; Mismatches 11; Indels 0; Gaps 0;

QY 1 CSMQZAGPCLASIPHWYKTKICSEFIYGGCGQNNNNFQTEAICLVTC 51
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 46 CEMPKEGTGCLAYFLHWYDKDNTCSMFYGGCGQNNNNFQSKANCLNTC 96

RESULT 11
US-09-852-659A-119
; Sequence 119, Application US/09852659A
; Patent No. US20020077287A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 28 Human Secreted Proteins
; FILE REFERENCE: P2003P4
; CURRENT APPLICATION NUMBER: US/09/852,659A
; CURRENT FILING DATE: 2001-05-11
; PRIOR APPLICATION NUMBER: 60/265,583
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: 09/152,060
; PRIOR FILING DATE: 1998-09-11
; PRIOR APPLICATION NUMBER: PCT/US98/04858
; PRIOR FILING DATE: 1998-03-12
; PRIOR APPLICATION NUMBER: 60/040,762
; PRIOR FILING DATE: 1997-03-14
; PRIOR APPLICATION NUMBER: 60/040,710
; PRIOR FILING DATE: 1997-03-14
; PRIOR APPLICATION NUMBER: 60/050,934
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/048,100
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/048,357
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/048,189
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: PCT/US98/04858
; PRIOR FILING DATE: 1998-03-12
; PRIOR APPLICATION NUMBER: 60/040,762
; PRIOR FILING DATE: 1997-03-14
; PRIOR APPLICATION NUMBER: 60/040,710
; PRIOR FILING DATE: 1997-03-14
; PRIOR APPLICATION NUMBER: 60/050,934
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/048,100
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/048,357
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/048,189
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/050,934
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/048,100
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/048,357
; PRIOR FILING DATE: 1997-05-30
; NUMBER OF SEQ ID NOS: 121
; SOFTWARE: Patent in Ver. 2.0
; SEQ ID NO 119
; LENGTH: 117
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-852-659A-119

Query Match          72.5%; Score 219; DB 9; Length 117;
Best Local Similarity 68.6%; Pred. No. 5.5e-19;
Matches 35; Conservative 5; Mismatches 11; Indels 0; Gaps 0;

QY 1 CSMQZAGPCLASIPHWYKTKICSEFIYGGCGQNNNNFQTEAICLVTC 51
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 61 CEMPKEGTGCLAYFLHWYDKDNTCSMFYGGCGQNNNNFQSKANCLNTC 111

RESULT 12
US-10-058-993-120
; Sequence 120, Application US/10058993
; Publication No. US20030225009A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 28 Human Secreted Proteins
; FILE REFERENCE: P2003P5
; CURRENT APPLICATION NUMBER: US/10/058,993
; CURRENT FILING DATE: 2002-01-30
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; PRIOR APPLICATION NUMBER: 09/852,659
; PRIOR FILING DATE: 2001-05-11
; PRIOR APPLICATION NUMBER: 09/852,797
; PRIOR FILING DATE: 2001-05-11
; PRIOR APPLICATION NUMBER: 09/853,161
; PRIOR FILING DATE: 2001-05-11
; PRIOR APPLICATION NUMBER: 60/265,583
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: 09/152,060
; PRIOR FILING DATE: 1998-09-11
; PRIOR APPLICATION NUMBER: PCT/US98/04858
; PRIOR FILING DATE: 1998-03-12
; PRIOR APPLICATION NUMBER: 60/068,368
; PRIOR FILING DATE: 1997-12-19
; PRIOR APPLICATION NUMBER: 60/057,765
; PRIOR FILING DATE: 1997-09-05
; PRIOR APPLICATION NUMBER: 60/048,970
; PRIOR FILING DATE: 1997-06-05
; PRIOR APPLICATION NUMBER: 60/050,934
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/048,100
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/048,189
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/048,357
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/040,710
; PRIOR FILING DATE: 1997-03-14
; PRIOR APPLICATION NUMBER: 60/040,762
; PRIOR FILING DATE: 1997-03-14
; NUMBER OF SEQ ID NOS: 122
; SOFTWARE: Patent in Ver. 2.0
; SEQ ID NO 120
; LENGTH: 117
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-058-993-120

Query Match          72.5%; Score 219; DB 15; Length 117;
Best Local Similarity 68.6%; Pred. No. 5.5e-19;
Matches 35; Conservative 5; Mismatches 11; Indels 0; Gaps 0;

QY 1 CSMQZAGPCLASIPHWYKTKICSEFIYGGCGQNNNNFQTEAICLVTC 51
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 61 CEMPKEGTGCLAYFLHWYDKDNTCSMFYGGCGQNNNNFQSKANCLNTC 111

RESULT 13
US-09-853-161-75
; Sequence 75, Application US/09853161
; Patent No. US20020076756A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 28 Human Secreted Proteins
; FILE REFERENCE: P2003P3
; CURRENT APPLICATION NUMBER: US/09/853,161
; CURRENT FILING DATE: 2001-05-11
; PRIOR APPLICATION NUMBER: 60/265,583
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: 09/152,060
; PRIOR FILING DATE: 1998-09-11
; PRIOR APPLICATION NUMBER: PCT/US98/04858
; PRIOR FILING DATE: 1998-03-12
; PRIOR APPLICATION NUMBER: 60/040,762
; PRIOR FILING DATE: 1997-03-14
; PRIOR APPLICATION NUMBER: 60/040,710
; PRIOR FILING DATE: 1997-03-14
; PRIOR APPLICATION NUMBER: 60/050,934
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/048,100
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/048,357
; PRIOR FILING DATE: 1997-05-30
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; PRIOR APPLICATION NUMBER: 60/048,189
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/057,765
; PRIOR FILING DATE: 1997-09-05
; PRIOR APPLICATION NUMBER: 60/048,970
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/068,368
; PRIOR FILING DATE: 1997-12-19
; NUMBER OF SEQ ID NOS: 118
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 75
; LENGTH: 133
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-853-161-75

Query Match      72.5%; Score 219; DB 9; Length 133;
Best Local Similarity 68.6%; Pred. No. 6.2e-19;
Matches 35; Conservative 5; Mismatches 11; Indels 0; Gaps 0;

QY 1 CSMPOEAGPCLASIPHHWYDKKNTCSMFVYGGCGGNNNFQSKANCLNTC 51
Db 77 CEMPKEGTGCLAYFLHWWYDKKNTCSMFVYGGCGGNNNFQSKANCLNTC 127

RESULT 14
US-09-852-659A-75
; Sequence 75, Application US/09852659A
; Patent No. US20020077287A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 28 Human Secreted Proteins
; FILE REFERENCE: PZ003P4
; CURRENT APPLICATION NUMBER: US/09/852,659A
; CURRENT FILING DATE: 2001-05-11
; PRIOR APPLICATION NUMBER: 60/265,583
; PRIOR FILING DATE: 1997-03-14
; PRIOR APPLICATION NUMBER: 60/048,189
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: PCT/US98/04859
; PRIOR FILING DATE: 1998-03-12
; PRIOR FILING DATE: 1997-03-14
; PRIOR APPLICATION NUMBER: 60/040,710
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/050,934
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/048,100
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/048,357
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/048,189
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/057,765
; PRIOR FILING DATE: 1997-09-05
; PRIOR APPLICATION NUMBER: 60/048,970
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/068,368
; PRIOR FILING DATE: 1997-12-19
; NUMBER OF SEQ ID NOS: 121
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 75
; LENGTH: 133
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-852-659A-75

Query Match      72.5%; Score 219; DB 9; Length 133;
Best Local Similarity 68.6%; Pred. No. 6.2e-19;
Matches 35; Conservative 5; Mismatches 11; Indels 0; Gaps 0;

QY 1 CSMPOEAGPCLASIPHHWYDKKNTCSMFVYGGCGGNNNFQTEAICLVTC 51
Db 77 CEMPKEGTGCLAYFLHWWYDKKNTCSMFVYGGCGGNNNFQSKANCLNTC 127

RESULT 14
US-09-852-659A-75
; Sequence 75, Application US/09852659A
; Patent No. US20020077287A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 28 Human Secreted Proteins
; FILE REFERENCE: PZ003P4
; CURRENT APPLICATION NUMBER: US/09/852,659A
; CURRENT FILING DATE: 2001-05-11
; PRIOR APPLICATION NUMBER: 60/265,583
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: 09/152,060
; PRIOR FILING DATE: 1998-09-11
; PRIOR APPLICATION NUMBER: PCT/US98/04859
; PRIOR FILING DATE: 1998-03-12
; PRIOR FILING DATE: 1997-03-14
; PRIOR APPLICATION NUMBER: 60/040,710
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/050,934
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/048,100
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/048,357
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/048,189
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/057,765
; PRIOR FILING DATE: 1997-09-05
; PRIOR APPLICATION NUMBER: 60/048,970
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/068,368
; PRIOR FILING DATE: 1997-12-19
; NUMBER OF SEQ ID NOS: 121
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 75
; LENGTH: 133
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-852-659A-75

Query Match      72.5%; Score 219; DB 9; Length 133;
Best Local Similarity 68.6%; Pred. No. 6.2e-19;
Matches 35; Conservative 5; Mismatches 11; Indels 0; Gaps 0;

QY 1 CSMPOEAGPCLASIPHHWYDKKNTCSMFVYGGCGGNNNFQTEAICLVTC 51
Db 77 CEMPKEGTGCLAYFLHWWYDKKNTCSMFVYGGCGGNNNFQSKANCLNTC 127
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Db 77 CEMPKEGTGCLAYFLHWWYDKKNTCSMFVYGGCGGNNNFQSKANCLNTC 127

RESULT 15
US-09-852-797-75
; Sequence 75, Application US/09852797
; Patent No. US20020172994A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 28 Human Secreted Proteins
; FILE REFERENCE: PZ003P2
; CURRENT APPLICATION NUMBER: US/09/852,797
; CURRENT FILING DATE: 2001-05-11
; PRIOR APPLICATION NUMBER: 60/265,583
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: 09/152,060
; PRIOR FILING DATE: 1998-09-11
; PRIOR APPLICATION NUMBER: PCT/US98/04858
; PRIOR FILING DATE: 1998-03-12
; PRIOR APPLICATION NUMBER: 60/040,762
; PRIOR FILING DATE: 1997-03-14
; PRIOR APPLICATION NUMBER: 60/040,710
; PRIOR FILING DATE: 1997-03-14
; PRIOR APPLICATION NUMBER: 60/050,934
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/048,100
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/048,357
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/048,189
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/057,765
; PRIOR FILING DATE: 1997-09-05
; PRIOR APPLICATION NUMBER: 60/048,970
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/068,368
; PRIOR FILING DATE: 1997-12-19
; NUMBER OF SEQ ID NOS: 118
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 75
; LENGTH: 133
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-852-797-75

Query Match      72.5%; Score 219; DB 9; Length 133;
Best Local Similarity 68.6%; Pred. No. 6.2e-19;
Matches 35; Conservative 5; Mismatches 11; Indels 0; Gaps 0;

QY 1 CSMPOEAGPCLASIPHHWYDKKNTCSMFVYGGCGGNNNFQTEAICLVTC 51
Db 77 CEMPKEGTGCLAYFLHWWYDKKNTCSMFVYGGCGGNNNFQSKANCLNTC 127

RESULT 16
US-10-058-993-75
; Sequence 75, Application US/10058993
; Publication No. US20030225009A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 28 Human Secreted Proteins
; FILE REFERENCE: PZ003P5
; CURRENT APPLICATION NUMBER: US/10/058,993
; CURRENT FILING DATE: 2002-01-30
; PRIOR APPLICATION NUMBER: 09/852,659
; PRIOR FILING DATE: 2001-05-11
; PRIOR APPLICATION NUMBER: 09/852,797
; PRIOR FILING DATE: 2001-05-11
; PRIOR APPLICATION NUMBER: 09/853,161
; PRIOR FILING DATE: 2001-05-11
; PRIOR APPLICATION NUMBER: 60/265,583
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: 09/152,060
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; PRIOR FILING DATE: 1998-09-11
; PRIOR APPLICATION NUMBER: PCT/US98/04858
; PRIOR FILING DATE: 1998-03-12
; PRIOR APPLICATION NUMBER: 60/068,368
; PRIOR FILING DATE: 1997-12-19
; PRIOR APPLICATION NUMBER: 60/057,765
; PRIOR FILING DATE: 1997-09-05
; PRIOR APPLICATION NUMBER: 60/048,970
; PRIOR FILING DATE: 1997-06-05
; PRIOR APPLICATION NUMBER: 60/050,934
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/048,100
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/048,189
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/048,357
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/040,710
; PRIOR FILING DATE: 1997-03-14
; PRIOR APPLICATION NUMBER: 60/040,762
; PRIOR FILING DATE: 1997-03-14
; NUMBER OF SEQ ID NOS: 122
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 75
; LENGTH: 133
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-058-993-75

Query Match 72.5%; Score 219; DB 15; Length 133;
Best Local Similarity 68.6%; Pred. No. 6.2e-19;
Matches 35; Conservative 5; Mismatches 11; Indels 0; Gaps 0;

QY 1 CSMPOEAGPCLASIPHHWYKTKICSEFIYGGCGNNNNFQTEAICLVTC 51
DB 77 CEMPETGCLAYFLHWYDKDNTCSMFYGGCGNNNNFQSKANCLNTC 127

RESULT 17

US-10-807-204-13
; Sequence 13, Application US/10807204
; Publication No. US20040229312A1
; GENERAL INFORMATION:
; APPLICANT: Bougueleret, Lydie
; APPLICANT: Bairoch, Amos
; APPLICANT: Niknejad, Anne
; TITLE OF INVENTION: Engineered Human Kunitz-Type Protease
; TITLE OF INVENTION: Inhibitor
; FILE REFERENCE: 54720-8015.US00
; CURRENT APPLICATION NUMBER: US/10/807,204
; PRIOR FILING DATE: 2004-03-22
; PRIOR APPLICATION NUMBER: PCT/EP03/01629
; PRIOR FILING DATE: 2003-02-18
; PRIOR APPLICATION NUMBER: US 60/358,683
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13
; LENGTH: 133
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-807-204-13

Query Match 72.5%; Score 219; DB 16; Length 133;
Best Local Similarity 68.6%; Pred. No. 6.2e-19;
Matches 35; Conservative 5; Mismatches 11; Indels 0; Gaps 0;

QY 1 CSMPOEAGPCLASIPHHWYKTKICSEFIYGGCGNNNNFQTEAICLVTC 51
DB 77 CEMPETGCLAYFLHWYDKDNTCSMFYGGCGNNNNFQSKANCLNTC 127

RESULT 18

US-10-807-204-14
; Sequence 14, Application US/10807204
; Publication No. US20040229312A1
; GENERAL INFORMATION:
; APPLICANT: Bougueleret, Lydie
; APPLICANT: Bairoch, Amos
; APPLICANT: Niknejad, Anne
; TITLE OF INVENTION: Engineered Human Kunitz-Type Protease
; TITLE OF INVENTION: Inhibitor
; FILE REFERENCE: 54720-8015.US00
; CURRENT APPLICATION NUMBER: US/10/807,204
; PRIOR FILING DATE: 2004-03-22
; PRIOR APPLICATION NUMBER: PCT/EP03/01629
; PRIOR FILING DATE: 2003-02-18
; PRIOR APPLICATION NUMBER: US 60/358,683
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14
; LENGTH: 134
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-807-204-14

Query Match 62.3%; Score 188; DB 16; Length 134;
Best Local Similarity 54.9%; Pred. No. 4e-15;
Matches 28; Conservative 10; Mismatches 13; Indels 0; Gaps 0;

QY 1 CSMPOEAGPCLASIPHHWYKTKICSEFIYGGCGNNNNFQTEAICLVTC 51
DB 77 CSLPKDGYCWAYFRWFWNKENSTCQVFIYGGCGNNNNFQSQICQVAC 127

RESULT 19

US-10-369-736-3
; Sequence 3, Application US/10369736
; Publication No. US20030162714A1
; GENERAL INFORMATION:
; APPLICANT: HILL, JENNIFER J.
; APPLICANT: WOLFMAN, NEIL M.
; TITLE OF INVENTION: FOLLISTATIN DOMAIN CONTAINING PROTEINS
; FILE REFERENCE: 08702.0015-00
; CURRENT APPLICATION NUMBER: US/10/369,736
; PRIOR FILING DATE: 2003-02-21
; PRIOR APPLICATION NUMBER: 60/357,846
; PRIOR FILING DATE: 2002-02-21
; PRIOR APPLICATION NUMBER: 60/434,645
; PRIOR FILING DATE: 2002-12-20
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 571
; TYPE: PRT
; ORGANISM: Mus sp.
US-10-369-736-3

Query Match 56.0%; Score 169; DB 14; Length 571;
Best Local Similarity 49.0%; Pred. No. 3.6e-12;
Matches 25; Conservative 9; Mismatches 17; Indels 0; Gaps 0;

QY 1 CSMPOEAGPCLASIPHHWYKTKICSEFIYGGCGNNNNFQTEAICLVTC 51
DB 381 CSLPALQGPCKAYVPRWAYNSQTGLCQSFVYGGCGNGNPFESRACESC 431

RESULT 20

US-10-369-736-49
; Sequence 49, Application US/10369736
; Publication No. US20030162714A1
; GENERAL INFORMATION:
; APPLICANT: HILL, JENNIFER J.
; APPLICANT: WOLFMAN, NEIL M.
; TITLE OF INVENTION: FOLLISTATIN DOMAIN CONTAINING PROTEINS


```
; LENGTH: 58
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Consensus Kunitz domain
US-10-038-722-5

Query Match      55.3%; Score 167; DB 14; Length 58;
Best Local Similarity 56.9%; Pred. No. 6.9e-13;
Matches 29; Conservative 5; Mismatches 17; Indels 0; Gaps 0;

Qy 1 CSMQEAGPCLASIPHHWYNNKTKICSEFIYGGCGGNNNNFQTEAICLVTC 51
    |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 5 CULPAETGFCRAMIPRFYNNAKSGKEPFIYGGCGGNNNNFTEECRTTC 55

RESULT 29
US-09-896-095-147
; Sequence 147, Application US/09896095
; Publication No. US20030219886A1
; GENERAL INFORMATION:
; APPLICANT: LADNER, Charles C.
; APPLICANT: GUTERMAN, Sonia K.
; APPLICANT: ROBERTS, Bruce L.
; APPLICANT: MARKLAND, William
; APPLICANT: LEY, Arthur C.
; APPLICANT: KENT, Rachel B.
; TITLE OF INVENTION: DIRECTED EVOLUTION OF NOVEL BINDING PROTEINS
; FILE REFERENCE: LADNER-7L
; CURRENT APPLICATION NUMBER: US/09/896,095
; CURRENT FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: 08/415,922
; PRIOR FILING DATE: 1995-03-04
; PRIOR APPLICATION NUMBER: 08/009,319
; PRIOR FILING DATE: 1993-01-26
; PRIOR APPLICATION NUMBER: 07/664,989
; PRIOR FILING DATE: 1991-03-01
; PRIOR APPLICATION NUMBER: 08/993,776
; PRIOR FILING DATE: 1997-12-18
; NUMBER OF SEQ ID NOS: 274
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 147
; LENGTH: 67
; TYPE: PRT
; ORGANISM: Bos taurus
US-09-896-095-147

Query Match      55.0%; Score 166; DB 10; Length 67;
Best Local Similarity 51.0%; Pred. No. 1e-12;
Matches 26; Conservative 8; Mismatches 17; Indels 0; Gaps 0;

Qy 1 CSMQEAGPCLASIPHHWYNNKTKICSEFIYGGCGGNNNNFQTEAICLVTC 51
    |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 8 CQLPARGPCKAALLRYFYNSTSNACEPFTYGGCGGNNNNFETTEMCLRIC 58

RESULT 30
US-10-038-722-90
; Sequence 90, Application US/10038722
; Publication No. US2003017591A1
; GENERAL INFORMATION:
; APPLICANT: LEY, Arthur C.
; APPLICANT: GUTERMAN, Sonia K.
; APPLICANT: MARKLAND, William
; APPLICANT: KENT, Rachel B.
; APPLICANT: ROBERTS, Bruce L.
; APPLICANT: LADNER, Robert C.
; TITLE OF INVENTION: ITI-D1 KUNITZ DOMAIN MUTANTS AS THE INHIBITORS
; FILE REFERENCE: LEY-1B
; CURRENT APPLICATION NUMBER: US/10/038,722
; CURRENT FILING DATE: 2002-01-08
; PRIOR APPLICATION NUMBER: US 08/849,406
; PRIOR FILING DATE: 1999-07-21
```

```
; PRIOR APPLICATION NUMBER: PCT/US95/16349
; PRIOR FILING DATE: 1995-12-15
; PRIOR APPLICATION NUMBER: US 08/358,160
; PRIOR FILING DATE: 1994-12-16
; NUMBER OF SEQ ID NOS: 129
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 90
; LENGTH: 67
; TYPE: PRT
; ORGANISM: Bos taurus
US-10-038-722-90

Query Match      55.0%; Score 166; DB 14; Length 67;
Best Local Similarity 51.0%; Pred. No. 1e-12;
Matches 26; Conservative 8; Mismatches 17; Indels 0; Gaps 0;

Qy 1 CSMQEAGPCLASIPHHWYNNKTKICSEFIYGGCGGNNNNFQTEAICLVTC 51
    |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 8 CQLPARGPCKAALLRYFYNSTSNACEPFTYGGCGGNNNNFETTEMCLRIC 58

RESULT 31
US-10-115-134-4
; Sequence 4, Application US/10115134
; Publication No. US20030223977A1
; GENERAL INFORMATION:
; APPLICANT: LEY, Arthur Charles
; APPLICANT: GUTERMAN, Sonia Kosow
; APPLICANT: MARKLAND, William
; APPLICANT: KENT, Rachel Baribault
; APPLICANT: ROBERTS, Bruce Lindsey
; APPLICANT: LADNER, Robert Charles
; TITLE OF INVENTION: DOMAIN MUTANTS AS CATHEPSIN G INHIBITORS
; FILE REFERENCE: LEY-1C
; CURRENT APPLICATION NUMBER: US/10/115,134
; CURRENT FILING DATE: 2002-04-04
; PRIOR APPLICATION NUMBER: 08/849,406
; PRIOR FILING DATE: 2001-07-21
; NUMBER OF SEQ ID NOS: 92
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 4
; LENGTH: 67
; TYPE: PRT
; ORGANISM: Bos taurus
US-10-115-134-4

Query Match      55.0%; Score 166; DB 15; Length 67;
Best Local Similarity 51.0%; Pred. No. 1e-12;
Matches 26; Conservative 8; Mismatches 17; Indels 0; Gaps 0;

Qy 1 CSMQEAGPCLASIPHHWYNNKTKICSEFIYGGCGGNNNNFQTEAICLVTC 51
    |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 8 CQLPARGPCKAALLRYFYNSTSNACEPFTYGGCGGNNNNFETTEMCLRIC 58

RESULT 32
US-09-910-430-8
; Sequence 8, Application US/09910430
; Patent No. US20020127235A1
; GENERAL INFORMATION:
; APPLICANT: Godfroi, Edmond
; APPLICANT: Bollen, Alex
; APPLICANT: Leboulle, Gerard
; TITLE OF INVENTION: IDENTIFICATION AND MOLECULAR CHARACTERIZATION OF
; TITLE OF INVENTION: PROTEINS, EXPRESSED IN THE IXODES RICINUS SALIVARY
; TITLE OF INVENTION: GLANDS
; FILE REFERENCE: VANM229.001CP1
; CURRENT APPLICATION NUMBER: US/09/910,430
; CURRENT FILING DATE: 2001-07-19
; PRIOR APPLICATION NUMBER: PCT/BE00/00061
; PRIOR FILING DATE: 2000-06-06
; PRIOR APPLICATION NUMBER: GB 9913425.6
; PRIOR FILING DATE: 1999-06-09
```



```
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 8
; LENGTH: 86
; TYPE: PRT
; ORGANISM: Ixodes ricinus
US-09-910-430-8

Query Match      55.0%; Score 166; DB 9; Length 86;
Best Local Similarity 49.0%; Pred. No. 1.3e-12;
Matches 25; Conservative 10; Mismatches 16; Indels 0; Gaps 0;

QY 1 CSMPQAGPCLASIPHWYNNKTKICSEFYGGCGQNNNNFQTEAICLVTC 51
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 31 CKLPDDGPCRARIPSYFDRKTKCKEPMYGGCEGNNNNFENITTCQEC 81

RESULT 33
US-10-165-605A-8
; Sequence 8, Application US/10165605A
; Publication No. US20030086937A1
; GENERAL INFORMATION:
; APPLICANT: Godfroid, Edmond
; APPLICANT: Bollen, Alex
; APPLICANT: Lebouille, Gerard
; TITLE OF INVENTION: IDENTIFICATION AND MOLECULAR CHARACTERIZATION OF
; TITLE OF INVENTION: PROTEINS, EXPRESSED IN THE IXODES RICINUS SALIVARY
; TITLE OF INVENTION: GLANDS
; FILE REFERENCE: VANW229.001CP2
; CURRENT APPLICATION NUMBER: US/10/165,605A
; CURRENT FILING DATE: 2002-06-07
; PRIOR APPLICATION NUMBER: 09/910,430
; PRIOR FILING DATE: 2001-07-19
; PRIOR APPLICATION NUMBER: PCT/BE00/00061
; PRIOR FILING DATE: 2000-06-06
; PRIOR APPLICATION NUMBER: GB9913425.6
; PRIOR FILING DATE: 1999-06-09
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 8
; LENGTH: 86
; TYPE: PRT
; ORGANISM: Ixodes ricinus
US-10-165-605A-8

Query Match      55.0%; Score 166; DB 14; Length 86;
Best Local Similarity 49.0%; Pred. No. 1.3e-12;
Matches 25; Conservative 10; Mismatches 16; Indels 0; Gaps 0;

QY 1 CSMPQAGPCLASIPHWYNNKTKICSEFYGGCGQNNNNFQTEAICLVTC 51
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 31 CKLPDDGPCRARIPSYFDRKTKCKEPMYGGCEGNNNNFENITTCQEC 81

RESULT 34
US-10-038-722-17
; Sequence 17, Application US/10038722
; Publication No. US20030175919A1
; GENERAL INFORMATION:
; APPLICANT: LEY, Arthur C.
; APPLICANT: GUTERMAN, Sonia K.
; APPLICANT: MARKLAND, William
; APPLICANT: KENT, Rachel B.
; APPLICANT: ROBERTS, Bruce L.
; APPLICANT: LADNER, Robert C.
; TITLE OF INVENTION: ITI-D1 KUNITZ DOMAIN MUTANTS AS rHE INHIBITORS
; FILE REFERENCE: LEY=18
; CURRENT APPLICATION NUMBER: US/10/038,722
; CURRENT FILING DATE: 2002-01-08
; PRIOR APPLICATION NUMBER: US 08/849,406
; PRIOR FILING DATE: 1999-07-21
; PRIOR APPLICATION NUMBER: PCT/US95/16349
; PRIOR FILING DATE: 1995-12-15
; NUMBER OF SEQ ID NOS: 129
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 18
; LENGTH: 58
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: MUTT26A
US-10-038-722-18

Query Match      53.3%; Score 161; DB 14; Length 58;
Best Local Similarity 51.0%; Pred. No. 3.7e-12;
Matches 26; Conservative 6; Mismatches 19; Indels 0; Gaps 0;

QY 1 CSMPQAGPCLASIPHWYNNKTKICSBFIYGGCGQNNNNFQTEAICLVTC 51
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 5 CQLGYSAGPCVAMFPFYNGTSMACQTFYGGCMGNGNNFVTEKDCLOTC 55

RESULT 35
US-10-038-722-18
; Sequence 18, Application US/10038722
; Publication No. US20030175919A1
; GENERAL INFORMATION:
; APPLICANT: LEY, Arthur C.
; APPLICANT: GUTERMAN, Sonia K.
; APPLICANT: MARKLAND, William
; APPLICANT: KENT, Rachel B.
; APPLICANT: ROBERTS, Bruce L.
; APPLICANT: LADNER, Robert C.
; TITLE OF INVENTION: ITI-D1 KUNITZ DOMAIN MUTANTS AS rHE INHIBITORS
; FILE REFERENCE: LEY=18
; CURRENT APPLICATION NUMBER: US/10/038,722
; CURRENT FILING DATE: 2002-01-08
; PRIOR APPLICATION NUMBER: US 08/849,406
; PRIOR FILING DATE: 1999-07-21
; PRIOR APPLICATION NUMBER: PCT/US95/16349
; PRIOR FILING DATE: 1995-12-15
; PRIOR APPLICATION NUMBER: US 08/358,160
; PRIOR FILING DATE: 1994-12-16
; NUMBER OF SEQ ID NOS: 129
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 18
; LENGTH: 58
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: MUTT26A
US-10-038-722-18

Query Match      53.3%; Score 161; DB 14; Length 58;
Best Local Similarity 51.0%; Pred. No. 3.7e-12;
Matches 26; Conservative 6; Mismatches 19; Indels 0; Gaps 0;

QY 1 CSMPQAGPCLASIPHWYNNKTKICSBFIYGGCGQNNNNFQTEAICLVTC 51
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 5 CQLGYSAGPCVAMFPFYNGTSMACQTFYGGCMGNGNNFVTEKDCLOTC 55

RESULT 36
US-10-038-722-19
; Sequence 19, Application US/10038722
; Publication No. US20030175919A1
; GENERAL INFORMATION:
; APPLICANT: LEY, Arthur C.
; APPLICANT: GUTERMAN, Sonia K.
; APPLICANT: MARKLAND, William
; APPLICANT: KENT, Rachel B.
; APPLICANT: ROBERTS, Bruce L.
; APPLICANT: LADNER, Robert C.
; TITLE OF INVENTION: ITI-D1 KUNITZ DOMAIN MUTANTS AS rHE INHIBITORS
; FILE REFERENCE: LEY=18
; CURRENT APPLICATION NUMBER: US/10/038,722
; CURRENT FILING DATE: 2002-01-08
; PRIOR APPLICATION NUMBER: US 08/849,406
; PRIOR FILING DATE: 1999-07-21
; PRIOR APPLICATION NUMBER: PCT/US95/16349
; PRIOR FILING DATE: 1995-12-15
```



```
; FILE REFERENCE: 3421.1001-002
; CURRENT APPLICATION NUMBER: US/10/456,986A
; PRIOR FILING DATE: 2003-06-06
; PRIOR APPLICATION NUMBER: 60/387,239
; PRIOR FILING DATE: 2002-06-07
; PRIOR APPLICATION NUMBER: 60/407,003
; PRIOR FILING DATE: 2002-08-28
; NUMBER OF SEQ ID NOS: 54
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 42
; LENGTH: 58
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: BIT1-E7-141 Sequence
US-10-456-986A-42

Query Match      53.3%; Score 161; DB 15; Length 58;
Best Local Similarity 51.0%; Pred. No. 3.7e-12;
Matches 26; Conservative 6; Mismatches 19; Indels 0; Gaps 0;

QY 1 CSMPOAGPCLASIPHHWYKTKICSEFIYGGCGGNNNFQTEAICLVTC 51
   : |||||: : : : : : : : : : : : : : : : : : : : :
Db 5 COLGYSAGPCVAMFPFRFYNGTSMACQTFVYGGCMGNGNNFVTEKDCLOTC 55

RESULT 41
US-10-456-986A-43
; Sequence 43, Application US/10456986A
; Publication No. US20040038893A1
; GENERAL INFORMATION:
; APPLICANT: Ladner, Robert C.
; APPLICANT: Ley, Arthur C.
; APPLICANT: Hirani, Shirish
; APPLICANT: Williams, Anthony
; TITLE OF INVENTION: Prevention and Reduction of Blood Loss
; FILE REFERENCE: 3421.1001-002
; CURRENT APPLICATION NUMBER: US/10/456,986A
; CURRENT FILING DATE: 2003-06-06
; PRIOR APPLICATION NUMBER: 60/387,239
; PRIOR FILING DATE: 2002-06-07
; PRIOR APPLICATION NUMBER: 60/407,003
; PRIOR FILING DATE: 2002-08-28
; NUMBER OF SEQ ID NOS: 54
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 43
; LENGTH: 58
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: MUTT26A Sequence
US-10-456-986A-43

Query Match      53.3%; Score 161; DB 15; Length 58;
Best Local Similarity 51.0%; Pred. No. 3.7e-12;
Matches 26; Conservative 6; Mismatches 19; Indels 0; Gaps 0;

QY 1 CSMPOAGPCLASIPHHWYKTKICSEFIYGGCGGNNNFQTEAICLVTC 51
   : |||||: : : : : : : : : : : : : : : : : : : : :
Db 5 COLGYSAGPCVAMFPFRFYNGTSMACQTFVYGGCMGNGNNFVTEKDCLOTC 55

RESULT 42
US-10-456-986A-44
; Sequence 44, Application US/10456986A
; Publication No. US20040038893A1
; GENERAL INFORMATION:
; APPLICANT: Ladner, Robert C.
; APPLICANT: Ley, Arthur C.
; APPLICANT: Hirani, Shirish
; APPLICANT: Williams, Anthony
; TITLE OF INVENTION: Prevention and Reduction of Blood Loss
; FILE REFERENCE: 3421.1001-002
```

```
; CURRENT APPLICATION NUMBER: US/10/456,986A
; CURRENT FILING DATE: 2003-06-06
; PRIOR APPLICATION NUMBER: 60/387,239
; PRIOR FILING DATE: 2002-06-07
; PRIOR APPLICATION NUMBER: 60/407,003
; PRIOR FILING DATE: 2002-08-28
; NUMBER OF SEQ ID NOS: 54
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 44
; LENGTH: 58
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: MUTQE Sequence
US-10-456-986A-44

Query Match      53.3%; Score 161; DB 15; Length 58;
Best Local Similarity 51.0%; Pred. No. 3.7e-12;
Matches 26; Conservative 6; Mismatches 19; Indels 0; Gaps 0;

QY 1 CSMPOAGPCLASIPHHWYKTKICSEFIYGGCGGNNNFQTEAICLVTC 51
   : |||||: : : : : : : : : : : : : : : : : : : : :
Db 5 COLGYSAGPCVAMFPFRFYNGTSMACQTFVYGGCMGNGNNFVTEKDCLOTC 55

RESULT 43
US-10-953-902A-42
; Sequence 42, Application US/10953902A
; Publication No. US20050164928A1
; GENERAL INFORMATION:
; APPLICANT: Ladner, Robert C.
; APPLICANT: Ley, Arthur C.
; APPLICANT: Hirani, Shirish
; APPLICANT: Williams, Anthony
; APPLICANT: De Simoni, Maria Garzia
; APPLICANT: Bergamaschini, Luigi
; TITLE OF INVENTION: KALLIKREIN-INHIBITOR THERAPIES
; FILE REFERENCE: 10280-120001
; CURRENT APPLICATION NUMBER: US/10/953,902A
; CURRENT FILING DATE: 2004-09-27
; PRIOR APPLICATION NUMBER: US 60/387,239
; PRIOR FILING DATE: 2002-06-07
; PRIOR APPLICATION NUMBER: US 60/407,003
; PRIOR FILING DATE: 2002-08-28
; PRIOR APPLICATION NUMBER: US 10/456,986
; PRIOR FILING DATE: 2003-06-06
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 42
; LENGTH: 58
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetically generated peptide
US-10-953-902A-42

Query Match      53.3%; Score 161; DB 18; Length 58;
Best Local Similarity 51.0%; Pred. No. 3.7e-12;
Matches 26; Conservative 6; Mismatches 19; Indels 0; Gaps 0;

QY 1 CSMPOAGPCLASIPHHWYKTKICSEFIYGGCGGNNNFQTEAICLVTC 51
   : |||||: : : : : : : : : : : : : : : : : : : : :
Db 5 COLGYSAGPCVAMFPFRFYNGTSMACQTFVYGGCMGNGNNFVTEKDCLOTC 55

RESULT 44
US-10-953-902A-43
; Sequence 43, Application US/10953902A
; Publication No. US20050164928A1
; GENERAL INFORMATION:
; APPLICANT: Ladner, Robert C.
; APPLICANT: Ley, Arthur C.
; APPLICANT: Hirani, Shirish
```

```
; APPLICANT: Williams, Anthony
; APPLICANT: De Simoni, Maria Garzia
; APPLICANT: Bergamaschini, Luigi
; TITLE OF INVENTION: KALLIKREIN-INHIBITOR THERAPIES
; FILE REFERENCE: 10280-120001
; CURRENT APPLICATION NUMBER: US/10/953,902A
; CURRENT FILING DATE: 2004-09-27
; PRIOR APPLICATION NUMBER: US 60/387,239
; PRIOR FILING DATE: 2002-06-07
; PRIOR APPLICATION NUMBER: US 60/407,003
; PRIOR FILING DATE: 2002-08-28
; PRIOR APPLICATION NUMBER: US 10/456,986
; PRIOR FILING DATE: 2003-06-06
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 43
; LENGTH: 58
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetically generated peptide
US-10-953-902A-43

Query Match          53.3%; Score 161; DB 18; Length 58;
Best Local Similarity 51.0%; Pred. No. 3.7e-12;
Matches 26; Conservative 6; Mismatches 19; Indels 0; Gaps 0;

QY 1 CSMQEAGPCLASIPHHWYNNKTKICSEFIYGGCGNNNNFQTEAICLVTC 51
   : ||||| : : : : : : : : : : : : : : : : : : : : : :
Db 5 CQLGYSAGPCVAMPFRPYFYNGASMACQTFVYGGCMGNGNFTVKDCLQTC 55
```

```
RESULT 45
US-10-953-902A-44
; Sequence 44, Application US/10953902A
; Publication No. US20050164928A1
; GENERAL INFORMATION:
; APPLICANT: Ladner, Robert C.
; APPLICANT: Ley, Arthur C.
; APPLICANT: Hirani, Shirish
; APPLICANT: Williams, Anthony
; APPLICANT: De Simoni, Maria Garzia
; APPLICANT: Bergamaschini, Luigi
; TITLE OF INVENTION: KALLIKREIN-INHIBITOR THERAPIES
; FILE REFERENCE: 10280-120001
; CURRENT APPLICATION NUMBER: US/10/953,902A
; CURRENT FILING DATE: 2004-09-27
; PRIOR APPLICATION NUMBER: US 60/387,239
; PRIOR FILING DATE: 2002-06-07
; PRIOR APPLICATION NUMBER: US 60/407,003
; PRIOR FILING DATE: 2002-08-28
; PRIOR APPLICATION NUMBER: US 10/456,986
; PRIOR FILING DATE: 2003-06-06
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 44
; LENGTH: 58
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetically generated peptide
US-10-953-902A-44

Query Match          53.3%; Score 161; DB 18; Length 58;
Best Local Similarity 51.0%; Pred. No. 3.7e-12;
Matches 26; Conservative 6; Mismatches 19; Indels 0; Gaps 0;

QY 1 CSMQEAGPCLASIPHHWYNNKTKICSEFIYGGCGNNNNFQTEAICLVTC 51
   : ||||| : : : : : : : : : : : : : : : : : : : : : :
Db 5 CQLGYSAGPCVAMPFRPYFYNGTSMACETTFVYGGCMGNGNFTVKDCLQTC 55
```

RESULT 46

```
US-10-007-280A-233
; Sequence 233, Application US/10007280A
; Publication No. US20030059784A1
; GENERAL INFORMATION:
; APPLICANT: Sun, Yongming
; APPLICANT: Recipon, Herve
; APPLICANT: Salceda, Susana
; APPLICANT: Chenghua, Liu
; TITLE OF INVENTION: Compositions and Methods Relating to Ovary Specific Genes and Pro
; FILE REFERENCE: DEX-0257
; CURRENT APPLICATION NUMBER: US/10/007,280A
; CURRENT FILING DATE: 2001-11-07
; PRIOR APPLICATION NUMBER: US 60/246,640
; PRIOR FILING DATE: 2000-11-08
; NUMBER OF SEQ ID NOS: 238
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 233
; LENGTH: 503
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-007-280A-233

Query Match          53.0%; Score 160; DB 14; Length 503;
Best Local Similarity 49.0%; Pred. No. 4e-11;
Matches 25; Conservative 7; Mismatches 19; Indels 0; Gaps 0;

QY 1 CSMQEAGPCLASIPHHWYNNKTKICSEFIYGGCGNNNNFQTEAICLVTC 51
   : ||||| : : : : : : : : : : : : : : : : : : : : : :
Db 317 CSLPALQGPCKAYAPRWAYNSQTGCQSFVYGGCEGNGNPFESREACEESC 367
```

```
RESULT 47
US-09-794-589-2
; Sequence 2, Application US/09794589
; Patent No. US20020004224A1
; GENERAL INFORMATION:
; APPLICANT: Sheppard, Paul O.
; TITLE OF INVENTION: KUNITZ DOMAIN POLYPEPTIDE ZKUN8
; FILE REFERENCE: 00-01
; CURRENT APPLICATION NUMBER: US/09/794,589
; CURRENT FILING DATE: 2001-02-27
; PRIOR APPLICATION NUMBER: US 60/186,069
; PRIOR FILING DATE: 2000-02-29
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 576
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-794-589-2

Query Match          53.0%; Score 160; DB 9; Length 576;
Best Local Similarity 49.0%; Pred. No. 4.6e-11;
Matches 25; Conservative 7; Mismatches 19; Indels 0; Gaps 0;

QY 1 CSMQEAGPCLASIPHHWYNNKTKICSEFIYGGCGNNNNFQTEAICLVTC 51
   : ||||| : : : : : : : : : : : : : : : : : : : : : :
Db 386 CSLPALQGPCKAYAPRWAYNSQTGCQSFVYGGCEGNGNPFESREACEESC 436
```

```
RESULT 48
US-10-315-380-2
; Sequence 2, Application US/10315380
; Publication No. US20030129577A1
; GENERAL INFORMATION:
; APPLICANT: Sheppard, Paul O.
; TITLE OF INVENTION: KUNITZ DOMAIN POLYPEPTIDE ZKUN8
; FILE REFERENCE: 00-01
; CURRENT APPLICATION NUMBER: US/10/315,380
; CURRENT FILING DATE: 2002-12-09
; PRIOR APPLICATION NUMBER: US/09/794,589
; PRIOR FILING DATE: 2001-02-27
; PRIOR APPLICATION NUMBER: US 60/186,069
```

```

: PRIOR FILING DATE: 2000-02-29
:
: NUMBER OF SEQ ID NOS: 7
:
: SOFTWARE: FastSEQ for Windows Version 3.0
:
: SEQ ID NO 2
:
: LENGTH: 576
:
: TYPE: PRT
:
: ORGANISM: Homo sapiens
:
: US-10-315-380-2

```

```

Query Match      53.0%; Score 160; DB 14; Length 576;
Best Local Similarity 49.0%; Pred.No. 4.6e-11;
Matches 25; Conservative 7; Mismatches 19; Indels 0; Gaps 0;

QY    1 CSMPOEAGPCLASIPHHWYNKTKICISFEIYGCGGNNNPNQTAEILVTC 51
       |||..|||..|||..|||..|||..|||..|||..|||..|||..|||..
db     CSIPALGGPCKAVAPRAYNSOTCCOSEFYVGCGEGNNPFSEACAECS 436

```

```

RESULT 49
US-10-369-736-7
; Sequence 7, Application US/10369736
; Publication No. US20030162714A1
; GENERAL INFORMATION:
; APPLICANT: HILL, JENNIFER J.
; APPLICANT: WOLFMAN, NEIL M.
; TITLE OF INVENTION: FOLLISTATIN DOMAIN CONTAINING PROTEINS
; FILE REFERENCE: 08702.0015-00
; CURRENT APPLICATION NUMBER: US/10/369,736
; CURRENT FILING DATE: 2003-02-21
; PRIOR APPLICATION NUMBER: 60/357,846
; PRIOR FILING DATE: 2002-02-21
; PRIOR APPLICATION NUMBER: 60/434,645
; PRIOR FILING DATE: 2002-12-20
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
; LENGTH: 576
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-369-736-7

```

Query Match	53.0%	Score 160;	DB 14;	Length 576;
Best Local Similarity	49.0%;	Ref. No. 4.6e-11;		
Matches 25;	Conservative 7;	Mismatches 19;	Indels 0;	Gaps 0;
Qy	1	CSMPQEAQPCILASIPHHWYNNKTKIKICSEFIYGGCGNNNNFQTEAICLVTC	51	
Dh	186	CSLPALQCGCKAYAPRWYNSOTGCGOSFVYGGCGEAGNNVFESREACBSC	436	

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RESULT 50
US-10-369-738-7
; Sequence 7, Application US/10369738
; Publication No. US20030180306A1
; GENERAL INFORMATION:
; APPLICANT: HILL, JENNIFER J.
; APPLICANT: WOLFMAN, NEIL M.
; TITLE OF INVENTION: FOLLISTATIN DOMAIN CONTAINING PROTEINS
; FILE REFERENCE: 08702.0014-00
; CURRENT APPLICATION NUMBER: US/10/369,738
; CURRENT FILING DATE: 2003-02-21
; PRIOR APPLICATION NUMBER: 60/357,846
; PRIOR FILING DATE: 2002-02-21
; PRIOR APPLICATION NUMBER: 60/434,645
; PRIOR FILING DATE: 2002-12-20
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
; LENGTH: 576
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-369-738-7

```

Query Match 53.0%; Score 160; DB 14; Length 576;
Best Local Similarity 49.0%; Pred. No. 4.6e-11;
Matches 25; Conservative 7; Mismatches 19; Indels 0;

[illegible]

Search completed: September 21, 2005, 16:45:54
Job time : 32.8938 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: September 21, 2005, 16:21:48 ; Search time 7.37168 Seconds
(without alignments)
665.663 Million cell updates/sec

Title: US-10-807-204-2_COPY_52_102
Perfect score: 302
Sequence: 1 CSMPOEAGPCLASIPHHWYN.....GGCQGNNNFQTEAICLVTC 51

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 50 summaries

Database : PIR 79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	ID	Description
1	170	56.3	110	1 TITRGC	basic proteinase i
2	163	54.0	67	1 TIBOC	trypsin inhibitor,
3	160	53.0	252	2 JG0185	hepatocyte growth
4	158	52.3	62	2 A44180	taicatoxin serine
5	154	51.0	747	2 JH0773	Alzheimer's disease
6	153	50.7	58	1 TIHABK	isolectin B4 (BP
7	153	50.7	62	2 S19327	venom basic protei
8	152	50.3	62	2 S07451	proteinase inhibit
9	152	50.3	922	2 T23573	hypothetical prote
10	149	49.3	57	2 A59204	basic proteinase i
11	148	49.0	65	1 TIVTVC	venom basic protei
12	147	48.7	76	2 S06678	Alzheimer's disease
13	147	48.7	76	2 S03607	Alzheimer's disease
14	147	48.7	484	4 A32761	hypothetical Alzhe
15	147	48.7	770	1 QRHUA4	Alzheimer's disease
16	146	48.3	111	2 S41082	amyloid precursor
17	146	48.3	751	2 A49374	beta-amyloid precu
18	146	48.3	763	2 A49321	amyloid beta (A4)
19	146	48.3	765	2 S42880	amyloid precursor-
20	145	48.0	57	1 TIFHBP	proteinase inhibit
21	145	48.0	122	1 A55115	uterine plasmin/tr
22	145	48.0	1599	2 T6210	hypothetical prote
23	144	47.7	62	2 S01802	chymotrypsin inhib
24	144	47.7	76	2 S04855	Alzheimer's disease
25	144	47.7	100	2 A32282	Alzheimer's disease
26	143	47.4	57	2 B59399	short epsilon-dendr
27	143	47.4	59	1 TIEFED	venom basic protei
28	143	47.4	59	2 A59399	long epsilon-dendr
29	143	47.4	62	2 S01803	chymotrypsin inhib

30	143	47.4	302	1 TITRGC	tissue factor path
31	143	47.4	352	1 HCHU	alpha-1-microglobu
32	143	47.4	372	2 JC2556	alpha-1-microglobu
33	142	47.0	61	1 TIVITI	venom basic protei
34	142	47.0	337	1 TIPGBI	alpha-1-microglobu
35	142	47.0	352	1 TIBOBI	alpha-1-microglobu
36	141	46.7	1522	2 H88380	protein T22F7.3 (i
37	140	46.4	123	2 A39652	inter-alpha-trypsi
38	140	46.4	1558	2 C89114	protein C3/C3.6a (
39	140	46.4	2167	2 T34395	hypothetical prote
40	138	45.7	61	1 TIHCBP	proteinase inhibit
41	138	45.7	125	1 TIHOBI	alpha-1-microglobu
42	138	45.7	265	2 A53390	Kunitz-type protei
43	137	45.4	235	2 A54951	tissue factor path
44	136	45.0	100	1 TIBO	basic proteinase i
45	136	45.0	805	2 T34212	hypothetical prote
46	135	44.7	1743	2 T26859	hypothetical prote
47	134	44.4	59	2 S00371	isoaprotinin G1 -
48	134	44.4	60	1 TIBOR	serum basic protei
49	134	44.4	1474	2 D88550	protein ZC84.6 (im
50	134	44.4	2844	2 S28291	hypothetical prote

ALIGNMENTS

RESULT 1

TITR

basic proteinase inhibitor - loggerhead

C:Species: Caretta caretta (loggerhead)

C>Date: 31-May-1979 #sequence_revision 23-Oct-1981 #text_change 09-Jul-2004

C:Accession: A01224

R:Kato, I.; Tominaga, N.

Fed. Proc. 38, 832, 1979

A:Title: Trypsin-subtilisin inhibitor from red sea turtle eggwhite consists of two tan

A:Reference number: A01224

A:Accession: A01224

A:Molecule type: protein

A:Residues: 1-110 <KAT>

A:Cross-references: UNIPROT:P00993

C:Comment: This inhibitor, isolated from egg white, consists of two nonhomologous domain

C:Superfamily: loggerhead basic proteinase inhibitor; animal Kunitz-type proteinase inh

C:Keywords: pyroglutamic acid; serine proteinase inhibitor

F:8-58/Domain: animal Kunitz-type proteinase inhibitor homology <BPI>

F:63-105/Domain: antileukoprotease repeat homology <ALP>

F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

F:8-58,17-41,33-54,67-93,76-97,80-92,86-101/Diaulfide bonds: #status predicted

F:18/inhibitory site: Lys (trypsin) #status predicted

Query Match 56.3%; Score 170; DB 1; Length 110;

Best Local Similarity 51.0%; Pred. No. 28-13;

Matches 26; Conservative 10; Mismatches 15; Indels 0; Gaps 0;

QY 1 CSMPOEAGPCLASIPHHWYNNKTKICSBEPIYGGCGGNNNFQTEAICLVTC 51

DB 8 CRLPPEQGCKGRIPRYFYNPASRMCESEFIYGGCKGNKNFNKTKAECVRC 58

RESULT 2

TIBOC

trypsin inhibitor, colostrum (BPI type) - bovine

C:Species: Bos primigenius taurus (cattle)

C>Date: 24-Apr-1984 #sequence_revision 31-Dec-1993 #text_change 09-Jul-2004

C:Accession: A01207

R:Cechova, D.; Jonakova, V.; Sorm, F.

Collect. Czech. Chem. Commun 36, 3342-3357, 1971

A:Title: Primary structure of trypsin inhibitor from cow colostrum (component B2).

A:Reference number: A09028

A:Accession: A01207

A:Molecule type: protein

A:Residues: 1-26,'B',28-67 <CEC>

A:Cross-references: UNIPROT:P00976

A:Note: the residue identified as Asx is bound to carbohydrate; therefore, we have show

```

Query Match          52.3%; Score 158; DB 2; Length 62;
Best Local Similarity 51.0%; Pred.No. 3.2e-12;
Matches      26; Conservative    8; Mismatches     17; Indels       0; Gaps        0;

QY   1 CSMQBAGPCLASIPHWYNKTKIGSEFTYGCGGNGNNNFQEAICLVTC 51
      :|::|||::|::|::|::|::|::|::|::|::|::|::|::|::|
Db    7 CHLPPFGPCRAIRPFVFNPHSKQEKEFYGGCHGNANKFKTPDECNYTC 57
      ||::|||::|::|::|::|::|::|::|::|::|::|::|::|::|

RESULT 5
JH0773
Alzheimer's disease amyloid beta protein precursor - African clawed frog
C:Species: Xenopus laevis (African clawed frog)
C>Date: 10-Jun-1993 #sequence_revision 10-Jun-1993 #text_change 13-Aug-1999
C:Accession: JH0773
R:Okado, H.; Okamoto, H. Biochem. Biophys. Res. Commun. 189, 1561-1568, 1992
A:Title: A Xenopus homologue of the human beta-amyloid precursor protein: developmentally regulated expression of the cDNA encoding the mature form
A:Reference number: JH0773; UID:93129227; PMID:1282805
A:Accession: JH0773
A:Molecule type: mRNA
A:Residues: 1-747 <OK>
A:Cross-references: GB:S52417; NID:g263150; PIDN:AAB24853.1; PID:g263151
A:Experimental source: larva
C:Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type protease domain
C:Keywords: alternative splicing; amyloid
F:287-337/Domain: animal Kunitz-type proteinase inhibitor homology <BPI>

Query Match          51.0%; Score 154; DB 2; Length 747;
Best Local Similarity 47.1%; Pred.No. 1e-10;
Matches      24; Conservative    8; Mismatches     19; Indels       0; Gaps        0;

QY   1 CSMQBAGPCLASIPHWYNKTKIGSEFTYGCGGNGNNNFQEAICLVTC 51
      |||::|||::|::|::|::|::|::|::|::|::|::|::|::|::|
Db    287 CSQAETGPCRAMISRWYDVTEKSQAQFIYGCGRNRFESDDYCMAVC 337
      ::|||::|||::|::|::|::|::|::|::|::|::|::|::|::|::|

RESULT 6
TIHABK
isoInhibitor K (BPI type) - Roman snail
C:Species: Helix pomatia (Roman snail)
C>Date: 23-Oct-1981 #sequence_revision 23-Oct-1981 #text_change 09-Jul-2004
C:Accession: A91232; A01225
R:Tschesche, H.; Dietl, T. Eur. J. Biochem. 58, 439-451, 1975
A:Title: The amino acid sequence of isoInhibitor K from snails (Helix pomatia).
A:Reference number: A91232; UID:76043680; PMID:1183446
A:Accession: A91232
A:Molecule type: protein
A:Residues: 1-58 <TCS>
A:Cross-references: UNIPROT:P00994
R:Dietl, T.; Tschesche, H. Hoppe-Seyler's Z. Physiol. Chem. 357, 139-145, 1976
A:Title: Die Disulfidbruecken des Trypsin-Kallikrein-Inhibitors K aus Weinbergschnecke Lymnaea stagnalis
A:Contents: annotation; disulfide bonds
C:Comment: This is one of several inhibitors of broad specificity that are members of the superfamily of basic serine proteases. It has been identified as a member of the superfamily of basic serine proteases by its primary structure and function.
C:Keywords: pyroglutamic acid; serine proteinase inhibitor
F:7-57/Domain: animal Kunitz-type proteinase inhibitor homology <BPI>
F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F:7-57,16-40,32-53/Disulfide Bonds: #status predicted

Query Match          50.7%; Score 153; DB 1; Length 58;
Best Local Similarity 49.0%; Pred.No. 1.2e-11;
Matches      25; Conservative    7; Mismatches     19; Indels       0; Gaps        0;

```


RESULT 7

S19327
venom basic proteinase inhibitor - leaf-nosed viper
N;Alternate names: trypsin inhibitor (Kunitz-type)
C;Species: Eristocophis macmahoni (leaf-nosed viper)
C;Date: 22-Nov-1993 #sequence_revision 03-Nov-1995 #text_change 09-Jul-2004
C;Accession: S19327
R;Siddiqui, A.R.; Zaidi, Z.H.; Joernvall, H.
FEBS Lett. 294, 141-143, 1991
A;Title: Purification and characterization of a Kunitz-type trypsin inhibitor from Leaf-Nosed Viper
A;Reference number: S19327; MUID:92077130; PMID:1743283
A;Accession: S19327
A>Status: preliminary
A:Molecule type: mRNA
A;Residues: 1-62 <SID>
A;Cross-references: UNIPROT:P24541
C;Superfamily: basic proteinase inhibitor; animal Kunitz-type proteinase inhibitor homologous
C;Keywords: serine proteinase inhibitor; venom
F;2-52/Domain: animal Kunitz-type proteinase inhibitor homology <BPI>

Query Match 50.7%; Score 153; DB 2; Length 62;
Best Local Similarity 51.0%; Pred. No. 1.3e-11;
Matches 26; Conservative 6; Mismatches 19; Indels 0; Gaps 0;

Qy 1 CSMPOEAGPCLASIPHWYNNKKTKICSEFYGGCGGNNTFTQAICLVTC 51
| : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 2 CYLPDDPGVCKAHIPRYYPNPASNKCNFIYGGCGGNANFPETRAECRHCTC 52
| : | : | : | : | : | : | : | : | : | : | : | : | : | :

RESULT 8

S07451
proteinase inhibitor 5.II - snake-larks sea anemone
C;Species: Anemonia sulcata (snake-larks sea anemone)
C;Date: 31-Dec-1990 #sequence_revision 09-May-1997 #text_change 09-Jul-2004
C;Accession: S07451; B27222
R;Wunderer, G.; Machleidt, W.; Pritz, H.
Meth. Enzymol. 80, 816-820, 1981
A;Title: The broad-specificity proteinase inhibitor 5 II from the sea anemone Anemonia sulcata
A;Reference number: S07451
A;Accession: S07451
A:Molecule type: protein
A;Residues: 1-59 <WN>
A;Cross-references: UNIPROT:P10280
A;Note: 13-Arg, 16-Gly, 17-Gly, 25-Leu, 28-Arg, and 39-Arg were also found
R;Krebs, H.C.; Habermehl, G.G.
Naturwissenschaften 74, 395-396, 1987
A;Title: Isolierung und strukturaufklärung eines haemolytisch aktiven peptids aus der Seeanemone Anemonia sulcata
A;Reference number: A94700
A;Accession: B27222
A:Molecule type: protein
A;Residues: 1-38,'R',40,'B',42,'BB',45-48,'ZZ','Z',53-62 <KRE>
C;Superfamily: basic proteinase inhibitor; animal Kunitz-type proteinase inhibitor homologous
C;Keywords: serine proteinase inhibitor
F;5-55/Domain: animal Kunitz-type proteinase inhibitor homology <BPI>

Query Match 50.3%; Score 152; DB 2; Length 62;
Best Local Similarity 49.0%; Pred. No. 1.7e-11;
Matches 25; Conservative 6; Mismatches 20; Indels 0; Gaps 0;

Qy 1 CSMPOEAGPCLASIPHWYNNKKTKICSEFYGGCGGNNTFTQAICLVTC 51
| : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 5 CELPKVGPCRRAPFRYYNSKRCEKFYGGCGGNANFPETLECEKVC 55
| : | : | : | : | : | : | : | : | : | : | : | : | : | :

RESULT 9

T23573
hypothetical protein K10D3.4 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T23573
R;McMurray, A.
submitted to the EMBL Data Library, June 1996
A;Reference number: Z19762

RESULT 7

S19327
venom basic proteinase inhibitor - leaf-nosed viper
N;Alternate names: trypsin inhibitor (Kunitz-type)
C;Species: Eristocophis macmahoni (leaf-nosed viper)
C;Date: 22-Nov-1993 #sequence_revision 03-Nov-1995 #text_change 09-Jul-2004
C;Accession: S19327
R;Siddiqui, A.R.; Zaidi, Z.H.; Joernvall, H.
FEBS Lett. 294, 141-143, 1991
A;Title: Purification and characterization of a Kunitz-type tryptic inhibitor from Leaf
F;5-55/Domain: animal Kunitz-type proteinase inhibitor homology <BPI>
A;Reference number: S19327; MUID:92077130; PMID:1743283
A;Accession: S19327
A>Status: preliminary
A:Molecule type: mRNA
A;Residues: 1-62 <SID>
A;Cross-references: UNIPROT:P24541
C;Superfamily: basic proteinase inhibitor; animal Kunitz-type proteinase inhibitor homolog
C;Keywords: serine proteinase inhibitor; venom
F;2-52/Domain: animal Kunitz-type proteinase inhibitor homology <BPI>

Query Match 50.7%; Score 153; DB 2; Length 62;
Best Local Similarity 51.0%; Pred. No. 1.3e-11;
Matches 26; Conservative 6; Mismatches 19; Indels 0; Gaps 0;

Qy 1 CSMPOEAGPCLASPHWYNNKYTKICSEFYGGCGGNNTFTBAICLVTC 51
| : | : | : | : | : | : | : | : | : | : | : | : | : ||
Db 2 CYLPDDPGVCKAHIFRYYPNPASNKNKFYGGCGGNANFPETRAECRHCTC 52
|| : || : || : || : || : || : || : || : || : || : || :

RESULT 8

S07451
proteinase inhibitor 5.II - snake-larks sea anemone
C;Species: Anemonia sulcata (snake-larks sea anemone)
C;Date: 31-Dec-1990 #sequence_revision 09-May-1997 #text_change 09-Jul-2004
C;Accession: S07451; B27222
R;Wunderer, G.; Machleidt, W.; Pritz, H.
Meth. Enzymol. 80, 816-820, 1981
A;Title: The broad-specificity proteinase inhibitor 5 II from the sea anemone Anemonia s
A;Reference number: S07451
A;Accession: S07451
A:Molecule type: protein
A;Residues: 1-59 <WN>
A;Cross-references: UNIPROT:P10280
A;Note: 13-Arg, 16-Gly, 17-Gly, 25-Leu, 28-Arg, and 39-Arg were also found
R;Krebs, H.C.; Habermehl, G.G.
Naturwissenschaften 74, 395-396, 1987
A;Title: Isolierung und strukturaufklärung eines haemolytisch aktiven peptids aus der
A;Reference number: A94700
A;Accession: B27222
A:Molecule type: protein
A;Residues: 1-38,'R', 40,'B','42','BB','45-48','Z','51','Z','53-62 <KRE>
C;Superfamily: basic proteinase inhibitor; animal Kunitz-type proteinase inhibitor homolog
C;Keywords: serine proteinase inhibitor
F;5-55/Domain: animal Kunitz-type proteinase inhibitor homology <BPI>

Query Match 50.3%; Score 152; DB 2; Length 62;
Best Local Similarity 49.0%; Pred. No. 1.7e-11;
Matches 25; Conservative 6; Mismatches 20; Indels 0; Gaps 0;

Qy 1 CSMPOEAGPCLASPHWYNNKYTKICSEFYGGCGGNNTFTBAICLVTC 51
| : | : | : | : | : | : | : | : | : | : | : | : | : ||
Db 5 CELPKVGPCRRAPFRYYNSKKRCFKFIYGCCGANNPTLECEKCVC 55
|||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| :

RESULT 9

T23573
hypothetical protein K10D3.4 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T23573
R;McMurray, A.
submitted to the EMBL Data Library, June 1996
A;Reference number: Z19762

RESULT 7

S19327
venom basic proteinase inhibitor - leaf-nosed viper
N;Alternate names: trypsin inhibitor (Kunitz-type)
C;Species: Eristocophis macmahoni (leaf-nosed viper)
C;Date: 22-Nov-1993 #sequence_revision 03-Nov-1995 #text_change 09-Jul-2004
C;Accession: S19327
R;Siddiqui, A.R.; Zaidi, Z.H.; Joernvall, H.
FEBS Lett. 294, 141-143, 1991
A;Title: Purification and characterization of a Kunitz-type trypsin inhibitor from Leaf
A;Reference number: S19327; MUID:92077130; PMID:1743283
A;Accession: S19327
A>Status: preliminary
A:Molecule type: mRNA
A;Residues: 1-62 <SID>
A;Cross-references: UNIPROT:P24541
C;Superfamily: basic proteinase inhibitor; animal Kunitz-type proteinase inhibitor homolog
C;Keywords: serine proteinase inhibitor; venom
F;2-52/Domain: animal Kunitz-type proteinase inhibitor homology <BPI>

Query Match 50.7%; Score 153; DB 2; Length 62;
Best Local Similarity 51.0%; Pred. No. 1.3e-11;
Matches 26; Conservative 6; Mismatches 19; Indels 0; Gaps 0;

Qy 1 CSMPOEAGPCLASIPHWYNNKYTKICSEFYGGCGGNNTFTQAICLVTC 51
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 2 CYLPDDPGVCKAHIFRYYPNPASNKCNFIYGGCGGNANFPETRAECRHCT 52
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :

RESULT 8

S07451
proteinase inhibitor 5.II - snake-locks sea anemone
C;Species: Anemonia sulcata (snake-locks sea anemone)
C;Date: 31-Dec-1990 #sequence_revision 09-May-1997 #text_change 09-Jul-2004
C;Accession: S07451; B27222
R;Wunderer, G.; Machleidt, W.; Pritz, H.
Meth. Enzymol. 80, 816-820, 1981
A;Title: The broad-specificity proteinase inhibitor 5 II from the sea anemone Anemonia s
A;Reference number: S07451
A;Accession: S07451
A:Molecule type: protein
A;Residues: 1-59 <WUN>
A;Cross-references: UNIPROT:P10280
A;Note: 13-Arg, 16-Gly, 17-Gly, 25-Leu, 28-Arg, and 39-Arg were also found
R;Krebs, H.C.; Habermehl, G.G.
Naturwissenschaften 74, 395-396, 1987
A;Title: Isolierung und strukturaufklärung eines haemolytisch aktiven peptids aus der
A;Reference number: A94700
A;Accession: B27222
A:Molecule type: protein
A;Residues: 1-38, 'R', 40, 'B', 42, 'BB', 45-48, 'Z', 51, 'Z', 53-62 <KRE>
C;Superfamily: basic proteinase inhibitor; animal Kunitz-type proteinase inhibitor homolog
C;Keywords: serine proteinase inhibitor
F;5-55/Domain: animal Kunitz-type proteinase inhibitor homology <BPI>

Query Match 50.3%; Score 152; DB 2; Length 62;
Best Local Similarity 49.0%; Pred. No. 1.7e-11;
Matches 25; Conservative 6; Mismatches 20; Indels 0; Gaps 0;

Qy 1 CSMPOEAGPCLASIPHWYNNKYTKICSEFYGGCGGNNTFTQAICLVTC 51
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 5 CELPKVGFCRRAPFRYYNSKKRCFKFIYGGCGGNANFPETLECEKCVC 55
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :

RESULT 9

T23573
hypothetical protein K10D3.4 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T23573
R;McMurray, A.
submitted to the EMBL Data Library, June 1996
A;Reference number: Z19762

A;Molecule type: DNA
A;Residues: 1-770 <YOS1>
A;Cross-references: GB:M33112; NID:G178613; PIDN:AAB59502.1; PID:G178616
A;Accession: I39451
A;Status: nucleic acid sequence not shown; translation not shown; translated from GB/EMBL
A;Molecule type: DNA
A;Residues: 1-530, 'QWLMNPVPAFWKAKGR' <YOS2>
A;Cross-references: GB:M34875; NID:G178608; PIDN:AAB59501.1; PID:G178615
R;Yoshikai, S.I.; Sasaki, H.; Doh-ura, K.; Furuya, H.; Sakaki, Y.
Gene 102, 291-292, 1991
A;Reference number: A59020; MUID:91340168; PMID:1908403
A;Contents: annotation; erratum
A;Note: revised physical map for reference I39451
R;Levy, E.; Carman, M.D.; Fernandez-Madrid, I.J.; Power, M.D.; Lieberburg, I.; van Duine
Science 248, 1124-1126, 1990
A;Title: Mutation of the Alzheimer's disease amyloid gene in hereditary cerebral hemorrh
A;Reference number: I39453; MUID:90260663; PMID:2111584
A;Accession: I39453
A;Status: translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 656-737 <LEV>
A;Cross-references: GB:M37896; NID:G178618; PIDN:AAA51727.1; PID:G178620
A;Note: a mutation with 693-Gln is presented
R;Murrell, J.; Farlow, M.; Ghetti, B.; Benson, M.D.
Science 254, 97-99, 1991
A;Title: A mutation in the amyloid precursor protein associated with hereditary Alzheimer
A;Reference number: I59562; MUID:92022553; PMID:1925564
A;Accession: I59562
A;Status: translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 689-716, 'F', 718-737 <MUR>
A;Cross-references: GB:S57665; NID:G236720; PIDN:AAB19991.1; PID:G236721
R;Kamino, K.; Ort, H.T.; Payami, H.; Wijisman, E.M.; Alonso, M.E.; Pulst, S.M.; Anderson,
arkis, S.E.; Korenberg, J.R.; Sharma, V.; Kukull, W.; Larson, E.; Heston, L.L.; Martin,
Am. J. Hum. Genet. 51, 998-1014, 1992
A;Title: Linkage and mutational analysis of familial Alzheimer disease kindreds for the
A;Reference number: A44017; MUID:93035397; PMID:1415269
A;Accession: A44017
A;Molecule type: DNA
A;Residues: 687-692, 'G', 694-718 <KAMI>
A;Cross-references: GB:S45135; NID:G257377; PIDN:AAB23645.1; PID:G257378
A;Experimental source: familial Alzheimer disease family SB
A;Note: sequence extracted from NCBI backbone (NCBI:P:115374)
A;Accession: B44017
A;Molecule type: DNA
A;Residues: 687-718 <KAM2>
A;Cross-references: GB:S45136; NID:G257379; PIDN:AAB23646.1; PID:G257380
A;Experimental source: familial Alzheimer disease family LIT
A;Note: sequence extracted from NCBI backbone (NCBI:P:115376)
A;Note: this sequence has a silent mutation
R;Kang, J.; Lemaire, H.G.; Unterbeck, A.; Salbaum, J.M.; Masters, C.L.; Grzeschik, K.H.;
Nature 325, 733-736, 1987
A;Title: The precursor of Alzheimer's disease amyloid A4 protein resembles a cell-surfac
A;Reference number: A03134; MUID:87144572; PMID:2881207
A;Accession: A03134
A;Molecule type: mRNA
A;Residues: 1-288, 'V', 365-770 <KAN>
A;Cross-references: GB:Y00264; NID:G28525; PIDN:CRA68374.1; PID:G28526
A;Note: alternative splice form APP(695)
R;Robakis, N.K.; Ramakrishna, N.; Wolfe, G.; Wisniewski, H.M.
Proc. Natl. Acad. Sci. U.S.A. 84, 4190-4194, 1987
A;Title: Molecular cloning and characterization of a cDNA encoding the cerebrovascular a
A;Reference number: A29030; MUID:87231971; PMID:3035574
A;Accession: A29030
A;Molecule type: mRNA
A;Residues: 284-288, 'V', 365-646, 'E', 648-770 <ROB>
A;Cross-references: GB:M1765; NID:G178539; PIDN:AAA51722.1; PID:G178540
A;Note: the authors translated the codon GAG for residue 647 as Asp
R;Goldgaber, D.; Lerman, M.I.; McBride, O.W.; Saffiotti, U.; Gajdusek, D.C.
Science 235, 877-880, 1987
A;Title: Characterization and chromosomal localization of a cDNA encoding brain amyloid
A;Reference number: A47584; MUID:87120328; PMID:3810169
A;Accession: A47584

A;Molecule type: mRNA
A;Residues: 674-756, 'S', 758-770 <GOL>
A;Cross-references: GB:M15533; NID:G178706; PIDN:AAA35540.1; PID:G178707
A;Experimental source: brain
R;Tanzi, R.E.; Gusella, J.F.; Watkins, P.C.; Bruns, G.A.P.; St George-Hyslop, P.; Van Ke
Science 235, 880-884, 1987
A;Title: Amyloid beta protein gene: cDNA, mRNA distribution, and genetic linkage near ti
A;Reference number: A47585; MUID:87120329; PMID:2949367
A;Accession: A47585
A;Molecule type: mRNA
A;Residues: 674-703 <TAN1>
A;Cross-references: GB:M15532; NID:G177957; PIDN:AAA51564.1; PID:G177958
R;Dyrks, T.; Weidemann, A.; Multhaup, G.; Salbaum, J.M.; Lemaire, H.G.; Kang, J.; Mueller
EMBO J. 7, 949-957, 1988
A;Title: Identification, transmembrane orientation and biogenesis of the amyloid A4 pre
A;Reference number: S02638; MUID:88296437; PMID:2900137
A;Accession: S02638
A;Molecule type: mRNA
A;Residues: 672-678 <DVR>
R;Tanzi, R.E.; McClatchey, A.I.; Lamperti, E.D.; Villa-Komaroff, L.; Gusella, J.F.; Nev
Nature 331, 528-530, 1988
A;Title: Protease inhibitor domain encoded by an amyloid protein precursor mRNA associa
A;Reference number: S00707; MUID:88122640; PMID:2893290
A;Accession: S00707
A;Molecule type: mRNA
A;Residues: 286-344, 'I', 365-366 <TAN2>
A;Cross-references: EMBL:X06982; NID:G28817; PIDN:CAA30042.1; PID:G929612
A;Experimental source: promyelocytic leukemia cell line HL60
A;Note: alternative splice form APP(751)
R;Ponte, P.; Gonzalez-DeWhitt, P.; Schilling, J.; Miller, J.; Heu, D.; Greenberg, B.; D
Nature 331, 525-527, 1988
A;Title: A new A4 amyloid mRNA contains a domain homologous to serine proteinase inhibi
A;Reference number: S00925; MUID:88122639; PMID:2893289
A;Accession: S00925
A;Molecule type: mRNA
A;Residues: 1-344, 'I', 365-770 <PO2>
A;Cross-references: GB:X06989; EMBL:Y00297; NID:G28720; PIDN:CAA30050.1; PID:G28721
A;Note: alternative splice form APP(751)
R;Kitaguchi, N.; Takahashi, Y.; Tokushima, Y.; Shiojiri, S.; Ito, H.
Nature 331, 530-532, 1988
A;Title: Novel precursor of Alzheimer's disease amyloid protein shows protease inhibito
A;Reference number: A38949; MUID:88122641; PMID:2893291
A;Accession: A38949
A;Molecule type: mRNA
A;Residues: 287-367 <KIT>
A;Cross-references: GB:X06981; NID:G28816; PIDN:CAA30041.1; PID:G929611
A;Experimental source: glioblastoma cell line
A;Note: alternative splice form APP(770)
R;Vitek, M.P.; Rasool, C.G.; de Sauvage, F.; Vitek, S.M.; Bartus, R.T.; Beer, B.; Ashton
Brain Res. Mol. Brain Res. 4, 121-131, 1988
A;Title: Absence of mutation in the beta-amyloid cDNAs cloned from the brains of three
A;Reference number: A30320
A;Accession: A30320
A;Status: not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 284-288, 'V', 365-770 <VIT1>
A;Accession: B30320
A;Status: not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 122-288, 'V', 365-770 <VIT2>
A;Accession: C30320
A;Status: not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 606-770 <VIT3>
R;Zain, S.B.; Salim, M.; Chou, W.G.; Sajdel-Sulkowska, E.M.; Majocha, R.E.; Marotta, C.
Proc. Natl. Acad. Sci. U.S.A. 85, 929-933, 1988
A;Title: Molecular cloning of amyloid cDNA derived from mRNA of the Alzheimer disease b
A;Reference number: A31087; MUID:88124954; PMID:2893379
A;Accession: A31087
A;Molecule type: mRNA
A;Residues: 507-770 <ZAI>
A;Cross-references: GB:M18734; NID:G178572; PIDN:AAA51726.1; PID:G178573
A;Note: the authors translated the codon GAA for residue 599 as Gly, ACC for residue 60

Query Match 48.3%; Score 146; DB 2; Length 765;
Best Local Similarity 45.1%; Pred. No. 9.8e-10;
Matches 23; Conservative 7; Mismatches 21; Indels 0; Gaps 0;

QY 1 CSMPQAGPCLASIPHHWYNNKTKICSEFIYGGCGNNNNFQTEAICLVTC 51
DB 312 CSQEAHTGCPRAVMPRWFDLSKGKCVRFIYGGCGNNRNFSEDYCMAVC 362

RESULT 20
TirHPB
protease inhibitor - flesh fly (Sarcophaga bullata)
C:Species: Sarcophaga bullata
C:Date: 07-Feb-1992 #sequence_revision 22-Jul-1994 #text_change 09-Jul-2004
C:Accession: A37294
R:Papayanopoulos, I.A.; Bienann, K.
Protein Sci. 1, 278-288, 1992
A:Title: Amino acid sequence of a protease inhibitor isolated from Sarcophaga bullata de
A:Reference number: A37294; MUID:93284121; PMID:1304909
A:Accession: A37294
A:Molecule type: protein
A:Residues: 1-57 <PAP>
A:Cross-references: UNIPROT:P26228
A:Experimental source: hemolymph
C:Superfamily: basic proteinase inhibitor
C:Keywords: serine proteinase inhibitor
F:6-56/Domain: animal Kunitz-type proteinase inhibitor homology <BPI>
F:6-56,15-39,31-52/Disulfide bonds: #status predicted
F:16/inhibitory site: Arg (chymotrypsin) #status predicted

Query Match 48.0%; Score 145; DB 1; Length 57;
Best Local Similarity 49.0%; Pred. No. 1.1e-10;
Matches 25; Conservative 7; Mismatches 19; Indels 0; Gaps 0;

QY 1 CSMPQAGPCLASIPHHWYNNKTKICSEFIYGGCGNNNNFQTEAICLVTC 51
DB 6 CLQPEVGPCKSDFFVFYNDTKACEEFLYGGCGNDNRNPTKBECEKLC 56

RESULT 21
A5515
uterine plasmin/trypsin inhibitor - pig
C:Species: Sus scrofa domestica (domestic pig)
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C:Accession: A55115
R:Stallings-Wann, M.L.; Burke, M.G.; Trout, W.E.; Roberts, R.M.
J. Biol. Chem. 269, 24090-24094, 1994
A:Title: Purification, characterization, and cDNA cloning of a Kunitz-type proteinase in
A:Reference number: A55115; MUID:95014140; PMID:7929061
A:Accession: A55115
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-122 <STA>
A:Cross-references: UNIPROT:Q29100; GB:L14282; NID:G682652; PIDN:AAAG2425.1; PID:G682653
A:Note: authors translated the codon GGC for residue 36 as Ala, AGC for residue 48 as Ar
C:Superfamily: basic proteinase inhibitor; animal Kunitz-type proteinase inhibitor homol
C:Keywords: serine proteinase inhibitor
F:38-88/Domain: animal Kunitz-type proteinase inhibitor homology <BPI>

Query Match 48.0%; Score 145; DB 1; Length 122;
Best Local Similarity 47.1%; Pred. No. 2.2e-10;
Matches 24; Conservative 5; Mismatches 22; Indels 0; Gaps 0;

QY 1 CSMPQAGPCLASIPHHWYNNKTKICSEFIYGGCGNNNNFQTEAICLVTC 51
DB 38 CREPPYTGPCSAHFVRYFNATTGLCQSFYGGCGKQNNFMDEKECLTTC 88

RESULT 22
T16210
hypothetical protein F30H5.3 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans

C:Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
C:Accession: T16210
R:Pauley, A.; Stellyes, L.
submitted to the EMBL Data Library, June 1995
A:Description: The sequence of C. elegans cosmid F30H5.
A:Reference number: Z18478
A:Accession: T16210
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-1599 <PAU>
A:Cross-references: UNIPROT:Q09983; EMBL:U29096; NID:G861393; PID:G861393; PIDN:AAA68408
A:Experimental source: strain Bristol N2
C:Genetics:
A:Gene: CESP:F30H5.3
A:Introns: 12/1; 59/2; 85/3; 124/3; 217/2; 534/3; 560/1; 1549/1

Query Match 48.0%; Score 145; DB 2; Length 1599;
Best Local Similarity 49.0%; Pred. No. 2.6e-09;
Matches 25; Conservative 5; Mismatches 21; Indels 0; Gaps 0;

QY 1 CSMPQAGPCLASIPHHWYNNKTKICSEFIYGGCGNNNNFQTEAICLVTC 51
DB 563 CSQPLRLGDCQSVRYVYNAVTRACETFDYTCQGNNDNPFLLCQNTC 613

RESULT 23
S01802
chymotrypsin inhibitor I - silkworm
C:Species: Bombyx mori (silkworm)
C:Date: 30-Sep-1989 #sequence_revision 30-Sep-1989 #text_change 09-Jul-2004
C:Accession: S01802
R:Sasaaki, T.
Biol. Chem. Hoppe-Seyler 369, 1235-1241, 1988
A:Title: Amino-acid sequences of two basic chymotrypsin inhibitors from silkworm larval
A:Reference number: S01802; MUID:89228538; PMID:3072972
A:Accession: S01802
A:Molecule type: protein
A:Residues: 1-62 <SAS>
A:Cross-references: UNIPROT:P10831
C:Superfamily: basic proteinase inhibitor
C:Keywords: serine proteinase inhibitor
F:9-60/Domain: animal Kunitz-type proteinase inhibitor homology <BPI>

Query Match 47.7%; Score 144; DB 2; Length 62;
Best Local Similarity 60.0%; Pred. No. 1.5e-10;
Matches 27; Conservative 4; Mismatches 14; Indels 0; Gaps 0;

QY 7 AGPCLASIPHHWYNNKTKICSEFIYGGCGNNNNFQTEAICLVTC 51
DB 16 SGPCFAYIKLYSNOKTKCEFIYGGCGNDNRNFTILAEQKC 60

RESULT 24
S04855
Alzheimer's disease amyloid A4 protein - mouse (fragment)
C:Species: Mus musculus domesticus (western European house mouse)
C:Date: 28-Feb-1990 #sequence_revision 28-Feb-1990 #text_change 09-Jul-2004
C:Accession: S04855
R:Fukuchi, K.I.; Martin, G.M.; Deeb, S.S.
Nucleic Acids Res. 17, 5396, 1989
A:Title: Sequence of the protease inhibitor domain of the A4 amyloid protein precursor
A:Reference number: S04855; MUID:89345111; PMID:2569710
A:Accession: S04855
A:Molecule type: mRNA
A:Residues: 1-76 <FUK>
A:Cross-references: UNIPROT:P12023; EMBL:X15210; NID:G49965; PIDN:CAA33280.1; PID:G9301
A:Note: the authors translated the codon GAR for residue 74 as Val
C:Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase
C:Keywords: alternative splicing; serine proteinase inhibitor; transmembrane protein
F:3-53/Domain: animal Kunitz-type proteinase inhibitor homology <BPI>

Query Match 47.7%; Score 144; DB 2; Length 76;
Best Local Similarity 47.1%; Pred. No. 1.9e-10;

Matches 24; Conservative 4; Mismatches 23; Indels 0; Gaps 0;

QY 1 CSMPEAGPCLASIPHWYNNKTKICSEFYGGCGGNNNFQTEAICLVTC 51
||| ||| :||| ||| ||| ||| ||| ||| :
DB 3 CSQAETGPCAMISRWFVDVTEGCKVPFFYGGCGGNRNFDTIEYCMAVC 53

RESULT 25
A32282
Alzheimer's disease amyloid beta protein precursor - mouse (fragment)
C:Species: Mus musculus (house mouse)
C>Date: 17-Aug-1989 #sequence_revision 17-Aug-1989 #text_change 09-Jul-2004
C:Accession: A32282
R;Yamada, T.; Sasaki, H.; Dohura, K.; Goto, I.; Sakaki, Y.
Biochem. Biophys. Res. Commun. 158, 906-912, 1989
A>Title: Structure and expression of the alternatively-spliced forms of mRNA for the monoclonal antibody 2B12
A:Reference number: A32282; MUID:89149813; PMID:2493250
A:Accession: A32282
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-100 <YAM>
A:Cross-references: UNIPROT:P12023; GB:M24397; NID:g200350; PIDN:AAA39929.1; PID:g200351
C:Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase inhibitor
C:Keywords: alternative splicing
F;11-61/Domain: animal Kunitz-type proteinase inhibitor homology <BPI>

Query Match 47.7%; Score 144; DB 2; Length 100;
Best Local Similarity 47.1%; Pred. No. 2.4e-10;
Matches 24; Conservative 4; Mismatches 23; Indels 0; Gaps 0;

QY 1 CSMPEAGPCLASIPHWYNNKTKICSEFYGGCGGNNNFQTEAICLVTC 51
||| ||| :||| ||| ||| ||| ||| ||| :
DB 11 CSQAETGPCAMISRWFVDVTEGCKVPFFYGGCGGNRNFDTIEYCMAVC 61

RESULT 26
B59399
short epsilon-dendrotoxin His55, subunit - Dendroaspis angusticeps
C:Species: Dendroaspis angusticeps
C>Date: 31-Dec-2001 #sequence_revision 31-Dec-2001 #text_change 09-Jul-2004
C:Accession: B59399
R;Sigle, R.; Hackett, M.; Aird, S.D.
Toxicol 40, 297-308, 2002
A>Title: Primary structure of four dendrotoxin E homologs from the venom of Dendroaspis
A:Reference number: A59399
A:Accession: B59399
A>Status: preliminary
A:Molecule type: protein
A:Residues: 1-57 <AIR>
A:Cross-references: UNIPROT:Q7LZE3
A>Note: trypsin inhibitor; K+ channel antagonist
C:Superfamily: basic proteinase inhibitor; animal Kunitz-type proteinase inhibitor homology
F;5-55/Dисульфидные связи: #status experimental
F;14-38/Dисульфидные связи: #status experimental
F;30-51/Dисульфидные связи: #status experimental

Query Match 47.4%; Score 143; DB 2; Length 57;
Best Local Similarity 51.0%; Pred. No. 1.9e-10;
Matches 26; Conservative 4; Mismatches 21; Indels 0; Gaps 0;

QY 1 CSMPEAGPCLASIPHWYNNKTKICSEFYGGCGGNNNFQTEAICLVTC 51
||| ||| :||| ||| ||| ||| ||| ||| :
DB 5 CKPAEPGPCASIPAFYYNWAKKCOLPHYGGCKGNANPFSTIEKRHCAC 55

RESULT 27
T1E2PD
venom basic proteinase inhibitor E - black mamba
C:Species: Dendroaspis polylepis polylepsis (black mamba)
C>Date: 30-Nov-1980 #sequence_revision 30-Nov-1980 #text_change 09-Jul-2004
C:Accession: A01215
R;Joubert, F.J.; Strydom, D.J.
Eur. J. Biochem. 87, 191-198, 1978

A;Title: Sanek venoms. The amino-acid sequence of trypsin inhibitor E of Dendroaspis pol
A;Reference number: A01215; MUID:78214615; PMID:668698
A;Accession: A01215
A;Molecule type: protein
A;Residues: 1-59 <JOU>
A;Cross-references: UNIPROT:P00984
A;Note: this protein inhibits trypsin and binds transition metal ions such as copper and
C;Superfamily: basic proteinase inhibitor; animal Kunitz-type proteinase inhibitor homol
C;Keywords: serine proteinase inhibitor; venom
F;7-57/Domain: animal Kunitz-type proteinase inhibitor homology <BPI>
F;7-57,16-40,32-53/Disuulfide bonds: #status predicted

Query Match 47.4%; Score 143; DB 1; Length 59;
Best Local Similarity 51.0%; Pred. No. 1.9e-10;
Matches 26; Conservative 4; Mismatches 21; Indels 0; Gaps 0;

Qy 1 CSMPOEAGPCLASIPHHWYNNKTKICSFYGGCGGNNNNFOTEAICLVTC 51
Db 7 CKLPAEPGPKASIPAFYNNWAAKCOLFHYGGCKGNANRFTIEKRRAC 57

RESULT 28
A59399
Long epsilon-dendrotoxin Arg55, subunit - Dendroaspis angusticeps
C;Species: Dendroaspis angusticeps
C;Date: 31-Dec-2001 #sequence_revision 31-Dec-2001 #text_change 09-Jul-2004
C;Accession: A59399
R;Sagle, R.; Hackett, M.; Aird, S.D.
Toxicon 40: 297-308, 2002
A;Title: Primary structure of four dendrotoxin E homologs from the venom of Dendroaspis
A;Reference number: A59399
A;Accession: A59399
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-59 <AIR>
A;Cross-references: UNIPROT:Q7LZS8
A;Note: trypsin inhibitor; K+ channel antagonist
C;Superfamily: basic proteinase inhibitor; animal Kunitz-type proteinase inhibitor homol
F;7-57/Disuulfide bonds: #status experimental
F;16-40/Disuulfide bonds: #status experimental
F;32-53/Disuulfide bonds: #status experimental

Query Match 47.4%; Score 143; DB 2; Length 59;
Best Local Similarity 51.0%; Pred. No. 1.9e-10;
Matches 26; Conservative 4; Mismatches 21; Indels 0; Gaps 0;

Qy 1 CSMPOEAGPCLASIPHHWYNNKTKICSFYGGCGGNNNNFOTEAICLVTC 51
Db 7 CKLPAEPGPKASIPAFYNNWAAKCOLFHYGGCKGNANRFTIEKRRAC 57

RESULT 29
S01803
chymotrypsin inhibitor II - silkworm
C;Species: Bombyx mori (silkworm)
C;Date: 30-Sep-1989 #sequence_revision 30-Sep-1989 #text_change 09-Jul-2004
C;Accession: S01803
R;Sasaki, T.
Biol. Chem. Hoppe-Seyler 369, 1235-1241, 1988
A;Title: Amino-acid sequences of two basic chymotrypsin inhibitors from silkworm larval
A;Reference number: S01802; MUID:89228538; PMID:3072972
A;Accession: S01803
A;Molecule type: protein
A;Residues: 1-62 <SAS>
A;Cross-references: UNIPROT:P10832
C;Superfamily: basic proteinase inhibitor; animal Kunitz-type proteinase inhibitor homol
C;Keywords: serine proteinase inhibitor
F;9-60/Domain: animal Kunitz-type proteinase inhibitor homology <BPI>

Query Match 47.4%; Score 143; DB 2; Length 62;
Best Local Similarity 57.8%; Pred. No. 2e-10;
Matches 26; Conservative 5; Mismatches 14; Indels 0; Gaps 0;

C;Comment: The amino acid at position P2' (228-Met) appears to determine the specificity and elastase; those with leucine interact strongly.
C;Superfamily: alpha-1-microglobulin and inter-alpha-trypsin inhibitor light chain precursor
C;Keywords: duplication; glycoprotein; plasma; serine proteinase inhibitor
F;20-173/Domain: lipocalin homology <LiP>
F;216-266/Domain: animal Kunitz-type proteinase inhibitor homology <BP1>
F;272-322/Domain: animal Kunitz-type proteinase inhibitor homology <BP2>
F;216-266,225-249,241-262,272-322,281-305,297-318/Diulfide bonds: #status predicted
F;226/Inhibitory site: Leu (chymotrypsin, elastase) #status predicted
F;235/Binding site: carbohydrate (Asn) (covalent) #status experimental
F;282/Inhibitory site: Arg (trypsin) #status predicted

Query Match 47.0%; Score 142; DB 1; Length 337;
Best Local Similarity 47.1%; Pred. No. 1.4e-09;
Matches 24; Conservative 5; Mismatches 22; Indels 0; Gaps 0;

Qy 1 CSMPEAGPCLASIPHWYNNKTKICSEFLYGGCGQNNNNFOTEALCLVTC 51
Db 216 CQLGYSGQPCLGIMKRYFFYSSMACETHYGGCMGNFVSEKCLQTC 266

RESULT 35

TIBOI

alpha-1-microglobulin / inter-alpha-trypsin inhibitor precursor [validated] - bovine
N;Alternate names: B1-14 (inhibitory fragment of IRI); bikunin; IRI
C;Species: Bos primigenius taurus (cattle)
C;Date: 25-Feb-1985 #sequence,revision 04-Feb-2000 #text_change 09-Jul-2004
C;Accession: S68149; A91717; A90685; S31219; A01209
R;Lindqvist, A.; Akerstrom, B.
Biochim. Biophys. Acta 1306, 98-106, 1996
A;Title: Bovine alpha(1)-microglobulin/bikunin. Isolation and characterization of liver
A;Reference number: S68149; PMID:96201710; PMID:8611630
A;Accession: S68149
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-352 <LIN>
A;Cross-references: UNIPROT:P00978; EMBL:U05642; NID:gl016297; PIDN:AAB07599.1; PID:gl016297
R;Hochstrasser, K.; Wachter, E.
Hoppe-Seyler's Z. Physiol. Chem. 364, 1679-1687, 1983
A;Title: Kunitz-type proteinase inhibitors derived by limited proteolysis of the inter-alpha-trypsin inhibitor
A;Reference number: A91717; PMID:84133807; PMID:6199275
A;Accession: A91717
A;Molecule type: protein
A;Residues: 227-267, 'L', 269-273, 'Q', 275-297, 'AF', 300-329, 'Q', 331-345, 'R', 347-348 <HOC>
R;Hochstrasser, K.; Wachter, E.; Albrecht, G.J.; Reisinger, P.
Biol. Chem. Hoppe-Seyler 366, 473-478, 1985
A;Title: Kunitz-type proteinase inhibitors derived by limited proteolysis of the inter-alpha-trypsin inhibitor
A;Reference number: A90685; PMID:85225967; PMID:2408637
A;Accession: A90685
A;Molecule type: protein
A;Residues: 347-349 <HOC2>
R;Hochstrasser, K.; Albrecht, G.J.; Schonberger, O.L.; Wachter, E.
Hoppe-Seyler's Z. Physiol. Chem. 364, 1689-1696, 1983
A;Title: Kunitz-type proteinase inhibitors derived by limited proteolysis of the inter-alpha-trypsin inhibitor
A;Reference number: A91718; PMID:84133808; PMID:6199276
A;Contents: annotation; reactive sites
R;Castillo, G.M.; Templeton, D.M.
FEBS Lett. 318, 292-296, 1993
A;Title: Subunit structure of bovine ESP (extracellular-matrix stabilizing factor(s))
A;Reference number: S31219; PMID:93178646; PMID:7680011
A;Accession: S31219
A;Status: preliminary
A;Molecule type: protein
A;Residues: 206-214, 'X', 216, 'X', 218-220 <CAS>
C;Superfamily: alpha-1-microglobulin and inter-alpha-trypsin inhibitor light chain precursor
C;Keywords: duplication; glycoprotein; plasma; serine proteinase inhibitor
F;235-188/Domain: lipocalin homology <LiP>
F;231-281/Domain: animal Kunitz-type proteinase inhibitor homology <BP1>
F;287-337/Domain: animal Kunitz-type proteinase inhibitor homology <BP2>
F;224/Inhibitory site: Leu (chymotrypsin, elastase) #status experimental
F;250/Binding site: carbohydrate (Asn) (covalent) #status experimental
F;297/Inhibitory site: Arg (trypsin) #status experimental

Query Match 47.0%; Score 142; DB 1; Length 352;
Best Local Similarity 45.1%; Pred. No. 1.4e-09;
Matches 23; Conservative 6; Mismatches 22; Indels 0; Gaps 0;

QY 1 CSMPOEAGPCLASIPHHWYNNKTKICSEFIYGGCGGNNNNFQTEAICLVTC 51
DB 231 CQLDYSQGPCLGFLKRYFYNGTSMACETFLYGGCGGNNNNFSEKELQTC 281

RESULT 36
H88380
protein T22F7.3 [imported] - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 10-May-2001
C:Accession: H88380
R:Anonymous, The C. elegans Sequencing Consortium.
Science 282, 2012-2018, 1998
A:Title: Genome sequence of the nematode C. elegans: a platform for investigating biology
A:Reference number: A75000; MUID:99069613; PMID:9851916
A:Note: see websites genome.wustl.edu/gsc/C_elegans/ and www.sanger.ac.uk/Projects/C_ele
A:Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; and
A:Accession: H88380
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-1522 <STO>
A:Cross-references: GB:chr.III; PIDN:AAA20672.1; PID:G529714; GSPDB:GN00021; CESP:T22F7.
A:Note: highly similar to ZC84.1
C:Genetics:
A:Gene: T22F7.3
A:Map position: 3

Query Match 46.7%; Score 141; DB 2; Length 1522;
Best Local Similarity 43.1%; Pred. No. 7.5e-09;
Matches 22; Conservative 8; Mismatches 21; Indels 0; Gaps 0;

QY 1 CSMPOEAGPCLASIPHHWYNNKTKICSEFIYGGCGGNNNNFQTEAICLVTC 51
DB 533 CTQPKRLGDCTSVAVRYWYNNATRCSEMPQYTGCGQNDNNFTLMACQCKC 583

RESULT 37
A29652
inter-alpha-trypsin inhibitor (BPI type) - sheep (fragment)
C:Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
C:Date: 31-Dec-1988 #sequence_revision 31-Dec-1988 #text_change 09-Jul-2004
C:Accession: A29652
R:Raap, G.; Hochstrasser, K.; Wächter, E.; Reisinger, P.W.M.
Biol. Chem. Hoppe-Seyler 368, 727-731, 1987
A:Title: The amino-acid sequence of the trypsin-released inhibitor from sheep inter-alpha
sin inhibitor, XI.).
A:Reference number: A29652; MUID:87299012; PMID:2441725
A:Accession: A29652
A:Molecule type: protein
A:Residues: 1-123 <RAS>
A:Cross-references: UNIPROT:PI3371
C:Superfamily: alpha-1-microglobulin and inter-alpha-trypsin inhibitor light chain precu
C:Keywords: serine proteinase inhibitor
F:5-55/Domain: animal Kunitz-type proteinase inhibitor homology <BP1>
F:61-111/Domain: animal Kunitz-type proteinase inhibitor homology <BP2>

Query Match 46.4%; Score 140; DB 2; Length 123;
Best Local Similarity 45.1%; Pred. No. 9e-10; 23; Indels 0; Gaps 0;

QY 1 CSMPOEAGPCLASIPHHWYNNKTKICSEFIYGGCGGNNNNFQTEAICLVTC 51
DB 5 CQLGYSQGPCLGMKRYFYNGTSMACETFLYGGCGGNNNNFPSEKELQTC 55

RESULT 38
C89114
protein C37C3.6a [imported] - Caenorhabditis elegans
C:Species: Caenorhabditis elegans

C:Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
C:Accession: C89114
R:Anonymous, The C. elegans Sequencing Consortium.
Science 282, 2012-2018, 1998
A:Title: Genome sequence of the nematode C. elegans: a platform for investigating biology
A:Reference number: A75000; MUID:99069613; PMID:9851916
A:Note: see websites genome.wustl.edu/gsc/C_elegans/ and www.sanger.ac.uk/Projects/C_ele
A:Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; and
A:Accession: C89114
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-1558 <STO>
A:Cross-references: UNIPROT:Q81710; GB:chr.V; PIDN:AAC25867.1; PID:G3294501; GSPDB:GN000
C:Genetics:
A:Gene: C37C3.6a
A:Map position: 5

Query Match 46.4%; Score 140; DB 2; Length 1558;
Best Local Similarity 43.1%; Pred. No. 1e-08;
Matches 22; Conservative 5; Mismatches 24; Indels 0; Gaps 0;

QY 1 CSMPOEAGPCLASIPHHWYNNKTKICSEFIYGGCGGNNNNFQTEAICLVTC 51
DB 1447 CDEAKDTGPTCTNFVTWKYNNKADGTCNRFHYGGCGGNNRPDNEQQCKAAC 1497

RESULT 39
T34395
hypothetical protein C37C3.6b - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 09-Jul-2004
C:Accession: T34395; T34394
R:Geisel, C.; Bradshaw, H.
submitted to the EMBL Data Library, July 1996
A:Description: The sequence of C. elegans cosmid C37C3.
A:Reference number: Z21518
A:Accession: T34395
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-2167 <GBI>
A:Cross-references: UNIPROT:O76840; EMBL:U64857; PIDN:AAC25868.1; GSPDB:GN00023; CESP:C
A:Experimental source: strain Bristol N2; clone C37C3
A:Accession: T34394
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-1555, 'SKF' <GB2>
A:Cross-references: EMBL:U64857; PIDN:AAC25867.1; GSPDB:GN00023; CESP:C37C3.6a
A:Experimental source: strain Bristol N2; clone C37C3
C:Genetics:
A:Gene: CESP:C37C3.6b; CESP:C37C3.6a
A:Map position: 5
A:Introns: 32/3; 104/2; 156/2; 207/1; 459/2; 536/3; 577/2; 1105/3; 1367/1; 1438/1; 1556/

Query Match 46.4%; Score 140; DB 2; Length 2167;
Best Local Similarity 43.1%; Pred. No. 1.4e-08;
Matches 22; Conservative 5; Mismatches 24; Indels 0; Gaps 0;

QY 1 CSMPOEAGPCLASIPHHWYNNKTKICSEFIYGGCGGNNNNFQTEAICLVTC 51
DB 1447 CDEAKDTGPTCTNFVTWKYNNKADGTCNRFHYGGCGGNNRPDNEQQCKAAC 1497

RESULT 40
TIHCBP
proteinase inhibitor (BPI-type) - horseshoe crab (Tachyplesus tridentatus)
C:Species: Tachyplesus tridentatus
C:Date: 08-Mar-1989 #sequence_revision 22-Jul-1994 #text_change 09-Jul-2004
C:Accession: A26923
R:Nakamura, T.; Hirai, T.; Tokunaga, F.; Kawabata, S.; Iwanaga, S.
J. Biochem. 101, 1297-1306, 1987
A:Title: Purification and amino acid sequence of Kunitz-type protease inhibitor found in
A:Reference number: A26923; MUID:88007472; PMID:3308864
A:Accession: A26923

A:Molecule type: protein
A:Residues: 1-61 <NAK>
A:Cross-references: UNIPROT:P16044
A:Experimental source: hemocytes
C:Comment: The inhibitory activity is similar to bovine basic proteinase inhibitor.
C:Superfamily: basic proteinase inhibitor; animal Kunitz-type proteinase inhibitor homolog
C:Keywords: serine proteinase inhibitor
F:8-58/Domain: animal Kunitz-type proteinase inhibitor homology <BPI>
F:8-58,17-41,33-54/Disulfide bonds: #status predicted
F:18/inhibitory site: Arg (chymotrypsin, elastase, trypsin, plasmin, plasma kallikrein)

Query Match 45.7%; Score 138; DB 1; Length 61;
Best Local Similarity 45.1%; Pred. No. 8e-10;
Matches 23; Conservative 7; Mismatches 21; Indels 0; Gaps 0;

QY 1 CSMPEAGPCLASIPHHWYKTKCSBFYGGCGGNNNNFQTEAICLVTC 51
DB 8 CTSPPVTGPRAGFRKRYNTRTKQCEPPKYGCKGNRYKSEQDCLDAC 58

RESULT 41
TIHOBI
alpha-1-microglobulin/inter-alpha-trypsin inhibitor - horse (fragment)
N:Alternate names: EI-14 (inhibitory fragment of ITI); ITI; trypsin inhibitor, E-UTI
C:Species: Equus caballus (domestic horse)
C:Date: 30-Jun-1987 #sequence_revision 04-Feb-2000 #text_change 09-Jul-2004
C:Accession: A01210; A45653
R:Hochstrasser, K.; Wächter, E.; Albrecht, G.J.; Reisinger, P.
Biol. Chem. Hoppe-Seyler 366, 473-478, 1985
A:Title: Kunitz-type proteinase inhibitors derived by limited proteolysis of the inter-alpha
A:Reference number: A90685; MUID:85225967; PMID:2408637
A:Accession: A01210
A:Molecule type: protein
A:Residues: 3-125 <HOC>
A:Cross-references: UNIPROT:P04355
R:Veeraragavan, K.; Singh, K.; Wächter, E.; Hochstrasser, K.
Biochem. Int. 26, 405-413, 1992
A:Title: Characterization of a trypsin inhibitor from equine urine.
A:Reference number: A45653; MUID:92328813; PMID:1627153
A:Accession: A45653
A>Status: preliminary
A:Molecule type: protein
A:Residues: 1-12, 'E', 14-33 <VEE>
A:Cross-references: PIDN:AAB22430.1; PID:G250858
A:Experimental source: urine
A:Note: sequence extracted from NCBI backbone (NCBIP:107966)
C:Comment: This inhibitory fragment, released from native ITI after limited proteolysis
first domain interacts weakly with PMN-granulocytic elastase and not at all with pancrea
C:Comment: The amino acid at position P2' (19-Met) appears to determine the specificity
d elastase; those with leucine interact strongly.
C:Superfamily: alpha-1-microglobulin and inter-alpha-trypsin inhibitor light chain precu
C:Keywords: duplication; glycoprotein; plasma; serine proteinase inhibitor
F:7-57/Domain: animal Kunitz-type proteinase inhibitor homology <BPI>
F:63-113/Domain: animal Kunitz-type proteinase inhibitor homology <BP2>
F:7-57,16-40,32-53,63-113,72-96,88-109/Disulfide bonds: #status predicted
F:17/inhibitory site: Leu (chymotrypsin, elastase) #status predicted
F:26/Binding site: carbohydrate (Asn) (covalent) #status experimental
F:73/inhibitory site: Arg (trypsin) #status predicted

Query Match 45.7%; Score 138; DB 1; Length 125;
Best Local Similarity 45.1%; Pred. No. 1.6e-09;
Matches 23; Conservative 6; Mismatches 22; Indels 0; Gaps 0;

QY 1 CSMPEAGPCLASIPHHWYKTKCSBFYGGCGGNNNNFQTEAICLVTC 51
DB 7 CQLDHAQGPCLGMSIRFYFNGTSMACETFGYGLGNGNNFASQKSLQTC 57

RESULT 42
A53390
Kunitz-type proteinase inhibitor precursor - sheep
C:Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
C:Date: 27-Jun-1994 #sequence_revision 27-Jun-1994 #text_change 09-Jul-2004

A:Accession: A53390
A:Residues: 1-61 <NAK>
A:Cross-references: UNIPROT:P16044
A:Experimental source: hemocytes
C:Comment: The inhibitory activity is similar to bovine basic proteinase inhibitor.
C:Superfamily: basic proteinase inhibitor; animal Kunitz-type proteinase inhibitor homolog
C:Keywords: serine proteinase inhibitor
F:8-58/Domain: animal Kunitz-type proteinase inhibitor homology <BPI>
F:8-58,17-41,33-54/Disulfide bonds: #status predicted
F:18/inhibitory site: Arg (chymotrypsin, elastase, trypsin, plasmin, plasma kallikrein)

Query Match 45.7%; Score 138; DB 2; Length 265;
Best Local Similarity 41.2%; Pred. No. 3.3e-09;
Matches 21; Conservative 12; Mismatches 18; Indels 0; Gaps 0;

QY 1 CSMPEAGPCLASIPHHWYKTKCSBFYGGCGGNNNNFQTEAICLVTC 51
DB 208 CLPEKVTGDCNATMTRYFNTQTGLCEQFVYTGCGNGNFFENLEDCKMTC 258

RESULT 43
A54951
tissue factor pathway inhibitor-2 precursor - human
N:Alternate names: placental protein 5 (PP5)
C:Species: Homo sapiens (man)
C:Date: 31-May-1996 #sequence_revision 31-May-1996 #text_change 09-Jul-2004
C:Accession: A54951; I55185; A34029; C34029; B34029
R:Spracher, C.A.; Kistel, W.; Mathewes, S.; Foster, D.C.
Proc. Natl. Acad. Sci. U.S.A. 91, 3353-3357, 1994
A:Title: Molecular cloning, expression, and partial characterization of a second human
A:Reference number: A54951; MUID:94211862; PMID:8159751
A:Accession: A54951
A>Status: translated from GB/EMBL/DBDJ
A:Molecule type: mRNA
A:Residues: 1-235 <RES>
A:Cross-references: UNIPROT:P48307; GB:L27624; NID:G441149; PIDN:AAA20094.1; PID:G44115
A:Experimental source: placenta
R:Miyagi, Y.; Koshikawa, N.; Yasumitsu, H.; Miyagi, E.; Hirahara, F.; Aoki, I.; Mäugli,
J. Biochem. 116, 939-942, 1994
A:Title: CDNA cloning and mRNA expression of a serine proteinase inhibitor secreted by
A:Reference number: I55185; MUID:95204397; PMID:7896752
A:Accession: I55185
A>Status: nucleic acid sequence not shown; translation not shown; translated from GB/EM

A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-805 <PAU>
A:Cross-references: UNIPROT:Q19305; EMBL:U41264; PIDN:AAA82427.1; CESP:F10E7.4
C:Genetics:
A:Introns: 9/1; 34/3; 57/1; 90/3; 128/3; 162/3; 205/1; 285/2; 417/1; 475/1; 606/1; 745/1

Query Match 45.0%; Score 136; DB 2; Length 805;
Best Local Similarity 41.2%; Pred. No. 1.6e-08;
Matches 21; Conservative 8; Mismatches 22; Indels 0; Gaps 0;

QY 1 CSMPQAGPCLASIPHWYNNKTKICSEFIYGGCGQNNNNFQTEAICLVTC 51
DB 608 CQEDKQAGCAGNFPYWNHKTQCEIFGTGCKGRNQFTEBCKQIC 658

RESULT 46
T26859
hypothetical protein Y43F8B.3 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C:Accession: T26859
R:Ainscough, R.
submitted to the EMBL Data Library, October 1998
A:Reference number: Z20278
A:Accession: T26859
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-1743 <WIL>
A:Cross-references: UNIPROT:Q9XWX5; EMBL:AL032623; PIDN:CAA21511.1; CESP:Y43F8B.3
A:Experimental source: clone Y43F8B
C:Genetics:
A:Gene: CESP:Y43F8B.3
A:Introns: 65/1; 92/2; 128/1; 229/1; 367/1; 422/1; 486/2; 523/1; 571/1; 628/1; 857/2; 94

Query Match 44.7%; Score 135; DB 2; Length 1743;
Best Local Similarity 36.6%; Pred. No. 4.5e-08;
Matches 26; Conservative 6; Mismatches 19; Indels 20; Gaps 1;

QY 1 CSMPQAGPCLASIPHWYNNKTKICSEFIYGGCGQNNNNFQTE----- 44
DB 1667 CLVRADPGPCNREIPRWAYDKASGCKKTFIFGCGQNNNFDNQCVAFETGCGGNLNN 1726

QY 45 ----AICLVTC 51
DB 1727 FVSIADCCQATC 1737

RESULT 47
S00371
isoaprotinin G1 - bovine hybrid
C:Species: Bos primigenius indicus x Bos primigenius taurus (cattle)
C:Date: 31-Dec-1990 #sequence_revision 31-Dec-1990 #text_change 09-Jul-2004
C:Accession: S00371
R:Siekemann, J.; Wenzel, H.R.; Schroeder, W.; Techesche, H.
Biol. Chem. Hoppe-Seyler 369, 157-163, 1988
A:Title: Characterization and sequence determination of six aprotinin homologues from bo
A:Reference number: S00371; MUID:88221840; PMID:2453200
A:Molecule type: protein
A:Accession: S00371
A:Residues: 1-59 <SIE>
A:Cross-references: UNIPROT:Q7M311
C:Superfamily: basic proteinase inhibitor; animal Kunitz-type proteinase inhibitor homolog
C:Keywords: pyroglutamic acid; serine proteinase inhibitor
F:6-56/Domain: animal Kunitz-type proteinase inhibitor homology <BPI>
F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status predicted
F:16/Inhibitory site: Lys (trypsin) #status predicted

Query Match 44.4%; Score 134; DB 2; Length 59;
Best Local Similarity 41.2%; Pred. No. 2.4e-09;
Matches 21; Conservative 10; Mismatches 20; Indels 0; Gaps 0;

QY 1 CSMPQAGPCLASIPHWYNNKTKICSEFIYGGCGQNNNNFQTEAICLVTC 51
DB 6 CLEPPYTGCKARMIRYFYNAKAGLCQPFVYGGCRKSNFNFKSAEDCMRTC 56

RESULT 48
T108
serum basic proteinase inhibitor - bovine
C:Species: Bos primigenius taurus (cattle)
C:Date: 31-Oct-1980 #sequence_revision 31-Oct-1980 #text_change 09-Jul-2004
C:Accession: A01206
R:Wachter, E.; Depner, K.; Hochstrasser, K.; Lempart, K.; Geiger, R.
FEBS Lett. 119, 58-62, 1980
A:Title: A new Kunitz-type inhibitor from bovine serum amino acid sequence determination
A:Reference number: A01206; MUID:81044408; PMID:7428928
A:Accession: A01206
A:Molecule type: protein
A:Residues: 1-60 <WAC>
A:Cross-references: UNIPROT:P00975
C:Comment: This inhibitor has activity very similar to that of the basic proteinase inhibi
C:Superfamily: basic proteinase inhibitor; animal Kunitz-type proteinase inhibitor homo
C:Keywords: serine proteinase inhibitor
F:7-57/Domain: animal Kunitz-type proteinase inhibitor homology <BPI>
F:17/Inhibitory site: Lys (trypsin) #status experimental

Query Match 44.4%; Score 134; DB 1; Length 60;
Best Local Similarity 41.2%; Pred. No. 2.4e-09;
Matches 21; Conservative 10; Mismatches 20; Indels 0; Gaps 0;

QY 1 CSMPQAGPCLASIPHWYNNKTKICSEFIYGGCGQNNNNFQTEAICLVTC 51
DB 7 CLEPPYTGCKARMIRYFYNAKAGCETPFVYGGCRKSNFNFKSAEDCMRTC 57

RESULT 49
D88550
protein ZC84.6 [imported] - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
C:Accession: D88550
R:anonymous, The C. elegans Sequencing Consortium.
Science 282, 2012-2018, 1998
A:Title: Genome sequence of the nematode C. elegans: a platform for investigating biolo
A:Reference number: A75000; MUID:99069613; PMID:9851916
A:Note: see websites genome.wustl.edu/gsc/C.elegans/ and www.sanger.ac.uk/Projects/C.el
A:Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; amo
A:Accession: D88550
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-1474 <STO>
A:Cross-references: UNIPROT:O62504; GB:chr_III; PIDN:CAA79570.1; PID:G3881447; GSPDB:GN
C:Genetics:
A:Gene: ZC84.6
A:Map position: 3

Query Match 44.4%; Score 134; DB 2; Length 1474;
Best Local Similarity 43.1%; Pred. No. 5.1e-08;
Matches 22; Conservative 7; Mismatches 22; Indels 0; Gaps 0;

QY 1 CSMPQAGPCLASIPHWYNNKTKICSEFIYGGCGQNNNNFQTEAICLVTC 51
DB 439 CTQPLRVGNCDRSVRRYWYSAATRECQSFYTCGQGNNDNNFETLVDCQTCF 489

RESULT 50
S28291
hypothetical protein ZC84.1 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004
C:Accession: S28291
R:Thomas, K.
submitted to the EMBL Data Library, December 1992
A:Reference number: S28285


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ID AC Q6IE19 PRELIMINARY; PRT; 182 AA.
DT Q6IE19;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE WAP four-disulfide core 6-like 1.
GN Name=wfdc611;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI TaxID=10116;
RN [1]_
RP SEQUENCE FROM N.A.
RC STRAIN=Sprague-Dawley;
RX PubMed=15060002; DOI=10.1101/gr.1946304;
RA Puente X.S., Lopez-Otin C.;
RT "A genomic analysis of rat proteases and protease inhibitors.";
RL Genome Res. 14:609-622(2004).
CC -!- SIMILARITY: Contains 1 BPTi/Kunitz inhibitor domain.
CC -!- MISCELLANEOUS: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ third party annotation (TPA) entry.
DR EMBL; EN000374; CAB51900.1; -.
DR HSSP; P00974; 1KGU.
DR GO; GO:0004867; F:serine-type endopeptidase inhibitor activity; IEA.
DR InterPro; IPR002223; Prot_inh_Kunz-m.
DR InterPro; IPR008197; WAP.
DR Pfam; PF00014; Kunitz_BPTI; 1.
DR Pfam; PF00095; WAP; 1.
DR PRINTS; PRO0003; 4DISULPHCORE.
DR PRINTS; PRO0759; BASICPTASE.
DR ProDom; PD000222; Prot_inh_Kunz-m; 1.
DR SMART; SM00131; KU; 1.
DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
DR PROSITE; PS0279; BPTI_KUNITZ_2; 1.
SQ SEQUENCE 182 AA; 21018 MW; EB12D7BFF756707E CRC64;

Query Match 73.8%; Score 223; DB 2; Length 182;
Best Local Similarity 66.7%; Pred. No. 1.3e-19;
Matches 34; Conservative 8; Mismatches 9; Indels 0; Gaps 0;

QY 1 CSMPEGAGPCLASIPHWYKTKICSEPIYGGCGGNNNFOTEICLVTC 51
Db 77 CSLPQDAGPCLAYLRWYKTKTNLCTQPIYGGCGGNTNNFLSKDICTSIC 127

RESULT 3
EPPI HUMAN
ID EPPI HUMAN STANDARD; PRT; 133 AA.
AC Q95975; Q96SD7; Q9HD30;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Eppin precursor (Epididymal protease inhibitor) (Serine protease
DE inhibitor-like with Kunitz and WAP domains 1) (WAP four-disulfide core
DE domain protein 7) (Protease inhibitor WAP7).
GN Name=SPINLW1; Synonyms=WAP7, WFDC7;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI TaxID=9606;
RN [1]_
RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
RC TISSUE=Epididymis, and Testis;
RX MEDLINE=21297183; PubMed=11404006; DOI=10.1016/S0378-1119(01)00462-0;
RA Richardson R.T., Sivashanmugam P., Hall S.H., Hamil K.G., Moore P.A.,
RA Ruben S.M., French F.S., O'Rand M.G.;
RT "Cloning and sequencing of human Eppin: a novel family of protease
RT inhibitors expressed in the epididymis and testis.";
RL Gene 270:93-102(2001).
[2]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RA Stavrides G.S., Huckie E.J., Deloukas P.;
RA Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
RN

[3]
RP SEQUENCE FROM N.A.
RX MEDLINE=21638749; PubMed=11780052; DOI=10.1038/414865a;
RA Deloukas P., Matthews L.H., Ashurst J.L., Burton J., Gilbert J.G.R.,
RA Jones M., Stavrides G., Almeida J.P., Babbage A.K., Bagguley C.L.,
RA Bailey J., Barlow K.F., Bates K.N., Bead L.M., Beare D.M.,
RA Beasley O.P., Bird C.P., Blakey S.E., Bridgeman A.M., Brown A.J.,
RA Buck D., Burrill W.D., Butler A.P., Carder C., Carter N.P.,
RA Chapman J.C., Clamp M., Clark G., Clark L.N., Clark S.Y., Clee C.M.,
RA Clegg S., Cobley V.E., Collier R.E., Connor R.E., Corby N.R.,
RA Coulson A., Coville G.J., Deadman R., Dhani P.D., Dunn M.,
RA Ellington A.G., Frankland J.A., Fraser A., French L., Garner P.,
RA Grafham D.V., Griffiths C., Griffiths M.N.D., Gwilliam R., Hall R.E.,
RA Hammond S., Harley J.L., Heath P.D., Ho S., Holden J.L., Howden P.J.,
RA Huckle E., Hunt A.R., Hunt S.E., Jekosch K., Johnson C.M., Johnson D.,
RA Kay M.P., Kimberley A.M., King A., Knights A., Laird G.K., Lawlor S.,
RA Leharvalaho M.H., Leversha M.A., Lloyd C., Lloyd D.M., Lovell J.D.,
RA Marsh V.L., Martin S.L., McConnachie L.J., McIay K., McMurray A.A.,
RA Milne S.A., Mistry D., Moore M.J.F., Mullikin J.C., Nickerson T.,
RA Oliver K., Parker A., Patel R., Pearce T.A.V., Peck A.I.,
RA Phillimore B.J.C.T., Prathalingam S.R., Plumb R.W., Ramsey H.,
RA Rice C.M., Ross M.T., Scott C.E., Sehra H.K., Showkneen R., Sims S.,
RA Skuce C.D., Smith M.L., Soderlund C., Steward C.A., Sulston J.E.,
RA Swann R.M., Symamore N., Taylor R., Tee L., Thomas D.W., Thorpe A.,
RA Tracey A., Tromans A.C., Vaudin M., Wall M., Wallis J.M.,
RA Whitehead S.L., Whittaker P., Willey D.L., Williams L., Williams S.A.,
RA Whiting M., Wray P.W., Hubbard T., Durbin R.M., Bentley D.R., Beck S.,
RA Rogers J.;
RT "The DNA sequence and comparative analysis of human chromosome 20.";
RL Nature 414:865-871(2001).
[4]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RC TISSUE=Brain;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Altschul R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Kleitner S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo A.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Boak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A.C., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallos D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC -!- SUBCELLULAR LOCATION: Secreted (Potential).
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=1;
CC IsoId=095925-1; Sequence=Displayed;
CC Name=2;
CC IsoId=095925-2; Sequence=VSP 006755;
CC -!- TISSUE SPECIFICITY: Expressed in epididymis and testis.
CC -!- SIMILARITY: Contains 1 BPTi/Kunitz inhibitor domain.
CC -!- SIMILARITY: Contains 1 WAP-type domain.
CC
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Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Fahey J., Helton E., Kettaman M., Madan A., Rodrigues S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S., Krzywiński M.I., Skaleka U., Smalilus D.E., Schnerch A., Schein J.E., Jones S.J., Marra M.A.;
and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
[2]
SEQUENCE FROM N.A.
TISSUE=Brain;
Strausberg R.;
Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
CC -I- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.
DR EMBL; BC044829; AAH44829.1; -.
DR HSP; P00974; IUAU.
DR GO; GO:0004867; F-serine-type endopeptidase inhibitor activity; IEA.
DR InterPro; IPRO02223; Prot_Inh_Kunz-m.
DR InterPro; IPRO08197; WAP.
DR Pfam; PF00014; Kunitz_BPTI; 1.
DR Pfam; PF00095; WAP; 1.
DR PRINTS; PR00003; 4DISULPHCORE.
DR PRINTS; PR00759; BASICPTASE.
DR PRODOM; PD000222; Prot_Inh_Kunz-m; 1.
DR SMART; SM00131; KU; 1.
DR SMART; SM00217; WAP; 1.
DR PROSITE; PS00317; 4 DISULFIDE CORE; 1.
DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
DR PROSITE; PSS0279; BPTI_KUNITZ_2; 1.
FT NON_TER
SQ SEQUENCE 143 AA; 16506 MW; 92BF56C2B7977508 CRC64;

Query Match 72.5%; Score 219; DB 2; Length 143;
Best Local Similarity 68.8%; Pred.No. 3.3e-19;
Matches 35; Conservative 5; Mismatches 11; Indels 0; Gaps 0;

QY 1 CSMPQBAGPCLASIPHWYNKTKICSEFYGGCGGNNNNFQTEAICLVTC 51
|||:|||:||||:||||:||||:||||:||||:||||:
DB 87 CEMPKEGTGCLAYFLHWYDKDNTCSMFVYGCGGNNNNFQSKANCLNLC 137

RESULT 5
Q8HZ45 PRELIMINARY; PRT; 133 AA.

ID Q8HZ45
AC Q8HZ45
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DD 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Epitdymal protease inhibitor 1.
GN Name-Eppin;
OS Papio papio (Guinea baboon).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecoidea; Papio.
OX NCBI_TaxID=100937;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Testis;
RA Sivasharmugam P., O'Rand M.G., Richardson R.T.;
RL Submitted (AUG-2002) to the EMBL/GenBank/DBJ databases.
CC -I- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.
DR EMBL; AY141973; AN08507.1; -.
DR HSP; P00974; IUAU.
DR GO; GO:0008233; F-peptidease activity; IEA.
DR GO; GO:0004867; F-serine-type endopeptidase inhibitor activity; IEA.
DR InterPro; IPRO02223; Prot_Inh_Kunz-m.
DR InterPro; IPRO08197; WAP.
DR Pfam; PF00014; Kunitz_BPTI; 1.
DR Pfam; PF00095; WAP; 1.
DR PRINTS; PR00759; BASICPTASE.

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DR Probom: P0000222; Prot_Inh_Kunz-m; 1.
DR SMART; SM00131; KU; 1.
DR SMART; SM00217; WAP; 1.
DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
DR PROSITE; PS0279; BPTI_KUNITZ_2; 1.
KW Protease.
SQ SEQUENCE 133 AA; 15277 MW; B33ABE57ECBBE84 CRC64;

Query Match 71.5%; Score 216; DB 2; Length 133;
Best Local Similarity 68.6%; Pred. No. 7.2e-19;
Matches 35; Conservative 3; Mismatches 13; Indels 0; Gaps 0;

Qy 1 CSMPEAGPCLASIPHHWYKTKICSEFIYGGCGGNNNFQTEAICLVTC 51
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 77 CEMPNETGCLAFFIRWYDKKNNTCTSFVHGCGGNNNFQSEANCLNTC 127

RESULT 6
EPPI_MACMU
ID EPPI_MACMU STANDARD; PRT; 133 AA.
AC Q9BDL1;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DE Eppin precursor (Epididymal protease inhibitor) (Serine protease
DE inhibitor-like with Kunitz and WAP domains 1).
GN Name=SPINLW1;
OS Macaca mulatta (Rhesus macaque).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae;
OC Cercopitheciinae; Macaca.
OX NCBI_TaxID=9544;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Epididymis, and Testis;
RA Sivashanmugam P., Hall S.H., Hamil K.G., French F.S., O'Rand M.G.,
RA Richardson R.T.;
RT "Characterization of monkey and mouse Eppin, a protease inhibitor from
RT epididymis and testis.";
RL Submitted (FEB-2001) to the EMBL/GenBank/DBSJ databases.
CC -!- SUBCELLULAR LOCATION: Secreted (Potential).
CC -!- TISSUE SPECIFICITY: Expressed in epididymis and testis.
CC -!- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.
CC -!- SIMILARITY: Contains 1 WAP-type domain.
CC
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CC
DR EMBL; AF346414; AAK31336.1; -.
DR HSP; P00974; 1BPTI
DR InterPro; IPR002223; Prot_Inh_Kunz-m.
DR Pfam; PF00014; Kunitz_BPTI; 1.
DR Pfam; PF00095; WAP; 1.
DR PRINTS; PR00759; BASICPTASE.
DR PRODOM; P0000222; Prot_Inh_Kunz-m; 1.
DR SMART; SM00131; KU; 1.
DR SMART; SM00217; WAP; 1.
DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
DR PROSITE; PS0279; BPTI_KUNITZ_2; 1.
KW Serine protease inhibitor; Signal.
FT SIGNAL 1 21 Potential.
FT CHAIN 22 133 Eppin.
FT DOMAIN 29 73 WAP.
FT DOMAIN 77 127 BPTI/Kunitz inhibitor.
FT DISULFID 33 61 By similarity.
FT DISULFID 40 65 By similarity.
FT DISULFID 48 60 By similarity.
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FT DISULFID 54 69 By similarity.
FT DISULFID 77 127 By similarity.
FT DISULFID 86 110 By similarity.
FT DISULFID 102 123 By similarity.
SQ SEQUENCE 133 AA; 15279 MW; 433ABE946E39A35E9 CRC64;

Query Match 69.9%; Score 211; DB 1; Length 133;
Best Local Similarity 66.7%; Pred. No. 3e-18;
Matches 34; Conservative 4; Mismatches 13; Indels 0; Gaps 0;

Qy 1 CSMPEAGPCLASIPHHWYKTKICSEFIYGGCGGNNNFQTEAICLVTC 51
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 77 CEMPNETGCLAFFIRWYDKKNNTCTSFVHGCGGNNNFQSEANCLNTC 127

RESULT 7
EPPI_MOUSE
ID EPPI_MOUSE STANDARD; PRT; 134 AA.
AC Q9DA01;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DE Eppin precursor (Epididymal protease inhibitor) (Serine protease
DE inhibitor-like with Kunitz and WAP domains 1).
GN Name=Spinlwl;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/c; TISSUE=Epididymis, and Testis;
RA Sivashanmugam P., Hall S.H., Hamil K.G., French F.S., O'Rand M.G.,
RA Richardson R.T.;
RT "Characterization of monkey and mouse Eppin, a protease inhibitor from
RT epididymis and testis.";
RL Submitted (FEB-2001) to the EMBL/GenBank/DBSJ databases.
CC -!- SUBCELLULAR LOCATION: Secreted (Potential).
CC -!- TISSUE SPECIFICITY: Expressed in epididymis and testis.
CC -!- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.
CC -!- SIMILARITY: Contains 1 WAP-type domain.
CC
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CC
DR EMBL; AF346414; AAK31336.1; -.
DR HSP; P00974; 1BPTI
DR InterPro; IPR002223; Prot_Inh_Kunz-m.
DR Pfam; PF00014; Kunitz_BPTI; 1.
DR Pfam; PF00095; WAP; 1.
DR PRINTS; PR00759; BASICPTASE.
DR PRODOM; P0000222; Prot_Inh_Kunz-m; 1.
DR SMART; SM00131; KU; 1.
DR SMART; SM00217; WAP; 1.
DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
DR PROSITE; PS0279; BPTI_KUNITZ_2; 1.
KW Serine protease inhibitor; Signal.
FT SIGNAL 1 21 Potential.
FT CHAIN 22 133 Eppin.
FT DOMAIN 29 73 WAP.
FT DOMAIN 77 127 BPTI/Kunitz inhibitor.
FT DISULFID 33 61 By similarity.
FT DISULFID 40 65 By similarity.
FT DISULFID 48 60 By similarity.
```


NCBI_TaxID=9606;
[1]
RN MEDLINE=22304654; PubMed=12206714; DOI=10.1042/BJ20020869;
RP CLaus A., Lilja H., Lundwall A.;
RX "A locus on human chromosome 20 contains several genes expressing
RT protease inhibitor domains with homology to whey acidic protein.";
RL Biochem. J. 368:233-242(2002).
[2]
RN MEDLINE=21638749; PubMed=11780052; DOI=10.1038/414865a;
RP Jones M., Matthews L.H., Ashurst J.L., Burton J., Gilbert J.G.R.,
RA Deloukas P., Stavrides G., Almeida J.P., Babbage A.K., Baguley C.L.,
RA Bailey J., Barlow K.F., Bates K.N., Beard L.M., Beare D.M.,
RA Beasley O.P., Bird C.P., Blakey S.E., Bridgman A.M., Brown A.J.,
RA Buck D., Burrill W.D., Butler A.P., Carder C., Carter N.P.,
RA Chapman J.C., Clamp M., Clark G., Clark L.N., Clark S.V., Clee C.M.,
RA Clegg S., Cobley V.E., Collier R.E., Connor R.E., Corby N.R.,
RA Coulson A., Coville G.J., Deadman R., Dhani P.D., Dunn M.,
RA Ellington A.G., Frankland J.A., Fraser A., French L., Garner P.,
RA Grafham D.V., Griffiths C., Griffiths M.N.D., Gwilliam R., Hall R.E.,
RA Hammond S., Harley J.L., Heath P.D., Ho S., Holden J.L., Howden P.J.,
RA Huckle E., Hunt A.R., Hunt S.E., Jekosch K., Johnson C.M., Johnson D.,
RA Kay M.P., Kimberley A.M., King A., Knights K., Laird G.K., Lawlor S.,
RA Lehaeslaih M.H., Leverha M.A., Lloyd C., Lloyd D.M., Lovell J.D.,
RA Marsh V.L., Martin S.L., McConachie L.J., McMay K., McMurray A.A.,
RA Milne S.A., Mistry D., Moore M.J.F., Mullikin J.C., Nickerson T.,
RA Oliver K., Parker A., Patel R., Pearce T.A.V., Peck A.I.,
RA Phillimore B.J.C.T., Prathalingam S.R., Plumb R.W., Ramsay H.,
RA Rice C.M., Ross M.T., Scott C.E., Sehra H.K., Shownkeen R., Sims S.,
RA Skuce C.D., Smith M.L., Soderlund C., Steward C.A., Sulston J.E.,
RA Swann R.M., Sycamore N., Taylor R., Tee L., Thomas D.W., Thorpe A.,
RA Tracey A., Tromans A.C., Vaudin M., Wall M., Wallis J.M.,
RA Whitehead S.L., Whittaker P., Willey D.L., Williams L., Williams S.A.,
RA Wilming L., Wray P.W., Hubbard T., Durbin R.M., Bentley D.R., Beck S.,
RA Rogers J.;
RT "The DNA sequence and comparative analysis of human chromosome 20.";
RL Nature 414:865-871(2001).
CC -1- SUBCELLULAR LOCATION: Secreted (Potential).
CC -1- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=1;
CC IsoId=Q9BQY6-1; Sequence=Displayed;
CC Name=2;
CC IsoId=Q9BQY6-2; Sequence=VSP_007550, VSP_007551;
CC -1- TISSUE SPECIFICITY: Ubiquitously expressed, but the highest levels
CC are found in epididymis, testis and trachea.
CC -1- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.
CC -1- SIMILARITY: Contains 1 WAP-type domain.
CC -----
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CC -----
CC EMBL; AF411861; AA03684.1; -;
CC EMBL; AL031663; CAC36264.1; -;
CC HSSP; P02760; IBIK.
CC Genew; HGNC:16164; WFDC6.
CC InterPro; IPR002223; Prot_Inh_Kunz-m.
CC InterPro; IPR008197; WAP_BPTI; 1.
CC Pfam; PF00014; Kunitz_BPTI; 1.
CC Pfam; PF00095; WAP; 1.
CC PRINTS; PR00759; BASICTPASE.
CC ProDom; PD000222; Prot_Inh_Kunz-m; 1.
CC SMART; SM00131; KU; 1.
CC SMART; SM00217; WAP; 1.
CC PROSITE; PS00317; 4-DISULFIDE CORE; FALSE_NEG.
CC PROSITE; PS00280; BPTI_KUNITZ_1; FALSE_NEG.
CC PROSITE; PS00279; BPTI_KUNITZ_2; 1.

Alternative splicing; Serine protease inhibitor; Signal.
KW SIGNAL 1 25 Potential.
FT CHAIN 26 131 WAP four-disulfide core domain protein 6.
FT DOMAIN 31 69 WAP.
FT BPTI/Kunitz inhibitor.
FT DISULFID 33 61 By similarity.
FT DISULFID 48 60 By similarity.
FT DISULFID 54 69 By similarity.
FT VARSPLIC 75 86 IYAVCHRLRLAPA -> VSLTYHKBELE (in isoform 2).
FT FTID=VSP_007550.
FT Missing (in isoform 2).
FT FTID=VSP_007551.
SQ SEQUENCE 131 AA; 14626 MW; 2F6D08E743EB7564 CRC64;
Query Match 54.6%; Score 165; DB 1; Length 131;
Best Local Similarity 96.8%; Pred. No. 1.5e-12;
Matches 30; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 21 KTKTKSEFIYGGCGNNNNFQTEAICLVTC 51
DB 97 KTKTKSEFIYGGCGNNNNFQTEAICLVTC 127
RESULT 13
Q6DJB6 PRELIMINARY; PRT; 750 AA.
AC Q6DJB6;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE App-prov protein.
GN Name=app-prov;
OS Xenopus tropicalis (Western clawed frog) (Silurana tropicalis).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8364;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Whole body;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Schuler G.D.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Caesant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Murty D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzyzanski M.I., Skalek A., Smailus D.E., Schnarch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RC and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
[2]
RN SEQUENCE FROM N.A.
RC TISSUE=Whole body;
RA Klein S., Gerhard D.S.;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.
CC EMBL; BC075266; AAF75266.1; -;
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0005488; F:binding; IEA.
DR GO; GO:0004867; F:serine-type endopeptidase inhibitor activity; IEA.
DR InterPro; IPR008155; A4_APP.

DR InterPro; IPR008154; A4_extra.
DR InterPro; IPR001255; Beta-APP.
DR InterPro; IPR002223; Prot_Inh_Kunz-m.
DR Pfam; PF02177; A4_EXTRA_1.
DR Pfam; PF03494; Beta-APP_1.
DR Pfam; PF00014; Kunitz_BPTI_1.
DR PRINTS; PR00203; AMYLOIDA4.
DR PRINTS; PR00759; BASICPTASE.
DR PRINTS; PR00204; BETAAMYLOID.
DR ProDom; PD000222; Prot_Inh_Kunz-m; 1.
DR SMART; SMO0006; A4_EXTEA; 1.
DR SMART; SMO0331; KU_1.
DR PROSITE; PS00319; A4_EXTRA; 1.
DR PROSITE; PS00320; A4_INTRA; 1.
DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
DR PROSITE; PS50279; BPTI_KUNITZ_2; 1.
DR PROSITE; PS50279; BPTI_KUNITZ_2; 1.

SQ SEQUENCE 750 AA; 84527 MW; 4222350843147CAF CRC64;

Query Match 54.6%; Score 165; DB 2; Length 750;
Best Local Similarity 51.0%; Pred. NO. 8.6e-12;
Matches 26; Conservative 7; Mismatches 18; Indels 0; Gaps 0

QY 1 CSMPEAGPCLASPHWYNKKIKCSFYGGCGNNNFQTAEICLVTC 51
DB 289 CSQAETGPCRAMIPRWYYDVTERKCAQFIYGCGGNRNFDSEDCNMCV 339
||| ||| ||| ||| : :: ||| ||| ||| |:: :|
C P E A G P C L A S P H W Y N K K I K C S F Y G G C G N N N F Q T A E I C L V T C 51

RESULT 14
IBPC_BOVIN STANDARD; PRT; 67 AA.
AC P00976;
DT 21-JUL-1986 (Rel. 01, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Colostrium trypsin inhibitor (Colostrium BPI).
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE.
RA Cecanova D., Jonakova V., Sorm F.;
RT "Primary structure of trypsin inhibitor from cow colostrum (component B2)".
RL Collect. Czech. Chem. Commun. 36:3342-3357(1971).
RN [2]
RP DISULFIDE BONDS.
RA Dischova D., Ber E.;
RT "Disulfide bonds of trypsin inhibitor from cow colostrum.";
RL Collect. Czech. Chem. Commun. 39:680-688(1974).
RN [3]
RP CHARACTERIZATION.
RX PubMed=11947537;
RA Cecanova D., Muszynska G.;
RT "Role of lysine 18 in active center of cow colostrum trypsin inhibitor."
RL FEBS Lett. 8:84-86(1970).
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.
FR; A01207; TIBOC.
HSSP; P02760; IBIK.
DR InterPro; IPR002223; Prot_Inh_Kunz-m.
DR Pfam; PF00014; Kunitz_BPTI_1.
DR PRINTS; PR00759; BASICPTASE.
DR ProDom; PD000222; Prot_Inh_Kunz-m; 1.
DR SMART; SMO0131; KU; 1.
DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
DR PROSITE; PS50279; BPTI_KUNITZ_2; 1.
KW Direct protein sequencing; Glycoprotein; Serine protease inhibitor.
FT SITE 18 19 Reactive bond for trypsin.
FT DISULFID 8 58
FT DISULFID 17 41

RT Kunitz-type serine proteinase inhibitor domain is a predominant
RT product in mouse but not in human.;
RL Biochem. Biophys. Res. Commun. 255:740-748(1999).
CC -!- FUNCTION: Inhibitor of HGF activator.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein (Potential).
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=3;
CC Name=1;
CC IsoId=Q9WU03-1; Sequence=Displayed;
CC Name=2;
CC IsoId=Q9WU03-2; Sequence=VSP_003034;
CC Name=3;
CC IsoId=Q9WU03-3; Sequence=VSP_003035, VSP_003036;
CC -!- TISSUE SPECIFICITY: Isoform 2 is more predominantly expressed than
CC isoform 1.
CC -!- DOMAIN: This inhibitor contains two inhibitory domains.
CC -!- SIMILARITY: Contains 2 BPTI/Kunitz inhibitor domains.
CC
CC This SWISS-PROT entry is copyrighted. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC
CC EMBL; AF099016; AAD22172.1; -;
CC EMBL; AF099019; AAD22173.1; -;
CC EMBL; AF099020; AAD22174.1; -;
CC HSSP; P00974; 1K09.
CC MGD; MGI:1338031; Spint2.
CC InterPro; IPR002223; Prot_Inh_Kunz-m.
CC Pfam; PF00014; Kunitz_BPTI; 2.
CC PRINTS; PR00759; BASICTPASE.
CC ProDom; PD000222; Prot_Inh_Kunz-m; 2.
CC SMART; SM00131; KU; 2.
CC PROSITE; PS00280; BPTI_KUNITZ_1; 2.
CC PROSITE; PS0279; BPTI_KUNITZ_2; 2.
CC KW Alternative splicing; Glycoprotein; Repeat; Serine protease inhibitor;
KW Signal; Transmembrane.
FT SIGNAL 1 27 Potential.
FT CHAIN 28 252 Kunitz-type protease inhibitor 2.
FT DOMAIN 28 197 Extracellular (Potential).
FT TRANSMEM 198 218 Potential.
FT DOMAIN 219 252 Cytoplasmic (Potential).
FT DOMAIN 38 88 BPTI/Kunitz inhibitor 1.
FT DOMAIN 133 183 BPTI/Kunitz inhibitor 2.
FT SITE 48 49 Reactive bond (By similarity).
FT SITE 143 144 Reactive bond (By similarity).
FT DISULFID 38 88 By similarity.
FT DISULFID 47 71 By similarity.
FT DISULFID 63 84 By similarity.
FT DISULFID 133 183 By similarity.
FT DISULFID 142 166 By similarity.
FT DISULFID 158 179 By similarity.
FT CARBOHYD 57 57 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 94 94 N-linked (GlcNAc...) (Potential).
FT VARSPLIC 37 93 Missing (in isoform 2 and isoform 3).
FT VARSPLIC 114 128 /FTID=VSP_003034.
FT PRKQSAEDLSAEIFN -> CFVLSVAALFLFYA (in
FT isoform 3).
FT /FTID=VSP_003035.
FT VARSPLIC 129 252 Missing (in isoform 3).
FT /FTID=VSP_003036.
FT SEQUENCE 252 AA; 27914 MW; B2FF4B86924D4F8F CRC64;
Query Match 53.0%; Score 160; DB 1; Length 252;
Best Local Similarity 49.0%; Pred. No. 1.2e-11;
Matches 25; Conservative 7; Mismatches 19; Indels 0; Gaps 0;

RESULT 17
Q6ZNI4 PRELIMINARY; PRT; 283 AA.
ID Q6ZNI4
AC Q6ZNI4
DT 05-JUL-2004 (TRENBLrel. 27, Created)
DT 05-JUL-2004 (TRENBLrel. 27, Last sequence update)
DE Hypothetical protein FLJ16032.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Tongue;
RA Ninomiya K., Wagatsuma M., Kanda K., Kondo H., Yokoi T., Kodaira H.,
RA Furuya T., Takahashi M., Kikkawa E., Omura Y., Abe K., Kamiyama K.,
RA Katsuta N., Sato K., Tanikawa M., Yamazaki M., Sugiyama T., Irie R.,
RA Otsuki T., Sato H., Wakamatsu A., Ishii S., Yamamoto J., Isono Y.,
RA Kawai-Hio Y., Saito K., Nishikawa T., Kimura K., Yamashita H.,
RA Matsuo K., Nakamura Y., Sekine M., Kikuchi H., Murakawa K.,
RA Katsuhori K., Takahashi-Fujii A., Oshima A., Sugiyama A., Kawakami B.,
RA Suzuki Y., Sugano S., Nagahara K., Masuho Y., Nagai K., Isogai T.,
RL Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.
CC EMBL; AK131196; BAD18391.1; -;
CC HSSP; P00974; 1K09.
CC GO; GO:0004867; F:serine-type endopeptidase inhibitor activity; IEA.
CC InterPro; IPR001134; Netrin_C.
CC InterPro; IPR002223; Prot_Inh_Kunz-m.
CC InterPro; IPR008993; TIMP-like.
CC Pfam; PF00014; Kunitz_BPTI; 2.
CC PRINTS; PR00759; BASICTPASE.
CC ProDom; PD000222; Prot_Inh_Kunz-m; 2.
CC SMART; SM00131; KU; 1.
CC PROSITE; PS00280; BPTI_KUNITZ_1; 1.
CC PROSITE; PS0279; BPTI_KUNITZ_2; 1.
CC PROSITE; PS0189; NTR; 1.
SQ SEQUENCE 283 AA; 31291 MW; 86206E7309866D30 CRC64;
Query Match 53.0%; Score 160; DB 2; Length 283;
Best Local Similarity 49.0%; Pred. No. 1.3e-11;
Matches 25; Conservative 7; Mismatches 19; Indels 0; Gaps 0;
QY 1 CSMQEGAGPCLASIPHWYNNKTKICSEFYGGCGGNNNNFQTEAICLVTC 51
DB 93 CSLPALQGFCKAYAPRWYNSQTGQSFVYGGCEGNGNFFESREACEESC 143
RESULT 18
Q8TEU8 PRELIMINARY; PRT; 576 AA.
ID Q8TEU8
AC Q8TEU8
DT 01-JUN-2002 (TRENBLrel. 21, Created)
DT 01-JUN-2002 (TRENBLrel. 21, Last sequence update)
DT 01-MAR-2004 (TRENBLrel. 26, Last annotation update)
DE Multivalent protease inhibitor protein.
GN Name=WFIKNRP;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21173622; PubMed=11274388; DOI=10.1073/pnas.061028398;
RA Trexler M., Banyai L., Pothay L.;
RT "A human protein containing multiple types of protease-inhibitory
RT modules";
RL Proc. Natl. Acad. Sci. U.S.A. 98:3705-3709(2001).
RN [2]
RP SEQUENCE FROM N.A.

```
RA Trexler M., Banyai L., Paddy L.;
RT "Distinct expression pattern of two related human proteins containing
RT multiple types of protease-inhibitory modules.";
RL Biol. Chem. 383:0-0(2002).
CC -!- SIMILARITY: Contains 2 BPTI/Kunitz inhibitor domains.
DR EMBL; AF468657; AAL7058.1; -.
DR HSSP; P00974; 1K09.
DR GO; GO:0008233; F:peptidase activity; IEA.
DR GO; GO:0004867; F:serine-type endopeptidase inhibitor activity; IEA.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003598; IG_c2.
DR InterPro; IPR001134; Netrin C.
DR InterPro; IPR002350; Prot_inh_Kazal.
DR InterPro; IPR011497; Prot_inh_Kazal_2.
DR InterPro; IPR002223; Prot_inh_Kunz-m.
DR InterPro; IPR008993; TIMP_like.
DR InterPro; IPR008197; WAP.
DR Pfam; PF07648; Kazal_2; 1.
DR Pfam; PF00014; Kunitz_BPTI; 2.
DR Pfam; PF00095; WAP; 1.
DR PRINTS; PR00003; 4DISULPHCORE.
DR PRINTS; PR00759; BASICPTASE.
DR PRODOM; PD00222; Prot_inh_Kunz-m; 2.
DR SMART; SM00408; IGC2; 1.
DR SMART; SM00280; KAZAL; 1.
DR SMART; SM00131; KU; 2.
DR SMART; SM00217; WAP; 1.
DR PROSITE; PS00317; 4_DISULFIDE_CORE; 1.
DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
DR PROSITE; PS0279; BPTI_KUNITZ_2; 2.
DR PROSITE; PS0835; IG LIKE; 1.
DR PROSITE; PS50189; NTR; 1.
KW Protease.
SQ SEQUENCE 576 AA; 63941 MW; 08B4F2EDB121F81 CRC64;

Query Match 53.0%; Score 160; DB 2; Length 576;
Best Local Similarity 49.0%; Pred. No. 2,7e-11;
Matches 25; Conservative 7; Mismatches 19; Indels 0; Gaps 0;

QY 1 CSMPOEAGPCLASIPHHWYKTKICSEFIYGGCGGNNNFQTEAICLVTC 51
Db 386 CSLPALQPCPKAYAPRWYNSQTGCQSFVYGCCEGNGNFFESRACEESC 436

RESULT 19
Q6UXZ9
ID Q6UXZ9 PRELIMINARY; PRT; 576 AA.
AC Q6UXZ9;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE Bikunin hlg.
GN ORFNames=UNQ9235;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22887296; PubMed=12975309; DOI=10.1101/gr.1293003;
RA Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D., Brugh J.,
RA Chen J., Chow B., Chui C., Crowley C., Currell B., Deuel B., Dowd P.,
RA Eaton D., Foster J., Grimaldi C., Gu Q., Hase P.E., Heldens S.,
RA Huang A., Kim H.S., Klinowski L., Jin Y., Johnson S., Lee J.,
RA Lewis L., Liao D., Mark M., Robbie E., Sanchez C., Schoenfeld J.,
RA Seshagiri S., Simmons L., Singh J., Smith V., Stinson J., Vagts A.,
RA Vandlen R., Watanabe C., Weiland D., Woods K., Xie M.H., Yansura D.,
RA Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A., Wood W.I.,
RA Godowski P.;
RT "The secreted protein discovery initiative (SPDI), a large-scale
RT effort to identify novel human secreted and transmembrane proteins: a
RT bioinformatics assessment.";
RL Genome Res. 13:2265-2270(2003).
```

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CC -!- SIMILARITY: Contains 2 BPTI/Kunitz inhibitor domains.
DR EMBL; AY358142; AAQ88509.1; -.
DR HSSP; P00974; 1K09.
DR GO; GO:0004867; F:serine-type endopeptidase inhibitor activity; IEA.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003598; IG_c2.
DR InterPro; IPR001134; Netrin C.
DR InterPro; IPR002223; Prot_inh_Kunz-m.
DR InterPro; IPR008993; TIMP_like.
DR InterPro; IPR008197; WAP.
DR Pfam; PF00014; Kunitz_BPTI; 2.
DR Pfam; PF00095; WAP; 1.
DR PRINTS; PR00003; 4DISULPHCORE.
DR PRINTS; PR00759; BASICPTASE.
DR PRODOM; PD00222; Prot_inh_Kunz-m; 2.
DR SMART; SM00408; IGC2; 1.
DR SMART; SM00131; KU; 2.
DR SMART; SM00217; WAP; 1.
DR PROSITE; PS00317; 4_DISULFIDE_CORE; 1.
DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
DR PROSITE; PS0279; BPTI_KUNITZ_2; 2.
DR PROSITE; PS0835; IG LIKE; 1.
DR PROSITE; PS50189; NTR; 1.
SQ SEQUENCE 576 AA; 63912 MW; 08B42DD50C3CF81 CRC64;

Query Match 53.0%; Score 160; DB 2; Length 576;
Best Local Similarity 49.0%; Pred. No. 2,7e-11;
Matches 25; Conservative 7; Mismatches 19; Indels 0; Gaps 0;

QY 1 CSMPOEAGPCLASIPHHWYKTKICSEFIYGGCGGNNNFQTEAICLVTC 51
Db 386 CSLPALQPCPKAYAPRWYNSQTGCQSFVYGCCEGNGNFFESRACEESC 436

RESULT 20
Q7PXZ1
ID Q7PXZ1 PRELIMINARY; PRT; 2419 AA.
AC Q7PXZ1;
DT 01-MAR-2004 (TrEMBLrel. 26, Created)
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE AGCP12609 (Fragment).
GN Name=agCG49342; ORFNames=ENSANGG00000019572;
OS Anopheles gambiae str. PEST.
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Anopheles.
OX NCBI_TaxID=180454;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=PEST;
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: Contains 9 BPTI/Kunitz inhibitor domains.
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; AAAB01008987; EAA01339.1; -.
DR HSSP; P10646; 1IRH.
DR GO; GO:0004867; F:serine-type endopeptidase inhibitor activity; IEA.
DR InterPro; IPR010294; ADAM_spacer1.
DR InterPro; IPR006209; EGF_like.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR010909; PLAC.
DR InterPro; IPR002223; Prot_inh_Kunz-m.
DR InterPro; IPR000884; TSP1.
DR InterPro; IPR008197; WAP.
DR Pfam; PF05986; ADAM_spacer1; 1.
DR Pfam; PF00014; Kunitz_BPTI; 9.
DR Pfam; PF00090; TSP_1; 7.
DR Pfam; PF00095; WAP; 1.
DR PRINTS; PR00003; 4DISULPHCORE.
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OC Ephydroidea: Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20196006; PubMed=10731132; DOI=10.1126/science.287.5461.2185;
RA Adame M.D., Celnikier S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutcon G.G., Workman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.H., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Gabor G.L.,
RA Abril J.F., Agbayani A., An H.J., Andrews-Pfannkuch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brothier P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahle C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,
RA Foster C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harries N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.H., Ibegwam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milhina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mout S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D., Scheeler F., Shen H.,
RA Shue B.C., Siden-Klanos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svireksas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.Y., Wassarman D.A., Weinstein G.M., Weisenbach J.,
RA Williams S.M., Woodgett, Worley K.C., Wu D., Yang S., Yao Q.A., Ye J.,
RA Yeh R.H., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.F., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster."
RN Science 287:2185-2195(2000).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=2426065; PubMed=12537568;
RA Celnikier S.E., Wheeler D.A., Kronmiller B., Carlson J.W., Halpern A.,
RA Patel S., Adams M., Champe M., Dugan S.P., Frise E., Hodgson A.,
RA George R.A., Hoskins R.A., Laverty T., Muzny D.M., Nelson C.R.,
RA Pacleb J.M., Park S., Pfeiffer B.D., Richards S., Sodergren E.J.,
RA Svireksas R., Tabor P.E., Wan K., Stapleton M., Sutton G.G., Venter C.,
RA Weinstein G., Scherer S.E., Myers E.W., Gibbs R.A., Rubin G.M.;
RT "Finishing a whole-genome shotgun. Release 3 of the Drosophila
melanogaster euchromatic genome sequence."
RN Genome Biol. 3:RESEARCH0079-RESEARCH0079(2002).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=2426070; PubMed=12537573;
RA Kaminker J.S., Bergman C.M., Kronmiller B., Carlson J., Svireksas R.,
RA Patel S., Frise E., Wheeler D.A., Lewis S.E., Rubin G.M.,
RA Ashburner M., Celnikier S.E.;
RT "The transposable elements of the Drosophila melanogaster euchromatin:
a genomics perspective."
RN Genome Biol. 3:RESEARCH0084-RESEARCH0084(2002).
RN [4]
RP SEQUENCE FROM N.A.
RX MEDLINE=2426069; PubMed=12537572;
RA Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
RA Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochnik S.E.,
RA Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Berman B.P.,
RA Bettencourt B.R., Celnikier S.E., de Grey A.D., Drysdale R.A.,
RA Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,
RA Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,

RA Lewis S.E.;
RT "Annotation of the Drosophila melanogaster euchromatic genome: a
systematic review."
RN Genome Biol. 3:RESEARCH0083-RESEARCH0083(2002).
RN [5]
RP SEQUENCE FROM N.A.
RG FlyBase;
RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
RN [6]
RP SEQUENCE FROM N.A.
RG FlyBase;
RL Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: Contains 10 BPTI/Kunitz inhibitor domains.
EMBL; AE003765; AAF56794.3; --
HSSP; P12111, 1KTH.
DR FlyBase; FBgn0003137; Ppn.
DR GO; GO:0005604; C:basement membrane; IDA.
DR InterPro; IPR010294; ADAM_spacer1.
DR InterPro; IPR006209; EGF_Like.
DR InterPro; IPR007110; Ig_Like.
DR InterPro; IPR003598; Ig_L2.
DR InterPro; IPR010909; PLAC.
DR InterPro; IPR002223; Prot_Inh_Kunz-m.
DR InterPro; IPR000884; TSP1.
DR InterPro; IPR008197; WAP.
DR Pfam; PF05986; ADAM_spacer1; 1.
DR Pfam; PF00047; Ig_2.
DR Pfam; PF00014; Kunitz_BPTI; 10.
DR Pfam; PF00090; TSP_1; 5.
DR Pfam; PF00095; WAP; 1.
DR PRINTS; PR00003; 4DISULPHCORE.
DR PRINTS; PR00759; BASICPTASE.
DR ProDom; PD000222; Prot_Inh_Kunz-m; 10.
DR SMART; SM00408; IGC2; 3.
DR SMART; SM00131; KU; 10.
DR SMART; SM00209; TSP1; 7.
DR SMART; SM00217; WAP; 1.
DR PROSITE; PS00317; 4_DISULFIDE_CORE; 1.
DR PROSITE; PS00280; BPTI_KUNITZ_1; 9.
DR PROSITE; PS0279; BPTI_KUNITZ_2; 10.
DR PROSITE; PS00022; EGF_1; UNKNOWN_1.
DR PROSITE; PS00835; IG_Like; 3.
DR PROSITE; PS00900; PLAC; 1.
DR PROSITE; PS00092; TSP1; 5.
SQ SEQUENCE 2772 AA; 299154 MW; 3965DC92D30CCAAA CRC64;

Query Match 52.6%; Score 159; DB 2; Length 2772;
Best Local Similarity 47.1%; Pred. No. 1.8e-10;
Matches 24; Conservative 7; Mismatches 20; Indels 0; Gaps 0;

QY 1 CSMQEQAGPCPLASIPHWYNNKTKICSEFIYGGCGGNNNFQTEAICLVTC 51
DB 1730 CEQPVESGFCAGNFERWYDNETDLCRPFYTGCKGNKNYPTEHACNYNC 1780

RESULT 24
Q869A0 PRELIMINARY; PRT; 2776 AA.
AC Q869A0;
DT 01-JUN-2003 (TReMBLrel. 24, Created)
DT 01-JUN-2003 (TReMBLrel. 24, Last sequence update)
DT 01-MAR-2004 (TReMBLrel. 26, Last annotation update)
DE Extracellular matrix protein papilin 2.
GN Name=Ppn;
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22552133; PubMed=1266201; DOI=10.1002/dvdy.10265;
RA Kramerova I.A., Kramerov A.A., Fessler J.H.;

RT "Alternative splicing of papilin and the diversity of Drosophila
 RL extracellular matrix during embryonic morphogenesis.";
 RL Dev. Dyn. 226:634-642(2003).

RN [2]

RP SEQUENCE FROM N.A.

RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: Contains 10 BPTI/Kunitz inhibitor domains.

DR EMBL; AF529179; AAO84907.1; -

DR HSSP; P12111; 1KTH.

DR FlyBase; F8gn0003137; Ppn.

DR GO; GO:0005604; C:basement membrane; IDA.

DR InterPro; IPR010294; ADAM spacer1.

DR InterPro; IPR006209; EGF like.

DR InterPro; IPR007110; EGF like.

DR InterPro; IPR003598; Iq c2.

DR InterPro; IPR010909; PLAC.

DR InterPro; IPR002223; Prot_Inh_Kunz-m.

DR InterPro; IPR000884; TSPI.

DR InterPro; IPR008197; WAP.

DR Pfam; PF05986; ADAM spacer1; 1.

DR Pfam; PF00047; ig; 2.

DR Pfam; PF00014; Kunitz_BPTI; 10.

DR Pfam; PF00090; TSP1; 5.

DR Pfam; PF00095; WAP; 1.

DR PRINTS; PR00003; 4DISULPHCORE.

DR PRINTS; PR00759; BASICPTASE.

DR ProDom; PD000222; Prot_Inh_Kunz-m; 10.

DR SMART; SM00408; ICG2; 3.

DR SMART; SM00131; KU; 10.

DR SMART; SM00209; TSP1; 7.

DR SMART; SM00217; WAP; 1.

DR PROSITE; PS00317; 4 DISULFIDE CORE; 1.

DR PROSITE; PS00280; BPTI_KUNITZ_1; 9.

DR PROSITE; PS0279; BPTI_KUNITZ_2; 10.

DR PROSITE; PS00022; EGF 1; UNKNOWN_1.

DR PROSITE; PS0835; Iq LIKE; 3.

DR PROSITE; PS0900; PLAC; 1.

DR PROSITE; PS0092; TSP1; 5.

DR Matrix protein.

KW SEQUENCE 2776 AA; 299741 MW; 92D38A17360D2D42 CRC64;

SQ Query Match 52.6%; Score 159; DB 2; Length 2776;

Best Local Similarity 47.1%; Pred. NO. 1.8e-10;

Matches 24; Conservative 7; Mismatches 20; Indels 0; Gaps 0;

QY 1 CSMPQAGCLASIPHWYTKKICSEFYGGCGGNNNFQTEALCLVTC 51

DB 1730 CEQPVESGFCAGNFERWYDNETDICRPFTYGGCKGNKNYPTEHACNYNC 1780

RESULT 25

Q7KRX2 PRELIMINARY; PRT; 2894 AA.

AC Q7KRX2;

DT 05-JUL-2004 (TrEMBLrel. 27, Created)

DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)

DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)

DE CG33103-PA.

GN Names:Ppn; ORFNames=CG33103;

OS Drosophila melanogaster (fruit fly).

OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;

OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;

OC Ephydroidea; Drosophilidae; Drosophila.

OX NCBI_TaxID=7227;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=20196006; PubMed=107311132; DOI=10.1126/science.287.5461.2185;

RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,

RA Anandates P.G., Scher S.E., Li P.W., Hoskins R.A., Galle R.F.,

RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,

RA Sutton G.G., Wortman J.R., Vandeil M.D., Zhang Q., Chen L.X.,

RA Brandon R.C., Rogers J.H., Blazej R.G., Champe M., Pfeiffer B.D.,

RA

Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Gabor G.L.,
 April J.F., Agbayani A., An H.J., Andrews-Pfannkuch C., Baldwin D.,
 Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
 Beeson K.Y., Benos P.V., Bernan P.P., Bhandari D., Bolshakov S.,
 Borkova D., Botchan M.R., Bouck J., Brokstein P., Brothier P.,
 Burtis K.C., Buser D.A., Butler H., Cadieu E., Center A., Chandra I.,
 Cherry J.M., Cawley S., Dahlke C., Vainport L.B., Davies P.,
 de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 Durbin K.J., Evangelista C.C., Ferraz C., Ferrera S., Fleischmann W.,
 Foslter C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,
 Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
 Hostin D., Houston K.A., Howland T.J., Wei M.H., Ibegwam C.,
 Jatali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Kechum K.A.,
 Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
 Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
 Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
 Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacle J.M.,
 Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 Reinert K., Remington K., Saunders R.D., Scheeler F., Shen H.,
 Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
 Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
 Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 Wang Z.Y., Wasserman D.A., Weinstein G.M., Weissenbach J.,
 Williams S.M., Woodage, Worley K.C., Wu D., Yang S., Yao Q.A., Ye J.,
 Yeh R.F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 "The genome sequence of Drosophila melanogaster.";
 Science 287:2185-2195(2000).

RL [2]

RP SEQUENCE FROM N.A.

RX MEDLINE=22426065; PubMed=12537568;

RA Celniker S.E., Wheeler D.A., Krommiller B., Carlson J.W., Halpern A.,

RA Patel S., Adams M., Champe M., Dugan S.P., Frise E., Hodgson A.,

RA George R.A., Hoskins R.A., Lavery T., Muzny D.M., Nelson C.R.,

RA Pacle J.M., Park S., Pfeiffer B.D., Richards S., Sodergren E.J.,

RA Svirskas R., Tabor P.E., Wan K., Stapleton M., Sutton G.G., Venter C.,

RA Weinstein G., Scherer S.E., Myers E.W., Gibbs R.A., Rubin G.M.,

RT "Finishing a whole-genome shotgun: Release 3 of the Drosophila

melanogaster euchromatic genome sequence.";

Genome Biol. 3:RESEARCH0079-RESEARCH0079(2002).

RL [3]

RP SEQUENCE FROM N.A.

RX MEDLINE=22426070; PubMed=12537573;

RA Kaminker J.S., Bergman C.M., Krommiller B., Carlson J., Svirskas R.,

RA Patel S., Frise E., Wheeler D.A., Lewis S.E., Rubin G.M.,

RA Ashburner M., Celniker S.E.;

RT "The transposable elements of the Drosophila melanogaster euchromatin:

a genomics perspective.";

Genome Biol. 3:RESEARCH0084-RESEARCH0084(2002).

RL [4]

RP SEQUENCE FROM N.A.

RX MEDLINE=22426069; PubMed=12537572;

RA Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,

RA Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochuk S.E.,

RA Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Berman B.P.,

RA Bettencourt B.R., Celniker S.E., de Grey A.D., Drysdale R.A.,

RA Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,

RA Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,

RA Lewis S.E.;

RT "Annotation of the Drosophila melanogaster euchromatic genome: a

systematic review.";

Genome Biol. 3:RESEARCH0083-RESEARCH0083(2002).

RL [5]

RP SEQUENCE FROM N.A.

RG FlyBase;

RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.

RP [6]

RP SEQUENCE FROM N.A.

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RG FlyBase;
RL Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: Contains 12 BPTI/Kunitz inhibitor domains.
DR EMBL; AE003765; AAF56795.3; -.
DR GO; GO:0004867; F:serine-type endopeptidase inhibitor activity; IEA.
DR HSSP; P10646; 1ADZ.
DR InterPro; IPR010294; ADAM_spacer1.
DR InterPro; IPR006209; EGF_Like.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003598; IG_c2.
DR InterPro; IPR010909; PLAC.
DR InterPro; IPR002223; Prot_Inh_Kunz-m.
DR InterPro; IPR000884; TSPI.
DR InterPro; IPR008197; WAP.
DR Pfam; PF05986; ADAM_spacer1; 1.
DR Pfam; PF00047; IG; 2.
DR Pfam; PF00014; Kunitz_BPTI; 12.
DR Pfam; PF00090; TSP_1; 5.
DR Pfam; PF00095; WAP; 1.
DR PRINTS; PRO0003; 4DISULPHCORE.
DR PRINTS; PRO0759; BASICPTASE.
DR ProDom; PD000222; Prot_Inh_Kunz-m; 12.
DR SMART; SM00409; IG; 3.
DR SMART; SM00131; KU; 12.
DR SMART; SM00209; TSP1; 7.
DR SMART; SM00217; WAP; 1.
DR PROSITE; PS00317; 4_DISULFIDE_CORE; 1.
DR PROSITE; PS00280; BPTI_KUNITZ_1; 11.
DR PROSITE; PS0279; BPTI_KUNITZ_2; 12.
DR PROSITE; PS00022; EGF_I; UNKNOWN_1.
DR PROSITE; PS50835; IG_LIKE; 3.
DR PROSITE; PS50900; PLAC; 1.
DR PROSITE; PS50092; TSP1; 5.
SQ SEQUENCE 2894 AA; 312663 MW; A1BFE1BAD9B214BC CRC64;

Query Match 52.6%; Score 159; DB 2; Length 2894;
Best Local Similarity 47.1%; Pred. No. 1.9e-10;
Matches 24; Conservative 7; Mismatches 20; Indels 0; Gaps 0;

OY 1 CSMPOEAGPCLASIPHWYNNKTKICSEFIYGGCGGNNNNFQTEAICLVTC 51
Db 1730 CEQPVESGFCAGNFERWYDNETDICRPTTYGGCKGNKNYPTEHACNYNC 1780

RESULT 26
ID Q86829 PRELIMINARY; PRT; 2898 AA.
AC Q86829;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Extracellular matrix protein papilin 3.
GN Name=Ppn;
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22552133; PubMed=12666201; DOI=10.1002/dvdy.10265;
RA Kramerova I.A., Kramerov A.A., Fessler J.H.;
RT "Alternative splicing of papilin and the diversity of Drosophila
RT extracellular matrix during embryonic morphogenesis.";
RL Dev. Dyn. 226:634-642(2003).
RN [2]
RP SEQUENCE FROM N.A.
RA Kramerova I., Fessler J.H.;
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: Contains 12 BPTI/Kunitz inhibitor domains.
DR EMBL; AF529180; AAO84908.1; -.
```

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DR FlyBase; P12111; 1KTH.
DR GO; GO:0005604; C:basement membrane; IDA.
DR InterPro; IPR010294; ADAM_spacer1.
DR InterPro; IPR006209; EGF_Like.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003598; IG_c2.
DR InterPro; IPR010909; PLAC.
DR InterPro; IPR002223; Prot_Inh_Kunz-m.
DR InterPro; IPR000884; TSPI.
DR InterPro; IPR008197; WAP.
DR Pfam; PF05986; ADAM_spacer1; 1.
DR Pfam; PF00047; IG; 2.
DR Pfam; PF00014; Kunitz_BPTI; 12.
DR Pfam; PF00090; TSP_1; 5.
DR Pfam; PF00095; WAP; 1.
DR PRINTS; PRO0003; 4DISULPHCORE.
DR PRINTS; PRO0759; BASICPTASE.
DR ProDom; PD000222; Prot_Inh_Kunz-m; 12.
DR SMART; SM00408; IGC2; 3.
DR SMART; SM00131; KU; 12.
DR SMART; SM00209; TSP1; 7.
DR SMART; SM00217; WAP; 1.
DR PROSITE; PS00317; 4_DISULFIDE_CORE; 1.
DR PROSITE; PS00280; BPTI_KUNITZ_1; 11.
DR PROSITE; PS0279; BPTI_KUNITZ_2; 12.
DR PROSITE; PS00022; EGF_I; UNKNOWN_1.
DR PROSITE; PS50835; IG_LIKE; 3.
DR PROSITE; PS50900; PLAC; 1.
DR PROSITE; PS50092; TSP1; 5.
KW Matrix protein.
SQ SEQUENCE 2898 AA; 313250 MW; 2F992742F2D64A00 CRC64;

Query Match 52.6%; Score 159; DB 2; Length 2898;
Best Local Similarity 47.1%; Pred. No. 1.9e-10;
Matches 24; Conservative 7; Mismatches 20; Indels 0; Gaps 0;

OY 1 CSMPOEAGPCLASIPHWYNNKTKICSEFIYGGCGGNNNNFQTEAICLVTC 51
Db 1730 CEQPVESGFCAGNFERWYDNETDICRPTTYGGCKGNKNYPTEHACNYNC 1780

RESULT 27
ID IVBT_OXYSC STANDARD; PRT; 62 AA.
AC Q7LZE4;
DT 05-JUL-2004 (Rel. 44, Created)
DT 05-JUL-2004 (Rel. 44, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Taicotoxin, serine protease inhibitor component (TCX).
OS Oxyuranus scutellatus scutellatus (Australian taipan).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Serpentes; Colubroidae;
OC Elapidae; Acanthophiinae; Oxyuranus.
OX NCBI_TaxID=8667;
RN [1]
RP SEQUENCE.
RX TISSUE=Venom;
RX PubMed=1485334; DOI=10.1016/0041-0101(92)90511-3;
RA Possani L.D., Martin B.M., Yatani A., Mochca-Morales J., Zamudio F.Z.,
RA Gurrola G.B., Brown A.M.;
RT "Isolation and physiological characterization of taicotoxin, a complex
RT toxin with specific effects on calcium channels.";
RL Toxincon 30:1343-1364(1992).
CC -!- FUNCTION: Taicotoxin blocks the high threshold calcium channel
CC current of excitable membranes in heart and does not affect the
CC low threshold calcium channel current. The block is selective for
CC calcium channels, reversible, does not affect single channel
CC conductance but only changes channel gating, and is voltage
CC dependent with higher affinity for inactivated channels. Is very
CC toxic to mice.
CC -!- SUBUNIT: Linked to an alpha-neurotoxin-like peptide of 8000 Da and
CC a neurotoxic phospholipase of 16000 Da by non-covalent bonds. The
```

ratio is approximately one phospholipase and one neurotoxin for four protease inhibitors.

-1- SUBCELLULAR LOCATION: Secreted.

-1- TISSUE SPECIFICITY: Expressed by the venom gland.

-1- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.

PIR: A44180; A44180; Prot Inh_Kunz-m.

DR InterPro; IPR002223; Prot Inh_Kunz-m.

DR PRINTS; PR00759; BASICPTASE.

DR ProDom; PD000222; Prot Inh_Kunz-m; 1.

DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.

DR PROSITE; PS00279; BPTI_KUNITZ_2; 1.

KW Calcium channel inhibitor; Direct protein sequencing; Toxin.

FT Ionic channel inhibitor; Neurotoxin; Serine protease inhibitor; Toxin.

FT DISULFID 7 57 By similarity.

FT DISULFID 16 40 By similarity.

FT DISULFID 32 53 By similarity.

SQ SEQUENCE 62 AA; 7045 MW; ABE0BEPBD1990605 CRC64;

Query Match 52.3%; Score 158; DB 1; Length 62;
Best Local Similarity 51.0%; Pred. No. 5.1e-12;
Matches 26; Conservative 8; Mismatches 17; Indels 0; Gaps 0;

QY 1 CSMQAEAGFCLASIPHWYNNKTKICSEFIYGGCGQNNNNFQTEAICLVTC 51
DB 7 CHLPKPGPCRAAIPRFYNNPHSKQCEKFIYGGCGHGNANKFTPDENYTC 57

RESULT 28

CRPT-BOOMI STANDARD; PRT; 69 AA.

AC F81162;

DT 15-DEC-1998 (Rel. 37, Created)

DT 15-DEC-1998 (Rel. 37, Last sequence update)

DT 05-JUL-2004 (Rel. 44, Last annotation update)

DE Protease inhibitor carapatin.

OS Boophilus microplus (Cattle tick).

OC Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Acari;

OC Parasitiformes; Ixodida; Ixodoidea; Ixodidae; Boophilus.

OX NCBI_TaxID=6941;

RN [1]

RP SEQUENCE.

RA Fuentes-Prior P., Pereira P.J.B., Mentale R., Bode W.;
Submitted (JAN-1998) to Swiss-Prot.

RL FUNCTION: Serine protease inhibitor.

CC -1- SUBCELLULAR LOCATION: Secreted.

CC -1- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.

DR HSP; P00980; IDTX.

DR InterPro; IPR002223; Prot Inh_Kunz-m.

DR Pfam; PF00014; Kunitz_BPTI; 1.

DR PRINTS; PR00759; BASICPTASE.

DR ProDom; PD000222; Prot Inh_Kunz-m; 1.

DR SMART; SM00131; KU; 1.

DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.

DR PROSITE; PS00279; BPTI_KUNITZ_2; 1.

KW Direct protein sequencing; Serine protease inhibitor.

FT SITE 18 19 Reactive bond (By similarity).

FT DISULFID 8 58 By similarity.

FT DISULFID 17 41 By similarity.

FT DISULFID 33 54 By similarity.

SQ SEQUENCE 69 AA; 7842 MW; E0B14312AC1533BB CRC64;

Query Match 52.3%; Score 158; DB 1; Length 69;
Best Local Similarity 51.0%; Pred. No. 5.6e-12;
Matches 26; Conservative 6; Mismatches 19; Indels 0; Gaps 0;

QY 1 CSMQAEAGFCLASIPHWYNNKTKICSEFIYGGCGQNNNNFQTEAICLVTC 51
DB 8 CVPTADPGCKGFMWYNNIFTSQCEFIYGGCGQNDNRYRTKEECDKTC 58

RESULT 29

Q6B8G1 PRELIMINARY; PRT; 142 AA.

ID Q6B8G1

Q6B8G1;
25-OCT-2004 (TrEMBLrel. 28, Created)
25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
KUN-5 (Fragment).
OS Ixodes pacificus (western blacklegged tick).
OC Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Acari;
OC Parasitiformes; Ixodida; Ixodidae; Ixodes.
OX NCBI_TaxID=29930;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Salivary gland;
RA Ribeiro J.M.C.;
RT "An insight into the transcriptome of the salivary glands of the adult female tick, Ixodes pacificus.";
RL Submitted (AUG-2004) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Salivary gland;
RA Francischetti I.M., Lane R.S., Pham V.M., Ribeiro J.M.C.;
RL Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Contains 2 BPTI/Kunitz inhibitor domains.
DR EMBL; AV674183; AAT92116.1; -.
DR GO; GO:0004867; F:serine-type endopeptidase inhibitor activity; IEA.
DR InterPro; IPR002223; Prot Inh_Kunz-m.
DR Pfam; PF00014; Kunitz_BPTI; 1.
DR PRINTS; PR00759; BASICPTASE.
DR ProDom; PD000222; Prot Inh_Kunz-m; 1.
DR SMART; SM00131; KU; 2.
DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
DR PROSITE; PS00279; BPTI_KUNITZ_2; 2.
FT NON_TER 142 142
SQ SEQUENCE 142 AA; 16458 MW; A618BE45CB812C4B CRC64;

Query Match 52.3%; Score 158; DB 2; Length 142;
Best Local Similarity 52.9%; Pred. No. 1.2e-11;
Matches 27; Conservative 7; Mismatches 17; Indels 0; Gaps 0;

QY 1 CSMQAEAGFCLASIPHWYNNKTKICSEFIYGGCGQNNNNFQTEAICLVTC 51
DB 29 CTEVVDGPGCRALIPRFYNNMETKCEEFYGGYGNNNFNFSSCTSTC 79

RESULT 30

Q6ITB4 PRELIMINARY; PRT; 83 AA.

ID Q6ITB4;
AC Q6ITB4;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Microlepidin-2.
OS Oxmyranus microlepidotus (Inland taipan).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC Elapidae; Acanthophiinae; Oxmyranus.
OX NCBI_TaxID=111177;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Venom gland;
RA Filippovich I.V., Sorokina N.I.;
RL Submitted (MAY-2004) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.
DR EMBL; AV626931; AAT45407.1; -.
DR HSP; P10646; 1ADZ.
DR GO; GO:0004867; F:serine-type endopeptidase inhibitor activity; IEA.
DR InterPro; IPR002223; Prot Inh_Kunz-m.
DR Pfam; PF00014; Kunitz_BPTI; 1.
DR PRINTS; PR00759; BASICPTASE.
DR ProDom; PD000222; Prot Inh_Kunz-m; 1.
DR SMART; SM00131; KU; 1.
DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
DR PROSITE; PS00279; BPTI_KUNITZ_2; 1.
SQ SEQUENCE 83 AA; 9074 MW; 3145E51757014221 CRC64;

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Query Match          52.0%; Score 157; DB 2; Length 83;
Best Local Similarity 51.0%; Pred. No. 9.1e-12;
Matches 26; Conservative 6; Mismatches 19; Indels 0; Gaps 0;

QY 1 CSMPOEAGPCLASIPHHWYNNKTKICSEFIYGGCGGNNNNFQTEAICLVTC 51
    : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 31 CELPADTGPCRVGFPSFYNNPDEKKCLEFIYGGCGGNNNNFITKECESTC 81

RESULT 31
Q61TB5 PRELIMINARY; PRT; 83 AA.
AC Q61TB5;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Microlepidin-1.
OS Oxyuranus microlepidotus (Inland taipan).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC Elapidae; Acanthophiinae; Oxyuranus.
OX NCBI_TaxID=111177;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Venom gland;
RA Filippovich I.V., Sorokina N.I.;
RL Submitted (MAY-2004) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.
EMBL; AY626930; AAT45406.1; -.
DR HSSP; P10646; 1ADZ.
DR GO; GO:0004867; F:serine-type endopeptidase inhibitor activity; IEA.
DR InterPro; IPR002223; Prot_Inh_Kunz-m.
DR Pfam; PF00014; Kunitz BPTI; 1.
DR PRINTS; PR00759; BASICPTASE.
DR ProDom; PD000222; Prot_Inh_Kunz-m; 1.
DR SMART; SM00131; KU; 1.
DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
DR PROSITE; PS50279; BPTI_KUNITZ_2; 1.
DR SEQUENCE 83 AA; 9040 MW; C84F551750CF94C CRC64;

Query Match          52.0%; Score 157; DB 2; Length 83;
Best Local Similarity 51.0%; Pred. No. 9.1e-12;
Matches 26; Conservative 6; Mismatches 19; Indels 0; Gaps 0;

QY 1 CSMPOEAGPCLASIPHHWYNNKTKICSEFIYGGCGGNNNNFQTEAICLVTC 51
    : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 31 CELPADTGPCRVGFPSFYNNPDEKKCLEFIYGGCGGNNNNFITKECESTC 81

RESULT 32
Q61TB6 PRELIMINARY; PRT; 83 AA.
AC Q61TB6;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Scutellin-2.
OS Oxyuranus scutellatus.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC Elapidae; Acanthophiinae; Oxyuranus.
OX NCBI_TaxID=8668;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Venom gland;
RA Filippovich I.V., Sorokina N.I.;
RL Submitted (MAY-2004) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.
EMBL; AY626929; 1ADZ.
DR HSSP; P10646; 1ADZ.
DR GO; GO:0004867; F:serine-type endopeptidase inhibitor activity; IEA.
DR InterPro; IPR002223; Prot_Inh_Kunz-m.
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DR Pfam; PF00014; Kunitz BPTI; 1.
DR PRINTS; PR00759; BASICPTASE.
DR ProDom; PD000222; Prot_Inh_Kunz-m; 1.
DR SMART; SM00131; KU; 1.
DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
DR PROSITE; PS50279; BPTI_KUNITZ_2; 1.
DR SEQUENCE 83 AA; 9074 MW; 3145E51757014221 CRC64;

Query Match          52.0%; Score 157; DB 2; Length 83;
Best Local Similarity 51.0%; Pred. No. 9.1e-12;
Matches 26; Conservative 6; Mismatches 19; Indels 0; Gaps 0;

QY 1 CSMPOEAGPCLASIPHHWYNNKTKICSEFIYGGCGGNNNNFQTEAICLVTC 51
    : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 31 CELPADTGPCRVGFPSFYNNPDEKKCLEFIYGGCGGNNNNFITKECESTC 81

RESULT 33
BTIA_BOOMI
ID BTIA_BOOMI STANDARD; PRT; 122 AA.
AC P83609;
DT 05-JUL-2004 (Rel. 44, Created)
DT 05-JUL-2004 (Rel. 44, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Kunitz-type serine protease inhibitor BmtI-A (Fragments).
OS Boophilus microplus (Cattle tick).
OC Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Acari;
OC Parasitiformes; Ixodida; Ixodoidea; Ixodidae; Boophilus.
OX NCBI_TaxID=6941;
RN [1]
RP SEQUENCE AND FUNCTION.
RC TISSUE=Larva;
RX PubMed=10615008; DOI=10.1016/S0162-3109(99)00074-0;
RA Tanaka A.S., Andreotti R., Gomes A., Torquato R.J.S., Sampaio M.U.,
RA Sampaio C.A.M.;
RT "A double headed serine proteinase inhibitor-human plasma kallikrein
RT and elastase inhibitor-from Boophilus microplus larvae";
RL Immunopharmacology 45:171-177(1999).
CC -!- FUNCTION: Inhibits bovine trypsin, bovine chymotrypsin, human
CC plasmin, human plasma kallikrein and human neutrophil elastase,
CC but not bovine thrombin, human factor Xa or porcine pancreatic
CC kallikrein. May play a role in blocking blood coagulation during
CC the larvae fixation on cattle.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: Contains 2 BPTI/Kunitz inhibitor domains.
DR InterPro; IPR002223; Kunitz BPTI.
DR PRINTS; PR00759; BASICPTASE.
DR ProDom; PD000222; Prot_Inh_Kunz-m; 2.
DR SMART; SM00131; KU; 2.
DR PROSITE; PS00280; BPTI_KUNITZ_1; 2.
DR PROSITE; PS50279; BPTI_KUNITZ_2; 2.
KW Direct protein sequencing; Repeat; Serine protease inhibitor.
FT DOMAIN 10 60
FT DISULFID 62 112 BPTI/Kunitz inhibitor 1.
FT DISULFID 10 60 BPTI/Kunitz inhibitor 2.
FT DISULFID 35 56 By similarity.
FT NON_CONS 69 70 By similarity.
FT DISULFID 71 121 By similarity.
FT DISULFID 80 104 By similarity.
FT DISULFID 96 117 By similarity.
FT SITE 19 20 Reactive bond (By similarity).
FT SITE 71 72 Reactive bond (By similarity).
FT NON_TER 122 122
DR SEQUENCE 122 AA; 13736 MW; 8F5B1F48E10C566F CRC64;

Query Match          52.0%; Score 157; DB 1; Length 122;
Best Local Similarity 52.9%; Pred. No. 1.3e-11;
Matches 27; Conservative 6; Mismatches 18; Indels 0; Gaps 0;

QY 1 CSMPOEAGPCLASIPHHWYNNKTKICSEFIYGGCGGNNNNFQTEAICLVTC 51
    : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 71 CLARPESGFCLAYMPMGYDCKGQCFEYIYGGCDGNDKNKYTEECIKSC 121
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RESULT 34
Q7YRQ8 PRELIMINARY; PRT; 234 AA.
AC Q7YRQ8;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Tissue factor pathway inhibitor-2.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22802738; PubMed=12921785; DOI=10.1016/S0003-9861(03)00332-1;
RA Du X., Deng F.W., Chand H.S., Kisiel W.;
RT "Molecular cloning, expression, and characterization of bovine tissue
RT factor pathway inhibitor-2."
RL Arch. Biochem. Biophys. 417:96-104(2003).
RN [2]
RP SEQUENCE FROM N.A.
RA Deng F.-W., Kisiel W., Sun T.-T.;
RL Submitted (FEB-2003) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Contains 3 BPTI/Kunitz inhibitor domains.
EMBL; AY234861; AA084035.1; -.
DR HSP; P00981; 1DTK
DR GO; GO:0004867; F:serine-type endopeptidase inhibitor activity; IEA.
DR InterPro; IPR002223; Prot_Inh_Kunz-m.
DR Pfam; PF00014; Kunitz_BPTI; 3.
DR ProDom; PD000222; Prot_Inh_Kunz-m; 3.
DR SMART; SM00131; KU; 3.
DR PROSITE; PS00280; BPTI_KUNITZ_1; 3.
DR PROSITE; PS00279; BPTI_KUNITZ_2; 3.
DR SQ SEQUENCE 234 AA; 26675 MW; 401EEC84D589B422 CRC64;

Query Match 52.0%; Score 157; DB 2; Length 234;
Best Local Similarity 49.0%; Pred. No. 2.6e-11;
Matches 25; Conservative 10; Mismatches 16; Indels 0; Gaps 0;

QY 1 CSMQOAGPCLASIPHWYNNKTKICSEFIYGGCGGNNNFQTEAICLVTC 51
| : : : : : : : : : : : : : : : : : : : : : : : :
Db 36 CLLPDDGPCRARIPSYDYRYTQSCREFYGGCGGNANNFTLEACNEAC 86

RESULT 35
Q8IT91 PRELIMINARY; PRT; 759 AA.
AC Q8IT91;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Kunitz-like protease inhibitor precursor.
OS Ancylostoma caninum (Dog hookworm).
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Strongylida;
OC Ancylostomatidae; Ancylostomatidae; Ancylostoma.
OX NCBI_TaxID=29170;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=Baltimore;
RX MEDLINE=22645137; PubMed=12760667;
RA Hawdon J.M., Datu B., Crowell M.;
RT "Molecular cloning of a novel multidomain Kunitz-type proteinase
RT inhibitor from the hookworm Ancylostoma caninum."
RL J. Parasitol. 89:402-407(2003).
CC -1- SIMILARITY: Contains 12 BPTI/Kunitz inhibitor domains.
EMBL; AF533590; AA010061.1; -.
DR HSP; P31713; 1SHP
DR GO; GO:0008233; F:peptidase activity; IEA.
DR GO; GO:0004867; F:serine-type endopeptidase inhibitor activity; IEA.
DR InterPro; IPR002223; Prot_Inh_Kunz-m.
DR Pfam; PF00014; Kunitz_BPTI; 12.

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DR PRINTS; PR00759; BASICPTASE.
DR SMART; SM00131; KU; 12.
DR PROSITE; PS00280; BPTI_KUNITZ_1; 10.
DR PROSITE; PS00279; BPTI_KUNITZ_2; 12.
KW Protease; Signal.
FT SIGNAL 1 16 Potential.
SQ SEQUENCE 759 AA; 84886 MW; C431A3C3F418F40A CRC64;

Query Match 52.0%; Score 157; DB 2; Length 759;
Best Local Similarity 51.0%; Pred. No. 8.5e-11;
Matches 26; Conservative 9; Mismatches 16; Indels 0; Gaps 0;

QY 1 CSMQOAGPCLASIPHWYNNKTKICSEFIYGGCGGNNNFQTEAICLVTC 51
| : : : : : : : : : : : : : : : : : : : : : : : :
Db 205 CSQPIAGPCMAWKRYAYDNKKKRCVQFIYGGCKGNKNFESMEECTRTC 255

RESULT 36
Q90WAL PRELIMINARY; PRT; 83 AA.
AC Q90WAL;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Textilin.
OS Pseudonaja textilis textilis.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC Elapidae; Acanthophiinae; Pseudonaja.
OX NCBI_TaxID=169397;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Venom gland;
RA Masci P.P., Lavin M.F., Gaffney P.J., Sorokina I.N., Flippovich I.V.;
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Venom gland;
RA Flippovich I.V., Sorokina N.I., Masci P.P., de Jersey J.,
RA Whitaker A.N., Gaffney P.J., Lavin M.F.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.
EMBL; AF40324; AA095519.1; -.
DR HSP; P25660; 1JC6.
DR GO; GO:0004867; F:serine-type endopeptidase inhibitor activity; IEA.
DR Pfam; PF00014; Kunitz_BPTI; 1.
DR PRINTS; PR00759; BASICPTASE.
DR ProDom; PD000222; Prot_Inh_Kunz-m; 1.
DR SMART; SM00131; KU; 1.
DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
DR PROSITE; PS00279; BPTI_KUNITZ_2; 1.
DR SQ SEQUENCE 83 AA; 9173 MW; 2045E50657014221 CRC64;

Query Match 51.7%; Score 156; DB 2; Length 83;
Best Local Similarity 51.0%; Pred. No. 1.2e-11;
Matches 26; Conservative 6; Mismatches 19; Indels 0; Gaps 0;

QY 1 CSMQOAGPCLASIPHWYNNKTKICSEFIYGGCGGNNNFQTEAICLVTC 51
| : : : : : : : : : : : : : : : : : : : : : : : :
Db 31 CELPADTGPCRVRFPSFYNPDEKKCLEFIYGGCGGNANNFTKECESTC 81

RESULT 37
Q6AX20 PRELIMINARY; PRT; 587 AA.
AC Q6AX20;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Alp2 A protein.
DR Names:alp2 A;
GN Xenopus laevis (African clawed frog).
OC Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

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OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Kidney;
RX MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;
RA Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
RA Richardson P.;
RT "Genetic and genomic tools for Xenopus research: The NIH Xenopus
RT initiative";
RN Dev. Dyn. 225:384-391(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Kidney;
RX PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altshul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young J.W., Green E.D., Dickson M.C.,
RA Blakesley R.W., Touchman J.W., Shevchenko Y., Bouffard G.G.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalek U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences";
RN Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Kidney;
RA Klein S., Gerhard D.S.;
RL Submitted (AUG-2004) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.
DR EMBL; BC079801; AAH79801.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0005488; F:binding; IEA.
DR GO; GO:0004867; F:serine-type endopeptidase inhibitor activity; IEA.
DR InterPro; IPR008155; A4 APP.
DR InterPro; IPR008154; A4 extra.
DR Pfam; PF02177; A4 EXTRA; I.
DR Pfam; PF00014; Kunitz_BPTI; 1.
DR PRINTS; PR00203; AMYLOIDA4.
DR ProDom; PD000222; Prot Inh_Kunz-m; 1.
DR SMART; SM00006; A4 EXTRA; I.
DR SMART; SM00131; KU; 1.
DR PROSITE; PS00320; A4 INTRA; 1.
DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
DR PROSITE; PS02079; BPTI_KUNITZ_2; 1.
KW SIGNAL.
FT SIGNAL.
FT CHAIN.
FT SEQUENCE.
SQ SEQUENCE 587 AA; 66870 MW; 7DF224C2138B94BF CRC64;
Query Match 51.7%; Score 156; DB 2; Length 587;
Best Local Similarity 49.0%; Pred. No. 8.7e-11;
Matches 25; Conservative 6; Mismatches 20; Indels 0; Gaps 0;
QY 1 CSMPOEAGPCLASIPHHWYKTKICSEFIYGGCGGNNNFQTEAICLVTC 51
DB 284 CSQEAITGFCRAMPRWYFNLGQKCFRIFYGGCGGNRRNFESDYCMVAC 334
RESULT 38
Q70820
ID Q70820 PRELIMINARY; PRT; 751 AA.

AC Q70820;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Amyloid-beta-like protein A precursor.
GN Name=aplp2 A;
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RA Collin R.W.J., van Strien D., Leunissen J.A., Martens G.J.M.;
RL Submitted (NOV-2003) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.
DR EMBL; AJ608932; CAE75662.1; -.
DR HSSP; Q16019; 1AAP.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0005488; F:binding; IEA.
DR GO; GO:0004867; F:serine-type endopeptidase inhibitor activity; IEA.
DR InterPro; IPR008155; A4 APP.
DR InterPro; IPR008154; A4 extra.
DR InterPro; IPR002223; Prot Inh_Kunz-m.
DR Pfam; PF02177; A4 EXTRA; I.
DR Pfam; PF00014; Kunitz_BPTI; 1.
DR PRINTS; PR00203; AMYLOIDA4.
DR PRINTS; PR00759; BASICPTASE.
DR ProDom; PD000222; Prot Inh_Kunz-m; 1.
DR SMART; SM00006; A4 EXTRA; I.
DR SMART; SM00131; KU; 1.
DR PROSITE; PS00320; A4 INTRA; 1.
DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
DR PROSITE; PS02079; BPTI_KUNITZ_2; 1.
KW SIGNAL.
FT SIGNAL.
FT CHAIN.
FT SEQUENCE.
SQ SEQUENCE 751 AA; 85200 MW; C5E8FE7302C36B58 CRC64;
Query Match 51.7%; Score 156; DB 2; Length 751;
Best Local Similarity 49.0%; Pred. No. 1.1e-10;
Matches 25; Conservative 6; Mismatches 20; Indels 0; Gaps 0;
QY 1 CSMPOEAGPCLASIPHHWYKTKICSEFIYGGCGGNNNFQTEAICLVTC 51
DB 292 CSQEAITGFCRAMPRWYFNLGQKCFRIFYGGCGGNRRNFESDYCMVAC 342
RESULT 39
Q91963
ID Q91963 PRELIMINARY; PRT; 747 AA.
AC Q91963;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE APP747.
GN Name=APP747;
OS Xenopus.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
OC Xenopodinae;
OX NCBI_TaxID=8353;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93129227; PubMed=1282805;
RA Okado H., Okamoto H.;
RT "A Xenopus homologue of the human beta-amyloid precursor protein:
RT developmental regulation of its gene expression";
RL Biochem. Biophys. Res. Commun. 189:1561-1568(1992).
CC -!- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.
DR EMBL; S52417; AAB24853.1; -.
DR HSSP; Q16019; 1H23.


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DR GO; GO:0016021; C: integral to membrane; IEA.
DR GO; GO:0005488; F: binding; IEA.
DR GO; GO:0004867; F: serine-type endopeptidase inhibitor activity; IEA.
DR Pfam; PF02177; A4 EXTRA; 1.
DR Pfam; PF03494; Beta-APP; 1.
DR Pfam; PF00014; Kunitz_BPTI; 1.
DR PRINTS; PR00203; AMYLOIDA4.
DR PRINTS; PR00759; BASICPTASE.
DR PRINTS; PR00204; BETAAMYLOID.
DR ProDom; PD000222; Prot_Inh_Kunz-m; 1.
DR SMART; SM00131; KU; 1.
DR PROSITE; PS00319; A4_EXTRA; 1.
DR PROSITE; PS00320; A4_INTRA; 1.
DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
DR PROSITE; PS0279; BPTI_KUNITZ_2; 1.
DR PROSITE; PS0279; BPTI_KUNITZ_2; 1.
SQ SEQUENCE 747 AA; 84893 MW; A75B81885681D948 CRC64;

Query Match 51.0%; Score 154; DB 2; Length 747;
Best Local Similarity 47.1%; Pred. No. 2e-10;
Matches 24; Conservative 8; Mismatches 19; Indels 0; Gaps 0;

QY 1 CSMPOAGPCLASIPHWYNNKTKICSEFIYGGCGGNNNNFQTEAICLVTC 51
Db 287 CSEQATGFCRAMISRWYDVTSKCAQFIYGGCGGNNRNFESDDYCMVAVC 337

RESULT 40
Q6NRR1 PRELIMINARY; PRT; 749 AA.
ID Q6NRR1
AC Q6NRR1;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE App protein.
GN Name:app;
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidea; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Kidney;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heien F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udén T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaby S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Vallalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Ketterman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smallos D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RL and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
[2]
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Kidney;
RX MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;
RA Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
RA Richardson P.;
RT "Genetic and genomic tools for Xenopus research: The NIH Xenopus
RT initiative.";
Dev. Dyn. 225:384-391 (2002).
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[3]
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Kidney;
RA Klein S., Strausberg R.;
RL Submitted (May-2004) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.
DR EMBL; BC070668; AAH70668.1; -.
DR HSSP; Q16019; 1BA4.
DR GO; GO:0016021; C: integral to membrane; IEA.
DR GO; GO:0005488; F: binding; IEA.
DR GO; GO:0004867; F: serine-type endopeptidase inhibitor activity; IEA.
DR InterPro; IPR008155; A4_APP.
DR InterPro; IPR008154; A4_extra.
DR InterPro; IPR001255; Beta-APP.
DR InterPro; IPR002223; Prot_Inh_Kunz-m.
DR Pfam; PF02177; A4 EXTRA; 1.
DR Pfam; PF03494; Beta-APP; 1.
DR Pfam; PF00014; Kunitz_BPTI; 1.
DR PRINTS; PR00203; AMYLOIDA4.
DR PRINTS; PR00759; BASICPTASE.
DR PRINTS; PR00204; BETAAMYLOID.
DR ProDom; PD000222; Prot_Inh_Kunz-m; 1.
DR SMART; SM00131; KU; 1.
DR PROSITE; PS00319; A4_EXTRA; 1.
DR PROSITE; PS00320; A4_INTRA; 1.
DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
DR PROSITE; PS0279; BPTI_KUNITZ_2; 1.
DR PROSITE; PS0279; BPTI_KUNITZ_2; 1.
SQ SEQUENCE 749 AA; 84766 MW; 33478C6B6A8C295D CRC64;

Query Match 51.0%; Score 154; DB 2; Length 749;
Best Local Similarity 47.1%; Pred. No. 2e-10;
Matches 24; Conservative 8; Mismatches 19; Indels 0; Gaps 0;

QY 1 CSMPOAGPCLASIPHWYNNKTKICSEFIYGGCGGNNNNFQTEAICLVTC 51
Db 289 CSEQATGFCRAMISRWYDVTSKCAQFIYGGCGGNNRNFESDDYCMVAVC 339

RESULT 41
Q9GQN1 PRELIMINARY; PRT; 984 AA.
ID Q9GQN1
AC Q9GQN1;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Peptidylglycine alpha-amidating monooxygenase.
GN Name:PAW;
OS Calliactis parasitica (Sea anemone).
OC Eukaryota; Metazoa; Chnidaria; Anthozoa; Zoantharia; Actiniaria;
OC Nynanthaeae; Hormathiidae; Calliactis.
OX NCBI_TaxID=6114;
RN [1]
RP SEQUENCE FROM N.A.
RA Williamson M., Hauser F., Grimmelikhuijzen C.J.P.;
RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.
DR EMBL; AF221986; AAG44251.1; -.
DR HSSP; P12111; 1KNT.
DR GO; GO:0016020; C: membrane; IEA.
DR GO; GO:0005507; F: copper ion binding; IEA.
DR GO; GO:0004504; F: peptidylglycine monooxygenase activity; IEA.
DR GO; GO:0004867; F: serine-type endopeptidase inhibitor activity; IEA.
DR GO; GO:0006518; P: peptide metabolism; IEA.
DR InterPro; IPR011044; Amine DH B-like.
DR InterPro; IPR000323; Cu2_monooxygenase.
DR InterPro; IPR001258; NHL.
DR InterPro; IPR000720; Pamonooxygenase.
DR InterPro; IPR008977; PHM_PNGase F.
DR InterPro; IPR002223; Prot_Inh_Kunz-m.
DR Pfam; PF01082; Cu2_monooxygen; 1.
DR Pfam; PF03712; Cu2_monoox C; 1.
DR Pfam; PF00014; Kunitz_BPTI; 1.
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DR Pfam: PF01436; NHL; 5.
DR PRINTS; PR00759; BASICPTASE.
DR PRINTS; PR00790; PAMONOXGNASE.
DR SMART; SM00131; KU; 1.
DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
DR PROSITE; PS0279; BPTI_KUNITZ_2; 1.
DR PROSITE; PS00084; CU2_MONOXYGENASE_1; 1.
KW Monooxygenase.
SQ SEQUENCE 984 AA; 110265 MW; 4224E4BCEB3480D CRC64;

Query Match 51.0%; Score 154; DB 2; Length 984;
Best Local Similarity 43.1%; Pred. No. 2.6e-10;
Matches 22; Conservative 11; Mismatches 18; Indels 0; Gaps 0;

QY 1 CSMPOEAGPCLASIPHWYNTKTKICSEFIYGGCGGNNNFQTEAICLVTC 51
DB 730 CMLEHDTGCRAMPWPYFDKARSCTRFIYGGCGSGNENNFASKRECAKC 780

RESULT 42
Q9GQN2 PRELIMINARY; PRT; 984 AA.
AC Q9GQN2;
DT 01-WAR-2001 (TrEMBLrel. 16, Created)
DT 01-WAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Peptidylglycine alpha-amidating monooxygenase.
GN Name=PAM;
OS Calliactis parasitica (Sea anemone).
OC Eukaryota; Metazoa; Cnidaria; Anthozoa; Zoantharia; Actiniaria;
OC Nynantheae; Hormathiidae; Calliactis.
OX NCBI_TaxID=6114;
RN [1]
RP SEQUENCE FROM N.A.
RA Williamson M., Hauser F., Grimmelikhuijzen C.J.P.;
RC Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
RL -1 SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.
DR EMBL; AF221985; AAG44250.1; -.
DR HSP; F12111; IKNT.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005507; F:copper ion binding; IEA.
DR GO; GO:0004504; F:peptidylglycine monooxygenase activity; IEA.
DR GO; GO:0004867; F:serine-type endopeptidase inhibitor activity; IEA.
DR GO; GO:0005518; P:peptide metabolism; IEA.
DR InterPro; IPR01044; A:amine DH_B-like.
DR InterPro; IPR000323; C:Cu2 monooxygenase.
DR InterPro; IPR001258; NHL.
DR InterPro; IPR000720; P:ammonooxygenase.
DR InterPro; IPR008977; PHM_PNGase_F.
DR InterPro; IPR002223; Prot_Inh_Kunz-m.
DR Pfam; PF01082; Cu2_monooxygen; 1.
DR Pfam; PF03712; Cu2_monoox_C; 1.
DR Pfam; PF00014; Kunitz_BPTI; 1.
DR Pfam; PF01436; NHL; 5.
DR PRINTS; PR00759; BASICPTASE.
DR PRINTS; PR00790; PAMONOXGNASE.
DR ProDom; PD000222; Prot_Inh_Kunz-m; 1.
DR SMART; SM00131; KU; 1.
DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
DR PROSITE; PS0279; BPTI_KUNITZ_2; 1.
DR PROSITE; PS00084; CU2_MONOXYGENASE_1; 1.
KW Monooxygenase.
SQ SEQUENCE 984 AA; 110266 MW; 7AFE2D1B74B78EBC CRC64;

Query Match 51.0%; Score 154; DB 2; Length 984;
Best Local Similarity 43.1%; Pred. No. 2.6e-10;
Matches 22; Conservative 11; Mismatches 18; Indels 0; Gaps 0;

QY 1 CSMPOEAGPCLASIPHWYNTKTKICSEFIYGGCGGNNNFQTEAICLVTC 51
DB 730 CMLEHDTGCRAMPWPYFDKARSCTRFIYGGCGSGNENNFASKRECAKC 780
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RESULT 43
ISIK_HELPO
ID ISIK_HELPO STANDARD; PRT; 58 AA.
AC P00994;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Isoinhibitor K.
OS Helix pomatia (Roman snail) (Edible snail).
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Pulmonata; Stylommatophora;
OC Sigmurethra; Helicoidea; Helicidae; Helix.
OX NCBI_TaxID=6536;
RN [1]
RP SEQUENCE.
RX MEDLINE=76043680; PubMed=1183446;
RA Tschesche H., Dietl T.;
RT "The amino-acid sequence of isoinhibitor K form snails (Helix pomatia). A sequence determination by automated Edman degradation and mass-spectral identification of the phenylthiohydantoins.";
RL Eur. J. Biochem. 58:439-451(1975).
RN [2]
RP DISULFIDE BONDS.
RX MEDLINE=76141310; PubMed=3462;
RA Dietl T., Tschesche H.;
RT "The disulfide bridges of the trypsin-kallikrein inhibitor K from snails (Helix pomatia). Thermal inactivation and proteolysis by thermolysin.";
RL Hoppe-Seyler's Z. Physiol. Chem. 357:139-145(1976).
CC -!- FUNCTION: This is one of several isoinhibitors of broad specificity that are secreted into the mucus of the snail.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.
DR PIR; A91232; TIHABK.
DR HSP; P00974; IKO9.
DR InterPro; IPR002223; Prot_Inh_Kunz-m.
DR Pfam; PF00014; Kunitz_BPTI; 1.
DR PRINTS; PR00759; BASICPTASE.
DR ProDom; PD000222; Prot_Inh_Kunz-m; 1.
DR SMART; SM00131; KU; 1.
DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
DR PROSITE; PS0279; BPTI_KUNITZ_2; 1.
KW Direct protein sequencing; Pyrrolidone carboxylic acid; Serine protease inhibitor.
FT MOD_RES 1 1 Pyrrolidone carboxylic acid.
FT SITE 17 18 Reactive bond (By similarity).
FT DISULFID 7 57
FT DISULFID 16 40
FT DISULFID 32 53
SQ SEQUENCE 58 AA; 6451 MW; 6796586C488453B7 CRC64;

Query Match 50.7%; Score 153; DB 1; Length 58;
Best Local Similarity 49.0%; Pred. No. 2e-11;
Matches 25; Conservative 7; Mismatches 19; Indels 0; Gaps 0;

QY 1 CSMPOEAGPCLASIPHWYNTKTKICSEFIYGGCGGNNNFQTEAICLVTC 51
DB 7 CNLPAETGFCASPRQYYNSKSGCCQFIYGGCGNGNRDFTTQCCQGV 57

RESULT 44
IVBT_ERIMA
ID IVBT_ERIMA STANDARD; PRT; 62 AA.
AC P24541;
DT 01-WAR-1992 (Rel. 21, Created)
DT 01-MAR-1992 (Rel. 21, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Venom trypsin inhibitor.
OS Eristocophis macmahoni (Leaf-nosed viper).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC Viperidae; Viperinae; Eristocophis.
OX NCBI_TaxID=8702;
RN [1]
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RP SEQUENCE.
RC TISSUE=Venom;
RX MEDLINE=92077130; PubMed=1743283; DOI=10.1016/0014-5793(91)81361-B;
RA Siddiqi A.R., Zaidi Z.H., Joernvall H.;
RT "Purification and characterization of a Kunitz-type trypsin inhibitor
RT from leaf-nosed viper venom.";
RL FEBS Lett. 294:141-143(1991).
CC -1- FUNCTION: This protein inhibits trypsin and kallikrein.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- TISSUE SPECIFICITY: Expressed by the venom gland.
CC -1- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.
DR PIR; S19327; S19327.
DR HSP; P25660; IJ06.
DR InterPro; IPR002223; Prot_Inh_Kunz-m.
DR Pfam; PF00014; Kunitz BPTI; 1.
DR PRINTS; PR00759; BASICTPASE.
DR ProDom; PD000222; Prot_Inh_Kunz-m; 1.
DR SMART; SM00131; KU; 1.
DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
DR PROSITE; PS50279; BPTI_KUNITZ_2; 1.
KW Direct protein sequencing; Serine protease inhibitor.
FT SITE 12 13 Reactive bond (By similarity).
FT DISULFID 2 52 By similarity.
FT DISULFID 11 35 By similarity.
FT DISULFID 27 48 By similarity.
SQ SEQUENCE 62 AA; 6772 MW; 0A2ED0ADB20DF938 CRC64;

Query Match 50.7%; Score 153; DB 1; Length 62;
Best Local Similarity 51.0%; Pred. No. 2.1e-11;
Matches 26; Conservative 6; Mismatches 19; Indels 0; Gaps 0;

QY 1 CSMPOBAGPCLASIPHHWYNNKTKICSEFYGGCGGNNNNFQTEAICLVTC 51
DB 2 CYLPDPGVCKAHPFYYPNPSKCKKQFYGGCGGNNNNFETREACRHTC 52

RESULT 45
Q6T6S5 PRELIMINARY; PRT; 90 AA.
AC Q6T6S5;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE Kunitz protease inhibitor 2.
OS Bitis gabonica (Gaboon viper).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidodonta; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC Viperidae; Viperinae; Bitis.
OX NCBI_TaxID=8694;
RN [1]
RP SEQUENCE FROM N.A.
RX PubMed=15274202; DOI=10.1016/j.gene.2004.03.024;
RA Francischetti I.M., My-Pham V., Harrison J., Garfield M.K.,
RA Ribeiro J.M.;
RT "Bitis gabonica (Gaboon viper) snake venom gland: toward a catalog for
RT the full-length transcripts (cDNA) and proteins.";
RL Gene 337:55-69(2004).
RN [2]
RP SEQUENCE FROM N.A.
RA Francischetti I.M.B., Pham V.M., Garfield M.K., Ribeiro J.M.C.;
RA Submitted (OCT-2003) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.
DR EMBL; AY430413; AAR24535.1; -.
DR HSP; Q16019; IAA.
DR GO; GO:0008233; F:peptidase activity; IEA.
DR GO; GO:0004867; F:serine-type endopeptidase inhibitor activity; IEA.
DR InterPro; IPR002223; Prot_Inh_Kunz-m.
DR Pfam; PF00014; Kunitz BPTI; 1.
DR PRINTS; PR00759; BASICTPASE.
DR ProDom; PD000222; Prot_Inh_Kunz-m; 1.
DR SMART; SM00131; KU; 1.
DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
DR PROSITE; PS50279; BPTI_KUNITZ_2; 1.

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KW Protease.
SQ SEQUENCE 90 AA; 10006 MW; 2BEDC1D2020852AF CRC64;

Query Match 50.7%; Score 153; DB 2; Length 90;
Best Local Similarity 45.1%; Pred. No. 3.1e-11;
Matches 23; Conservative 10; Mismatches 18; Indels 0; Gaps 0;

QY 1 CSMPOBAGPCLASIPHHWYNNKTKICSEFYGGCGGNNNNFQTEAICLVTC 51
DB 31 CYLPADTGPCMANFPFRFYDSASKCKKFTYGGCHGNANNFETRECKKC 81

RESULT 46
Q7T0Z5 PRELIMINARY; PRT; 224 AA.
AC Q7T0Z5;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE MGC68843 protein.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RX TISSUE=Embryo;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Xiauner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udutin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Butterfield Y.S.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RX TISSUE=Embryo;
RX MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;
RA Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
RA Richardson P.;
RT "Genetic and genomic tools for Xenopus research: The NIH Xenopus
RT initiative.";
RL Dev. Dyn. 225:384-391(2002).
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Embryo;
RA Klein S., Strausberg R.;
RA Submitted (AUG-2003) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Contains 3 BPTI/Kunitz inhibitor domains.
DR EMBL; BC055972; AAH55972.1; -.
DR HSP; P00974; IBPI.
DR GO; GO:0004867; F:serine-type endopeptidase inhibitor activity; IEA.
DR InterPro; IPR002223; Prot_Inh_Kunz-m.
DR Pfam; PF00014; Kunitz BPTI; 3.
DR ProDom; PD000222; Prot_Inh_Kunz-m; 3.
DR SMART; SM00131; KU; 3.
DR PROSITE; PS00280; BPTI_KUNITZ_1; 3.
DR PROSITE; PS50279; BPTI_KUNITZ_2; 3.

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SQ SEQUENCE 224 AA; 25538 MW; 11C2D1C4C789445B CRC64;
 Query Match 50.7%; Score 153; DB 2; Length 224;
 Best Local Similarity 49.0%; Pred. No. 7.7e-11;
 Matches 25; Conservative 8; Mismatches 18; Indels 0; Gaps 0;

Qy 1 CSMPOEAGPCLASIPHWYNNKTKICSEFYIYGCGGNNNFQTEAICLVTC 51
 | : | | | | | : | : | : | : | : | : | : | : | : | : | : |
 Db 30 CLLPLDEGPCKALPHYYVDYRTQTCCQEFFYGGCGGNANFVMSDECCEKFC 80

RESULT 47
 IP52 ANESU STANDARD; PRT; 62 AA.
 ID _IP52 ANESU STANDARD; PRT; 62 AA.
 AC P10280;
 DT 01-MAR-1989 (Rel. 10, Created)
 DT 01-FEB-1991 (Rel. 17, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Protease inhibitor 5 II (SA5 II).
 OS Anemonia sulcata (Snake-locks sea anemone).
 OC Eukaryota; Metazoa; Cnidaria; Anthozoa; Zoantharia; Actiniaria;
 OC Nynanthese; Actinidae; Anemonia.
 NCBI_Taxid=6108;
 [1]
 SEQUENCE OF 1-59.
 RWunderer G., Machleidt W., Fritz H.;
 RA "The broad-specificity proteinase inhibitor 5 II from the sea anemone
 RT Anemonia sulcata.";
 RL Meth. Enzymol. 80:816-820(1981).
 [2]
 SEQUENCE.
 RA Krebs H.C., Habermehl G.G.;
 RP "Isolation and structural determination of a hemolytic active peptide
 RT from the sea anemone Metridium senile";
 RL Naturwissenschaften 74:395-396(1987).
 CC -1- FUNCTION: Inhibitor of kallikreins.
 CC -1- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.
 DR PIR; S07451; S07451.
 DR HGSP; P31713; LSHP.
 DR InterPro; IPR002223; Prot_Inh_Kunz-m.
 DR Pfam; PF00014; Kunitz_BPTI; 1.
 DR PRINTS; PR00759; BASICTPASE.
 DR ProDom; PD000222; Prot_Inh_Kunz-m; 1.
 DR SMART; SM00131; KU; 1.
 DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
 DR PROSITE; PSS0279; BPTI_KUNITZ_2; 1.
 KW Direct protein sequencing; Serine protease inhibitor.
 FT SITE 15 16 Reactive bond (By similarity).
 FT FT DISULFID 5 55 By similarity.
 FT FT DISULFID 14 38 By similarity.
 FT FT DISULFID 30 51 By similarity.
 FT VARIANT 13 13 P -> R.
 FT VARIANT 16 16 A -> G.
 FT VARIANT 17 17 R -> G.
 FT VARIANT 25 25 S -> L.
 FT VARIANT 28 28 K -> R.
 FT VARIANT 39 39 G -> R.
 SQ SEQUENCE 62 AA; 6937 MW; 7262D0D28CA567BC8 CRC64;

Query Match 50.3%; Score 152; DB 1; Length 62;
 Best Local Similarity 49.0%; Pred. No. 2.8e-11;
 Matches 25; Conservative 6; Mismatches 20; Indels 0; Gaps 0;

Qy 1 CSMPOEAGPCLASIPHWYNNKTKICSEFYIYGCGGNNNFQTEAICLVTC 51
 | : | | | | | : | : | : | : | : | : | : | : | : | : | : |
 Db 5 CELPKVVGPCRPFRRYYNSSKRCEKFYIYGCGGNNNFHTLECEKVC 55

RESULT 48
 Q90WA0 PRELIMINARY; PRT; 83 AA.
 ID Q90WA0
 AC Q90WA0;
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)

Job time : 29.1327 sec

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - protein search, using frame_plus_n2p model

Run on: September 21, 2005, 16:47:56 ; Search time 79 Seconds

(without alignments)
3877.395 Million cell updates/sec

Title: US-10-807-204-11

Perfect score: 764

Sequence: 1 atgggactctcaggacttct.....cctgcaaaaataaccattaa 396

Scoring table:

BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 4211384

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 50 summaries

Command line parameters:

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-DB=A Geneseq_16Dec04 -QFMT=fastan -SUFFIX=std.rag -MINMATCH=0.1 -LOOPCPU=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=50 -DOCALLIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=50
-MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEADSIZE=500 -MINLEN=0 -MAXLEN=2000000000
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-NO MWAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

A Geneseq_16Dec04:.*
1: Geneseqp1980s:.*
2: Geneseqp1990s:.*
3: Geneseqp2000s:.*
4: Geneseqp2001s:.*
5: Geneseqp2002s:.*
6: Geneseqp2003as:.*
7: Geneseqp2003bs:.*
8: Geneseqp2004s:.*

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	741	97.0	131	ADA19800	Ada19800 Engineere
2	741	97.0	131	ADA19811	Ada19811 Engineere
3	739	96.7	131	ADA19814	Ada19814 Human DJ1
4	613	80.2	106	ADA19801	Ada19801 Mature fo
5	559	73.2	98	ADA19808	Ada19808 Engineere
6	480	62.8	136	ADA19815	Ada19815 Mouse DJ1
7	455	59.6	133	AAW75219	Aaw75219 Human sec
8	455	59.6	133	AAE26982	Aae26982 Human gen
9	455	59.6	133	AAE27120	Aae27120 Human gen
10	455	59.6	133	ABU64993	Abu64993 Human sec

11	455	59.6	133	7	ADA19812	Ada19812 Human EPP
12	455	59.6	133	8	ADG89802	Adg89802 Human Pro
13	455	59.6	164	3	AAAY70010	Aay70010 Human Pro
14	455	59.6	179	8	ABM85103	Abm85103 Human dia
15	455	59.6	86	5	ABP69809	Abp69809 Human pol
16	412	53.9	86	6	ABJ26667	Abj26667 Human pro
17	412	53.9	101	4	ABB12236	Abb12236 Human epp
18	389.5	51.0	117	5	AAE27094	Aae27094 Human sec
19	389.5	51.0	117	5	AAE27165	Aae27165 Human gen
20	389.5	51.0	117	6	ABU65038	Abu65038 Human sec
21	389.5	51.0	117	8	ADG89847	Adg89847 Human sec
22	388	50.8	102	5	AAE27095	Aae27095 Human sec
23	388	50.8	102	5	AAE28009	Aae28009 Human gen
24	388	50.8	102	5	ABU65039	Abu65039 Human gen
25	388	50.8	102	8	ADG89848	Adg89848 Human sec
26	386	50.5	134	7	ADA19813	Ada19813 Mouse EPP
27	254	33.2	43	7	ADA19804	Ada19804 Engineere
28	242	31.7	64	4	AAE13093	Aae13093 Human eer
29	236.5	31.0	101	8	ADG66734	Adg66734 Novel hum
30	236	30.9	58	4	AAE13084	Aae13084 Human eer
31	236	30.9	58	4	AAE13084	Aae13084 Human eer
32	236	30.9	58	7	ADF41997	Adf41997 Human CAB
33	236	30.9	58	8	ADL16838	Adl16838 Human Kun
34	236	30.9	58	8	ADR89980	Adr89980 Human CAB
35	219	28.7	51	2	AAW75257	Aaw75257 Fragment
36	219	28.7	51	5	AAE27025	Aae27025 Human gen
37	219	28.7	51	5	AAE27163	Aae27163 Human gen
38	219	28.7	51	8	ADG89845	Adg89845 Human sec
39	182.5	23.9	560	2	AAE62523	Aae62523 Hookworm
40	181	23.7	2858	4	ABB71150	Abb71150 Drosophil
41	181	23.7	3060	4	ABE58064	AbE58064 Drosophil
42	180.5	23.6	571	7	AAE39498	Aae39498 Cloned mo
43	180.5	23.6	571	7	AAE39459	Aae39459 Mouse GDF
44	180.5	23.6	571	7	ADD93670	Add93670 Mouse GDF
45	180	23.6	33	7	ADA19806	Ada19806 Engineere
46	180	23.6	33	7	ADA19809	Ada19809 Engineere
47	177	23.2	58	2	AAE99146	Aae99146 Aprotinin
48	175	22.9	43	4	AAE13096	Aae13096 Human eer
49	175	22.9	54	4	AAE13092	Aae13092 Trypsin i
50	173	22.6	58	2	AAE27402	Aae27402 Human neu

ALIGNMENTS

RESULT 1
ADA19800
ID ADA19800 standard; protein; 131 AA.
XX
AC ADA19800;
XX
DT 20-NOV-2003 (first entry)
XX
DE Engineered human DJ11 protein SEQ ID NO:1.
XX
KW DJ11; Kunitz-type protease inhibitor domain; antiinflammatory;
KW antiallergic; thrombolytic; anticoagulant; cardiant; vasotropic;
KW antibacterial; immunosuppressive; antirheumatic; antiarthritic;
KW nephrotropic; antipsoriatic; vulnery; protease inhibitor; gene therapy;
KW acute pancreatitis; pulmonary injury; allergy-induced protease release;
KW deep vein thrombosis; myocardial infarction; shock; septic shock;
KW hyperfibrinolytic haemorrhage; inflammatory disorder; emphysema;
KW idiopathic pulmonary fibrosis; rheumatoid arthritis; glomerulonephritis;
KW chronic inflammatory bowel disease; psoriasis.
XX
OS Synthetic.
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Misc-difference 1..131 /note= "eppin-like precursor"
FT Peptide 1..25 /label= signal
FT Protein 26..131

FT Disulfide-bond /note= "mature DJ11 protein"
 FT 33. .61
 FT /note = predicted disulfide bond
 FT Disulfide-bond 40. .65
 FT /note = predicted disulfide bond
 FT Disulfide-bond 48. .60
 FT /note = predicted disulfide bond
 FT Disulfide-bond 54. .69
 FT /note = predicted disulfide bond
 FT 77. .127
 FT /note = predicted disulfide bond
 FT Domain
 FT /note = Kunitz domain predicted by pfscan
 FT 77. .127
 FT /note = predicted disulfide bond
 FT Disulfide-bond 86. .110
 FT /note = predicted disulfide bond
 FT Disulfide-bond 102. .123
 FT /note = predicted disulfide bond

WO2003070770-A2.

28-AUG-2003.

18-FEB-2003; 2003WO-EP001629.

21-FEB-2002; 2002US-0358683P.

(GENE-) GENEPROT INC.

Bougueleret L, Bairoch A, Niknejad A;

WPI; 2003-663849/62.

N-PSDB; ADA19810.

XX New engineered human Kunitz-type protease inhibitor for diagnosing,
 PT preventing or treating conditions associated with excessive proteinase
 PT activity, e.g. inflammation, pulmonary injuries, myocardial infarction or
 PT hemorrhage.

XX Claim 5; Page 69-70; 87pp; English.

XX The present invention describes an isolated, purified or recombinant DJ11
 CC polypeptide comprising a Kunitz-type protease inhibitor domain or its
 CC biologically active portion. The polypeptide comprises at least 98 %
 CC identity to residues 77-127 of a 131 amino acid sequence (S1, see
 CC ADA19800), or to residues 52-102 of a 106 amino acid sequence (S2, see
 CC ADA19801). DJ11 has antiinflammatory, antiallergic, thrombolytic,
 CC anticoagulant, cardiant, vasotropic, antibacterial, immunosuppressive,
 CC antirheumatic, antiarthritic, nephrotropic, antiporiatic and vulnary
 CC activities, and can be used as a protease inhibitor and in gene therapy.
 CC Composition and methods from the present invention can be used in
 CC diagnosing, preventing or treating conditions associated with excessive
 CC proteinase activity, such as acute pancreatitis, pulmonary injury,
 CC allergy-induced protease release, deep vein thrombosis, myocardial
 CC infarction, shock (including septic shock), hyperfibrinolytic
 CC haemorrhage, and especially, inflammatory disorders (e.g. emphysema,
 CC idiopathic pulmonary fibrosis, rheumatoid arthritis, glomerulonephritis,
 CC chronic inflammatory bowel disease or psoriasis). The DJ11 proteins may
 CC be used in preserving platelet function, organ preservation or in wound
 CC healing. The polynucleotide sequence encoding DJ11 may be used as
 CC hybridisation probes, in chromosome and gene mapping, in the generation
 CC of antisense RNA and DNA, and as targets for pharmaceutical intervention.
 CC The present sequence represents an engineered human DJ11 protein from the
 CC present invention.

XX Sequence 131 AA;

Alignment Scores:
 Pred. No.: 1,64e-68 Length: 131
 Score: 741.00 Matches: 130
 Percent Similarity: 99.24% Conservative: 0
 Best Local Similarity: 99.24% Mismatches: 1
 Query Match: 96.99% Indels: 0
 DB: 7 Gaps: 0

US-10-807-204-11 (1-396) x ADA19800 (1-131)
 QY 1 ATGGGACTCTCAGGACTTCTGCCAAATCCTGGTACCATTATCCTTTGGGGACATCCAG 60
 |||||
 Db 1 MetGlyLeuSerGlyLeuLeuProIleLeuValProPheIleLeuLeuGlyAspIleGln 20
 |||||
 QY 61 GAACCTGGGACGCTGAAGGCATCCTTTGGCAAGCCGTGCCAAAATCAAAGTGAATGC 120
 |||||
 Db 21 GluProGlyHisAlaGluGlyIleLeuGlyLysProCysProLysIleValGluCys 40
 |||||
 QY 121 GAAGTGGAGAATAATAGACCAAGTGTACCAACCCAGAGATTGCCAGAAAAACATGAAGTGT 180
 |||||
 Db 41 GluValGluGluIleAspGlnCysThrLysProArgAspCysProGluAenMetLysCys 60
 |||||
 QY 181 TGCCCGTTACGCCGTGGAAAGAAATGTTAGACTTCAGAAAGATATATCAGTATGCCA 240
 |||||
 Db 61 CysProPheSerCysGlyLysCysLeuAspPheArgLysAspIleCysSerMetPro 80
 |||||
 QY 241 CAGGAGGCTGGCCCTGGCTCCATACCACTGGTGGTACATAATAAAAAAATAAG 300
 |||||
 Db 81 GlnGluAlaGlyProCysLeuAlaSerIleProHisIleTrpTrpTyrAenLysThrLys 100
 |||||
 QY 301 ATCTGCTCGAATTCTATATGGCGTTGCCAGGGGAACAATAACAATTCCTCAAACTGAA 360
 |||||
 Db 101 IleCysSerGluPheIleTyrGlyCysGlnGlyAenAenAenAenPheGlnThrGlu 120
 |||||
 QY 361 GCTATCTGTCTGCTCACCTGCCAAAAAATACCAT 393
 |||||
 Db 121 AlaIleCysLeuValThrCysLysLysTyrHis 131

RESULT 2

ADA19811

ID ADA19811 standard; protein; 131 AA.

XX AC

ADA19811;

XX AC

20-NOV-2003 (first entry)

XX DT

Engineered human DJ11 protein SEQ ID NO:12.

XX DE

DJ11; Kunitz-type protease inhibitor domain; antiinflammatory;

XX KW

antiallergic; thrombolytic; anticoagulant; cardiant; vasotropic;

XX KW

antibacterial; immunosuppressive; antirheumatic; antiarthritic;

XX KW

nephrotropic; antiporiatic; vulnary; protease inhibitor; gene therapy;

XX KW

acute pancreatitis; pulmonary injury; allergy-induced protease release;

XX KW

deep vein thrombosis; myocardial infarction; shock; septic shock;

XX KW

hyperfibrinolytic haemorrhage; inflammatory disorder; emphysema;

XX KW

idiopathic pulmonary fibrosis; rheumatoid arthritis; glomerulonephritis;

XX KW

chronic inflammatory bowel disease; psoriasis.

XX OS

Synthetic.

XX OS

Homo sapiens.

XX XX

WO2003070770-A2.

XX XX

28-AUG-2003.

XX XX

18-FEB-2003; 2003WO-EP001629.

XX XX

21-FEB-2002; 2002US-0358683P.

XX PR

(GENE-) GENEPROT INC.

XX PA

Bougueleret L, Bairoch A, Niknejad A;

XX FI

WPI; 2003-663849/62.

XX DR

New engineered human Kunitz-type protease inhibitor for diagnosing,

PT preventing or treating conditions associated with excessive proteinase

PT activity, e.g. inflammation, pulmonary injuries, myocardial infarction or

PT hemorrhage.

XX PT

PS Disclosure; Page 84; 87pp; English.

XX The present invention describes an isolated, purified or recombinant DJ11
XX polypeptide comprising a Kunitz-type protease inhibitor domain or its
XX biologically active portion. The polypeptide comprises at least 98 %
XX identity to residues 77-127 of a 131 amino acid sequence (S1, see
XX ADA19800). DJ11 has antiinflammatory, antiallergic, thrombolytic,
XX anticoagulant, cardiant, vasotropic, antibacterial, immunosuppressive,
XX antirheumatic, antiarthritic, nephrotropic, antiporiatic and vulnerary
XX activities, and can be used as a protease inhibitor and in gene therapy.
XX Composition and methods from the present invention can be used in
XX diagnosing, preventing or treating conditions associated with excessive
XX proteinase activity, such as acute pancreatitis, pulmonary injury,
XX allergy-induced protease release, deep vein thrombosis, myocardial
XX infarction, shock (including septic shock), hyperfibrinolytic
XX haemorrhage, and especially, inflammatory disorders (e.g. emphysema,
XX idiopathic pulmonary fibrosis, rheumatoid arthritis, glomerulonephritis,
XX chronic inflammatory bowel disease or psoriasis). The DJ11 proteins may
XX be used in preserving platelet function, organ preservation or in wound
XX healing. The polynucleotide sequence encoding DJ11 may be used as
XX hybridisation probes, in chromosome and gene mapping, in the generation
XX of antisense RNA and DNA, and as targets for pharmaceutical intervention.
XX The present sequence represents an engineered human DJ11 protein from the
XX present invention.

SQ Sequence 131 AA;

Alignment Scores:

Pred. No.: 1.64e-68 Length: 131
Score: 741.00 Matches: 130
Percent Similarity: 99.24% Conservativity: 0
Best Local Similarity: 99.24% Mismatches: 1
Query Match: 96.93% Indels: 0
DB: 7 Gaps: 0

US-10-807-204-11 (1-396) x ADA19811 (1-131)

QY 1 ATGGAGCTCTCAGGACTTCTGCCAATCTGTGGTACCATTTCCTTTTGGGGACATCCAG 60
DB 1 MetGlyLeuSerGlyLeuLeuProLeuValProPheLeuLeuGlyAspIleGln 20
QY 61 GAACCTGGCCAGCGTGAAGGCATCTTGGCAAGCGTGTCCCAAAATCAAAAGTGAATGC 120
DB 21 GluProGlyHisAlaGluGlyLeuGlyLysProCysProLysIleLysValGluCys 40
QY 121 GAAGTGGGAAGAAATAGACAGTGTACCAACCCAGAGATGGCCAGAAAACATGAAGTGT 180
DB 41 GluValGluGluLeuAspGlnCysThrLysProArgAspCysProGluAsnMetLysCys 60
QY 181 TGCCCGTTCCAGCGTGGGAAAGAAATGTTTAGACTTCAGAAAGATATATGCAATATGCCA 240
DB 61 CysProPheSerCysGlyLysLysCysLeuAspPheArgLysAspIleCysSerMetPro 80
QY 241 CAGGAGGCTGGCCCTGCTGCTCCATACCACACTGGTGTAACAATAAAAACTAAG 300
DB 81 GlnGluAlaGlyProCysLeuAlaSerIleProHisTyrTrpTyrAsnLysLysThrLys 100
QY 301 ATCTGCTCGAATTATCATCTATGGCGGTGCCAGGGGACAAATAACAACTTCCAAACTGGA 360
DB 101 IleCysSerGluPheIleTyrGlyGlyCysGlnGlyAsnAsnAsnAsnPheGlnThrGlu 120
QY 361 GCTATCTGTCTGCTACCTGCAAAAATAACCAT 393
DB 121 AlaIleCysLeuValThrCysLysLysIleHis 131

RESULT 3

ADA19814

ID ADA19814 standard; protein; 131 AA.

XX ADA19814;

AC ADA19814;

XX 20-NOV-2003 (first entry)

QY 1 ATGGAGCTCTCAGGACTTCTGCCAATCTGTGGTACCATTTCCTTTTGGGGACATCCAG 60

XX Human DJ11 protein SEQ ID NO:15.

XX DJ11; Kunitz-type protease inhibitor domain; antiinflammatory;
XX antiallergic; thrombolytic; anticoagulant; cardiant; vasotropic;
XX antibacterial; immunosuppressive; antirheumatic; antiarthritic;
XX nephrotropic; antiporiatic; vulnerary; protease inhibitor; gene therapy;
XX acute pancreatitis; pulmonary injury; allergy-induced protease release;
XX deep vein thrombosis; myocardial infarction; shock; septic shock;
XX hyperfibrinolytic haemorrhage; inflammatory disorder; emphysema;
XX idiopathic pulmonary fibrosis; rheumatoid arthritis; glomerulonephritis;
XX chronic inflammatory bowel disease; psoriasis.

XX Homo sapiens.

OS WO2003070770-A2.

XX 28-AUG-2003.

XX 18-FEB-2003; 2003WO-EP001629.

XX 21-FEB-2002; 2002US-0358683P.

XX (GENE-) GENEPROT INC.

XX Bougueleret L, Bairoch A, Niknejad A;

XX WPI; 2003-663849/62.

XX New engineered human Kunitz-type protease inhibitor for diagnosing,
XX preventing or treating conditions associated with excessive proteinase
XX activity, e.g. inflammation, pulmonary injuries, myocardial infarction or
XX hemorrhage.

PS Disclosure; Fig 1; 87pp; English.

XX The present invention describes an isolated, purified or recombinant DJ11
XX polypeptide comprising a Kunitz-type protease inhibitor domain or its
XX biologically active portion. The polypeptide comprises at least 98 %
XX identity to residues 77-127 of a 131 amino acid sequence (S1, see
XX ADA19800), or to residues 52-102 of a 106 amino acid sequence (S2, see
XX ADA19801). DJ11 has antiinflammatory, antiallergic, thrombolytic,
XX anticoagulant, cardiant, vasotropic, antibacterial, immunosuppressive,
XX antirheumatic, antiarthritic, nephrotropic, antiporiatic and vulnerary
XX activities, and can be used as a protease inhibitor and in gene therapy.
XX Composition and methods from the present invention can be used in
XX diagnosing, preventing or treating conditions associated with excessive
XX proteinase activity, such as acute pancreatitis, pulmonary injury,
XX allergy-induced protease release, deep vein thrombosis, myocardial
XX infarction, shock (including septic shock), hyperfibrinolytic
XX haemorrhage, and especially, inflammatory disorders (e.g. emphysema,
XX idiopathic pulmonary fibrosis, rheumatoid arthritis, glomerulonephritis,
XX chronic inflammatory bowel disease or psoriasis). The DJ11 proteins may
XX be used in preserving platelet function, organ preservation or in wound
XX healing. The polynucleotide sequence encoding DJ11 may be used as
XX hybridisation probes, in chromosome and gene mapping, in the generation
XX of antisense RNA and DNA, and as targets for pharmaceutical intervention.
XX The present sequence represents a human DJ11 protein given in comparison
XX with DJ11 proteins in the exemplification of the present invention.

XX Sequence 131 AA;

Alignment Scores:

Pred. No.: 2.65e-68 Length: 131
Score: 739.00 Matches: 130
Percent Similarity: 99.24% Conservativity: 0
Best Local Similarity: 99.24% Mismatches: 1
Query Match: 96.73% Indels: 0
DB: 7 Gaps: 0

US-10-807-204-11 (1-396) x ADA19814 (1-131)

Db 1 MetGlyLeuSerGlyLeuLeuProIleLeuValProPheIleLeuLeuGlyAspIleGln 20
 Qy 61 GAACCTGGGACGCTGAAGGCATCTTGGCAAGCCGTGTCCCAAAATCAAAGTGGATGC 120
 Db 21 GluProGlyHisAlaGluGlyIleLeuGlyLysProCysProLysIleLeuValGluCys 40
 Qy 121 GAGTGTGAAGAAATAGACCATGTTACCAACCCAGAGATTGCCAGAAACATGAAGTGT 180
 Db 41 GluValGluGluIleAspGlnCysThrLysProArgAspCysProGluAsnMetLysCys 60
 Qy 181 TGCCCGCTTCAGCCGCTGGAAGAAATGTTAGACTTCAGAAAGGATATATGAGTATGCCA 240
 Db 61 CysProPheSerArgGlyLysLysCysLeuAspPheArgLysAspLleCysSerMetPro 80
 Qy 241 CAGAGGCTGCCCTGCCTGCCTGCCATACCACTGGTGGTACATATAAAAACTAAG 300
 Db 81 GlnGluAlaGlyProCysLeuAlaSerIleProHisTrpTyrAsnLysLysThrLys 100
 Qy 301 ATCTGCTCCGAATTCATCTATGCGGTGGCGGTGCCAGGGGACATACAACTTCCAACTCAA 360
 Db 101 IleCysSerGluPheIleTyrGlyGlySerGlnGlyAsnAsnAsnPheGlnThrGlu 120
 Qy 361 GCTATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 393
 Db 121 AlaIleCysLeuValThrCysLysLysTyrHis 131
 RESULT 4
 ID ADA19801 standard; protein; 106 AA.
 AC ADA19801;
 XX
 DT 20-NOV-2003 (first entry)
 DE Mature form of engineered human DJ11 protein SEQ ID NO:2.
 KW DJ11; Kunitz-type protease inhibitor domain; antiinflammatory;
 KW antiallergic; thrombolytic; anticoagulant; cardiant; vasotrophic;
 KW antibacterial; immunosuppressive; antirheumatic; antiarthritic;
 KW nephrotropic; antipsoriatic; vulnery; protease inhibitor; gene therapy;
 KW acute pancreatitis; pulmonary injury; allergy-induced protease release;
 KW deep vein thrombosis; myocardial infarction; shock; septic shock;
 KW hyperfibrinolytic haemorrhage; inflammatory disorder; emphysema;
 KW idiopathic pulmonary fibrosis; rheumatoid arthritis; glomerulonephritis;
 KW chronic inflammatory bowel disease; psoriasis.
 OS Synthetic.
 OS Homo sapiens.
 XX
 XX Key Location/Qualifiers
 FT Disulfide-bond 8..36 /note = predicted disulfide bond
 FT Disulfide-bond 15..40 /note = predicted disulfide bond
 FT Disulfide-bond 23..35 /note = predicted disulfide bond
 FT Disulfide-bond 29..44 /note = predicted disulfide bond
 FT Domain 52..102 /note = Kunitz domain predicted by pfscan
 FT Disulfide-bond 52..102 /note = predicted disulfide bond
 FT Disulfide-bond 61..85 /note = predicted disulfide bond
 FT Disulfide-bond 77..98 /note = predicted disulfide bond
 XX WO2003070770-A2.
 XX 28-AUG-2003.
 XX 18-FEB-2003; 2003WO-EP001629.

XX 21-FEB-2002; 2002US-0358683P.
 XX (GENE-) GENEPROT INC.
 XX Bougueleret L, Bairoch A, Niknejad A;
 XX WPI; 2003-663849/62.
 XX New engineered human Kunitz-type protease inhibitor for diagnosing,
 XX preventing or treating conditions associated with excessive proteinase
 XX activity, e.g. inflammation, pulmonary injuries, myocardial infarction or
 XX hemorrhage.
 PS Claim 5; Page 71; 87pp; English.
 XX The present invention describes an isolated, purified or recombinant DJ11
 CC polypeptide comprising a Kunitz-type protease inhibitor domain or its
 CC biologically active portion. The polypeptide comprises at least 98 %
 CC identity to residues 77-127 of a 131 amino acid sequence (S1, see
 CC ADA19800), or to residues 52-102 of a 106 amino acid sequence (S2, see
 CC ADA19801). DJ11 has antiinflammatory, antiallergic, thrombolytic,
 CC anticoagulant, cardiant, vasotrophic, antibacterial, immunosuppressive,
 CC antirheumatic, antiarthritic, nephrotropic, antipsoriatic and vulnery
 CC activities, and can be used as a protease inhibitor and in gene therapy.
 CC Composition and methods from the present invention can be used in
 CC diagnosing, preventing or treating conditions associated with excessive
 CC proteinase activity, such as acute pancreatitis, pulmonary injury,
 CC allergy-induced protease release, deep vein thrombosis, myocardial
 CC infarction, shock (including septic shock), hyperfibrinolytic
 CC haemorrhage, and especially, inflammatory disorders (e.g. emphysema,
 CC idiopathic pulmonary fibrosis, rheumatoid arthritis, glomerulonephritis,
 CC chronic inflammatory bowel disease or psoriasis). The DJ11 proteins may
 CC be used in preserving platelet function, organ preservation or in wound
 CC healing. The polynucleotide sequence encoding DJ11 may be used as
 CC hybridisation probes, in chromosome and gene mapping, in the generation
 CC of antisense RNA and DNA, and as targets for pharmaceutical intervention.
 CC The present sequence represents the mature form of an engineered human
 CC DJ11 protein from the present invention.
 XX
 SQ Sequence 106 AA;
 Alignment Scores:
 Pred. No.: 3-72e-55 Length: 106
 Score: 613.00 Matches: 105
 Percent Similarity: 99.06% Conservative: 0
 Best Local Similarity: 99.06% Mismatches: 1
 Query Match: 80.24% Indels: 0
 DB: 7 Gaps: 0
 US-10-807-204-11 (1-396) x ADA19801 (1-106)
 Qy 76 GAAGGCATCTTGGCAAGCCGTGTCCCAAAATCAAAGTGGATGCGAAGTGAAGAATA 135
 Db 1 GluGlyIleLeuGlyLysProCysProLysIleLysValGluCysGluValGluGlu 20
 Qy 136 GACCACTGTACCAACCCAGAGATTGCCAGAAACATGAAGTGTGCCCGTTCAGCCGT 195
 Db 21 AspGlnCysThrLysProArgAspCysProGluAsnMetLysCysCysProPheSerCys 40
 Qy 196 GGAAGAAGAAATGTTAGACTTCAGAAAGGATATATGAGTATGCCAGAGAGGTGGCCCC 255
 Db 41 GlyIlyLysCysLeuAspPheArgLysAspLleCysSerMetProGlnGluAlaGlyPro 60
 Qy 256 TGCTGTGCTCCATACACACTGGTGGTACAAATAAAAACTAAGATCTCTCCGAATTC 315
 Db 61 CysLeuAlaSerIleProHisTrpTyrAsnLysLysThrLysIleCysSerGluPhe 80
 Qy 316 ATCTATGGCGGTGGCCAGGGGACATACAACTTCCAACTGATCTCTGCTGTC 375
 Db 81 IleTyrGlyGlyCysGlnGlyAsnAsnAsnPheGlnThrGluAlaIleCysLeuVal 100
 Qy 376 ACCTGCAAAAAAATATACCAT 393

```
Db      101 ThrCysLysTyrHis 106
|||||
RESULT 5
ADAL9808
ID      ADA19808 standard; protein; 98 AA.
XX
XX
AC      ADAL9808;
XX
XX
DT      20-NOV-2003 (first entry)
XX
XX      Engineered human DJ11 partial amino acid sequence SEQ ID NO:9.
DE
XX      DJ11; Kunitz-type protease inhibitor domain; antiinflammatory;
KW      anti-allergic; thrombolytic; anticoagulant; cardiant; vasotropic;
KW      antibacterial; immunosuppressive; antirheumatic; antiarthritic;
KW      nephrotropic; antipsoriatic; vulnery; protease inhibitor; gene therapy;
KW      acute pancreatitis; pulmonary injury; allergy-induced protease release;
KW      deep vein thrombosis; myocardial infarction; shock; septic shock;
KW      hyperfibrinolytic haemorrhage; inflammatory disorder; emphysema;
KW      idiopathic pulmonary fibrosis; rheumatoid arthritis; glomerulonephritis;
KW      chronic inflammatory bowel disease; psoriasis.
XX
XX      Synthetic.
OS      Homo sapiens.
XX
XX      WO2003070770-A2.
XX
XX      28-AUG-2003.
XX
XX      18-FEB-2003; 2003WO-EP001629.
XX
XX      21-FEB-2002; 2002US-0358683P.
XX
XX      (GENE-) GENEPROT INC.
XX
XX      Bougueleret L, Bairoch A, Niknejad A;
XX
XX      WPI; 2003-663849/62.
XX
XX      New engineered human Kunitz-type protease inhibitor for diagnosing,
PT      preventing or treating conditions associated with excessive proteinase
PT      activity, e.g. inflammation, pulmonary injuries, myocardial infarction or
PT      hemorrhage.
XX
XX      Disclosure; Page 82; 87pp; English.
XX
XX      The present invention describes an isolated, purified or recombinant DJ11
CC      polypeptide comprising a Kunitz-type protease inhibitor domain or its
CC      biologically active portion. The polypeptide comprises at least 98 %
CC      identity to residues 77-127 of a 131 amino acid sequence (S1, see
CC      ADA19800), or to residues 52-102 of a 106 amino acid sequence (S2, see
CC      ADA19801). DJ11 has antiinflammatory, anti-allergic, thrombolytic,
CC      anticoagulant, cardiant, vasotropic, antibacterial, immunosuppressive,
CC      antirheumatic, antiarthritic, nephrotropic, antipsoriatic and vulnery
CC      activities, and can be used as a protease inhibitor and in gene therapy.
CC      Composition and methods from the present invention can be used in
CC      diagnosing, preventing or treating conditions associated with excessive
CC      proteinase activity, such as acute pancreatitis, pulmonary injury,
CC      allergy-induced protease release, deep vein thrombosis, myocardial
CC      infarction, shock (including septic shock), hyperfibrinolytic
CC      haemorrhage, and especially, inflammatory disorders (e.g. emphysema,
CC      idiopathic pulmonary fibrosis, rheumatoid arthritis, glomerulonephritis,
CC      chronic inflammatory bowel disease or psoriasis). The DJ11 proteins may
CC      be used in preserving platelet function, organ preservation or in wound
CC      healing. The polynucleotide sequence encoding DJ11 may be used as
CC      hybridisation probes, in chromosome and gene mapping, in the generation
CC      of antisense RNA and DNA, and as targets for pharmaceutical intervention.
CC      The present sequence represents a partial engineered human DJ11 protein
CC      amino acid sequence from the present invention.
XX
XX      Sequence 98 AA;
SQ
```

```
Alignment Scores:
Pred. No.: 1.6e-49 Length: 98
Score: 559.00 Matches: 98
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 73.17% Indels: 0
DB: 7 Gaps: 0

US-10-807-204-11 (1-396) x ADA19808 (1-98)
QY      1 ATGGGACTCTCAGGACTTCTGCCAATCTGGTACCATTTCATCTTTTGGGGGACATCCAG 60
DB      1 MetGlyLeuSerGlyLeuLeuProIleLeuValProPheIleLeuLeuGlyAspIleGln 20
QY      61 GAACCTGGGCACGCTGAAGGCATCTTGGCAAGCCGTGTCCCAAAATCAAAAGTGAATGC 120
DB      21 GluProGlyHisAlaGluGlyIleLeuGlyLysProCysProLysIleLysValGluCys 40
QY      121 GAAGTGGAGAAATAGACCACTGTACCAACCCAGAGATTGCCAGAAACATCAAGTGT 180
DB      41 GluValGluGluIleAspGlnCysThrLysProArgAspCysProGluAsnMetLysCys 60
QY      181 TGCCCGTTTCAGCCGCTGGAAAGAAATGTTAGACTTCAGAAAGGATATATGTCAGTATGCCA 240
DB      61 CysProPheSerArgGlyLysLysCysLeuAspPheArgLysAspIleCysSerMetPro 80
QY      241 CAGGAGGCTGGCCCTGCCTGCCCTCCATACCACACTGGTGGTACAAATAAAAAA 294
DB      81 GlnGluAlaGlyProCysLeuAlaSerIleProHisTrpTrpTyrAsnLysLys 98

RESULT 6
ADAL9815
ID      ADA19815 standard; protein; 136 AA.
XX
XX      ADAL9815;
XX
XX      20-NOV-2003 (first entry)
XX
XX      Mouse DJ11 protein SEQ ID NO:16.
XX
XX      DJ11; Kunitz-type protease inhibitor domain; antiinflammatory;
KW      anti-allergic; thrombolytic; anticoagulant; cardiant; vasotropic;
KW      antibacterial; immunosuppressive; antirheumatic; antithrombotic;
KW      nephrotropic; antipsoriatic; vulnery; protease inhibitor; gene therapy;
KW      acute pancreatitis; pulmonary injury; allergy-induced protease release;
KW      deep vein thrombosis; myocardial infarction; shock; septic shock;
KW      hyperfibrinolytic haemorrhage; inflammatory disorder; emphysema;
KW      idiopathic pulmonary fibrosis; rheumatoid arthritis; glomerulonephritis;
KW      chronic inflammatory bowel disease; psoriasis.
XX
XX      Mus musculus.
XX
XX      WO2003070770-A2.
XX
XX      28-AUG-2003.
XX
XX      18-FEB-2003; 2003WO-EP001629.
XX
XX      21-FEB-2002; 2002US-0358683P.
XX
XX      (GENE-) GENEPROT INC.
XX
XX      Bougueleret L, Bairoch A, Niknejad A;
XX
XX      WPI; 2003-663849/62.
XX
XX      New engineered human Kunitz-type protease inhibitor for diagnosing,
PT      preventing or treating conditions associated with excessive proteinase
PT      activity, e.g. inflammation, pulmonary injuries, myocardial infarction or
PT      hemorrhage.
XX
XX      Disclosure; Fig 1; 87pp; English.
XX
XX
```


AC	ABU64993;	CC	proteins, their fragment, polypeptide domain, epitope, secreted form,
XX		CC	variant, allelic variant, or species homologue, or the encoded sequence
DT		CC	included in ATCC 97921 and 97922. Also included are the encoding nucleic
XX	15-MAY-2003 (first entry)	CC	acids, recombinant vectors, host cells, antibodies, and genes. The
DE	Human secreted protein gene 24, protein #1.	CC	proteins and nucleic acids are useful for diagnosing, preventing,
XX		CC	treatment, prognosis or ameliorating a medical condition e.g.
KW	Secreted protein; immunodeficiency; multiple sclerosis;	CC	immunodeficiencies (e.g. X-linked agammaglobulinemia, B cell
KW	severe combined immunodeficiency; autoimmune disorder; cancer;	CC	immunodeficiencies, severe combined immunodeficiencies), autoimmune
KW	rheumatoid arthritis; diabetes mellitus; haematopoietic disorder;	CC	disorders (e.g. systemic erythematous, rheumatoid arthritis, multiple
KW	inflammatory condition; septic shock; inflammatory bowel disease;	CC	sclerosis, autoimmune thyroiditis, autoimmune haemolytic anaemia,
KW	Crohn's disease; respiratory disorder; asthma; allergy; stroke;	CC	Goodpasture's syndrome, Grave's disease, diabetes mellitus, dermatitis,
KW	gastrointestinal disorder; central nervous system disorder;	CC	haematopoietic disorders, inflammatory conditions (e.g. septic shock,
KW	ischaemic brain injury; neurodegenerative disorder; Parkinson's disease;	CC	sepsis, reperfusion injury, inflammatory bowel disease, Crohn's disease),
KW	Alzheimer's disease; cardiovascular disorder; atherosclerosis;	CC	respiratory disorders (e.g. asthma and allergy), gastrointestinal
KW	blood-related disorder; thrombosis; atherosclerosis; renal disorder;	CC	disorders, cancers (e.g. gastric, ovarian, lung, bladder, liver and
KW	hyperproliferative disorder; acute glomerulonephritis; Addison's disease;	CC	breast), central nervous system (CNS) disorders (e.g. ischaemic brain
KW	endocrine disorder; liver disease; reproductive system disorder;	CC	injury and/or stroke, traumatic brain injury), neurodegenerative
KW	endometriosis; infectious disease; pancreatic disorder; vaccine;	CC	disorders (e.g. Parkinson's disease and Alzheimer's disease, AIDS-related
KW	wound repair; angiogenesis; lymphatic disorder; hair loss; body weight;	CC	dementia, and prion disease), cardiovascular disorders (e.g.
KW	body height; hair colour; human.	CC	atherosclerosis, myocarditis, cardiovascular disease, and cardiopulmonary
OS	Homo sapiens.	CC	bypass complications), inflammation (e.g. hepatitis, gout, trauma,
XX		CC	pancreatitis, sarcoidosis, dermatitis, allogenic transplant rejection),
PN	US2002172994-A1.	CC	blood-related disorders (thrombosis, arterial thrombosis),
XX	21-NOV-2002.	CC	hyperproliferative disorders, renal disorders (e.g. acute
XX		CC	glomerulonephritis), endocrine disorders (e.g. Addison's disease,
PF	11-MAY-2001; 2001US-00852797.	CC	hyperthyroidism, hyperpituitarism), liver diseases and disorders,
XX		CC	reproductive system disorders (e.g. endometriosis), infectious diseases,
PR	14-MAR-1997; 97US-0040710P.	CC	and pancreatic disorders. Many other diseases and disorders are listed in
PR	14-MAR-1997; 97US-0040762P.	CC	the specification. They also useful as a vaccine adjuvant. Further they
PR	30-MAY-1997; 97US-0048100P.	CC	are useful to enhance or inhibit complement mediated cell lysis, for
PR	30-MAY-1997; 97US-0048189P.	CC	stimulating wound and tissue repair, angiogenesis, and the repair of
PR	30-MAY-1997; 97US-0048357P.	CC	vascular or lymphatic diseases or disorders. They are also useful to
PR	30-MAY-1997; 97US-0050934P.	CC	prevent hair loss, to modulate mammalian characteristics such as body
PR	06-JUN-1997; 97US-0048970P.	CC	height, weight, hair colour, and to increase or decrease storage
PR	05-SEP-1997; 97US-0057765P.	CC	capabilities, fat content, lipid, protein, carbohydrate, vitamins,
PR	19-DEC-1997; 97US-0068368P.	CC	minerals, cofactors or other nutritional components. The proteins are
PR	12-MAR-1998; 98WO-US004858.	CC	also useful for identifying binding partners. The present sequence
PR	11-SEP-1998; 98US-0015206P.	CC	represents a secreted protein of the invention
PR	02-FEB-2001; 2001US-0265583P.	XX	SQ Sequence 133 AA;
PA	(RUBE/) RUBEN S M.	Alignment Scores:	
PA	(ROSE/) ROSEN C A.	Pred. No.:	1.26e-38 Length: 133
PA	(LIYV/) LI Y.	Score:	455.00 Matches: 77
PA	(ZENG/) ZENG Z.	Percent Similarity:	74.22% Conservative: 18
PA	(KYAW/) KYAW H.	Best Local Similarity:	60.16% Mismatches: 33
PA	(FISC/) FISCHER C L.	Query Match:	59.55% Indels: 0
PA	(LIHH/) LI H.	DB:	6 Gaps: 0
PA	(SOPP/) SOPPET D R.		
PA	(GENT/) GENTZ R L.		
PA	(WEIY/) WEI Y.		
PA	(MOOR/) MOORE P A.		
PA	(YOUN/) YOUNG P E.		
PA	(GREEN/) GREENE J M.		
PA	(FERR/) FERRIE A M.		
XX			
PI	Ruben SM, Rosen CA, Li Y, Zeng Z, Kyaw H, Fischer CL, Li H;		
PI	Soppet DR, Gentz RL, Wei Y, Moore PA, Young PE, Greene JM;		
PI	Ferrie AM;		
XX			
DR	WPI: 2003-310989/30.		
DR	N-PSDB; ABX96989.		
XX			
PT	New human secreted polypeptides and polynucleotides for diagnosing,		
PT	prognosing, preventing and treating immune, hyperproliferative, liver,		
PT	kidney, reproductive disorders and for identifying modulators of		
PT	therapeutic use.		
XX			
PS	Claim 11; Page 185; 209pp; English.		
XX			
CC	The invention relates to an isolated polypeptide comprising an amino acid		
CC	sequence at least 95% identical to sequence of 28 human secreted		

101 ThrCysSerMetPheValTyrGlyCysGlnGlyAsnAsnAsnPheGlnSerLys 120

361 GCTATCTGCTGGTCACCTGCAAA 384

121 AlaAsnCysLeuAenThrCysLys 128

RESULT 11

ADA19812

ID ADA19812 standard; protein; 133 AA.

XX AC ADA19812;

XX DT 20-NOV-2003 (first entry)

XX DE Human EPPIN protein SEQ ID NO:13.

XX DJ11; Kunitz-type protease inhibitor domain; antiinflammatory;

KW antiallergic; thrombolytic; anticoagulant; cardiant; vasotrophic;

KW antibacterial; immunosuppressive; antirheumatic; antiarthritic;

KW nephrotropic; antipsoriatic; vulnary; protease inhibitor; gene therapy;

KW acute pancreatitis; pulmonary injury; allergy-induced protease release;

KW deep vein thrombosis; myocardial infarction; shock; septic shock;

KW hyperfibrinolytic haemorrhage; inflammatory disorder; emphysema;

KW idiopathic pulmonary fibrosis; rheumatoid arthritis; glomerulonephritis;

KW chronic inflammatory bowel disease; psoriasis; EPPIN.

XX OS Homo sapiens.

XX WO2003070770-A2.

XX 28-AUG-2003.

XX 18-FEB-2003; 2003WO-EP001629.

XX 21-FEB-2002; 2002US-0358683P.

XX (GENE-) GENEPROT INC.

XX Bougueleret L, Bairoch A, Niknejad A;

XX WPI; 2003-663849/62.

XX New engineered human Kunitz-type protease inhibitor for diagnosing,

PT preventing or treating conditions associated with excessive proteinase

PT activity, e.g. inflammation, pulmonary injuries, myocardial infarction or

PT hemorrhage.

XX Disclosure; Fig 1; 87pp; English.

XX The present invention describes an isolated, purified or recombinant DJ11

CC polypeptide comprising a Kunitz-type protease inhibitor domain or its

CC biologically active portion. The polypeptide comprises at least 98 %

CC identity to residues 77-127 of a 131 amino acid sequence (S1, see

CC ADA19800), or to residues 52-102 of a 106 amino acid sequence (S2, see

CC ADA19801). DJ11 has antiinflammatory, antiallergic, thrombolytic,

CC anticoagulant, cardiant, vasotrophic, antibacterial, immunosuppressive,

CC antirheumatic, antiarthritic, nephrotropic, antipsoriatic and vulnary

CC activities, and can be used as a protease inhibitor and in gene therapy.

CC Composition and methods from the present invention can be used in

CC diagnosing, preventing or treating conditions associated with excessive

CC proteinase activity, such as acute pancreatitis, pulmonary injury,

CC allergy-induced protease release, deep vein thrombosis, myocardial

CC infarction, shock (including septic shock), hyperfibrinolytic

CC haemorrhage, and especially, inflammatory disorders (e.g. emphysema,

CC idiopathic pulmonary fibrosis, rheumatoid arthritis, glomerulonephritis,

CC chronic inflammatory bowel disease or psoriasis). The DJ11 proteins may

CC be used in preserving platelet function, organ preservation or in wound

CC healing. The polynucleotide sequence encoding DJ11 may be used as

CC hybridisation probes, in chromosome and gene mapping, in the generation

CC of antisense RNA and DNA, and as targets for pharmaceutical intervention.

CC The present sequence represents a human EPPIN protein given in comparison

CC with DJ11 proteins in the exemplification of the present invention.

SQ Sequence 133 AA;

Alignment Scores:

Pred. No.: 1.26e-38 Length: 133

Score: 455.00 Matches: 77

Percent Similarity: 74.22% Conservative: 18

Best Local Similarity: 60.16% Mismatches: 33

Query Match: 59.55% Indels: 0

DB: 7 Gaps: 0

US-10-807-204-11 (1-396) x ADA19812 (1-133)

Qy 1 ATGGGACTCTCAGGACTTCTGCAATCCTGGTACCATTCTCTTTGGGGGACATCCAG 60

Db 1 MetGlySerSerGlyLeuLeuSerLeuLeuValLeuPheValLeuLeuAlaAsnValGln 20

Qy 61 GAACCTGGGCACGCTGAAGSCATCCTTGGCAAGCCGTGTCCCAAAATCAAAGTGAATGC 120

Db 21 GlyProGlyLeuThrAspTrpLeuPheProArgCysProLysIleArgGluGluCys 40

Qy 121 GAAGTGGAGAATAGACACAGTGTACCAACCCAGAGATTGCCAGAAAACATGNAAGTGT 180

Db 41 GluPheGlnGluArgAspValCysThrLysAspArgGlnCysGlnAspAsnLysLysCys 60

Qy 181 TGCCCGTTACGCCGTGGAAAGAAATGTTAGACTTCAGAAAGGATATATGCAGTATGCCCA 240

Db 61 CysValPheSerCysGlyLysLysCysLeuAspLeuLysGlnAspValCysGluMetPro 80

Qy 241 CAGGAGGCTGGCCCTGCTGCTCCATACCACTGTGGTGTACATAAATAAATACTAAG 300

Db 81 LysGluThrGlyProCysLeuAlaTyrPheLeuHisTrpTrpTyrAspLysLysAspAsn 100

Qy 301 ATCTGCTCCGAATTCATCTATGCGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 360

Db 101 ThrCysSerMetPheValTyrGlyCysGlnGlyCysGlnGlyCysGlnGlyCysGln 120

Qy 361 GCTATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 384

Db 121 AlaAsnCysLeuAsnThrCysLys 128

RESULT 12

ADG89802

ID ADG89802 standard; protein; 133 AA.

XX AC ADG89802;

XX DT 11-MAR-2004 (first entry)

XX DE Human protein from secreted protein gene 24 #1.

XX KW Secreted protein; gene therapy; neural disorder; immune system disorders;

KW muscular disorder; reproductive disorder; gastrointestinal disorder;

KW pulmonary disorder; cardiovascular disorder; renal disorder;

KW proliferative disorder; cancer; systemic lupus erythematosus;

KW rheumatoid arthritis; multiple sclerosis; thyroiditis; anaemia;

KW Grave's disease; diabetes; hepatitis; asthma; allergy; nephritis;

KW Parkinson's disease; Alzheimer's disease; atherosclerosis;

XX myocardial infarction; AIDS; infection; human.

XX OS Homo sapiens.

XX US2003225009-A1.

XX 04-DEC-2003.

XX 30-JAN-2002; 2002US-00058993.

XX 14-MAR-1997; 97US-0040710P.

XX 14-MAR-1997; 97US-0040762P.

XX 30-MAY-1997; 97US-0048100P.

XX 30-MAY-1997; 97US-0048189P.

XX 30-MAY-1997; 97US-0048357P.

XX 30-MAY-1997; 97US-0050934P.

US-10-807-204-11 (1-396) x ABM85103 (1-179)

```
QY 1 ATGGGACTCTCAGGACTTCTGCAATCTGTCATTCACATTCATCTTTGGGGGACATCCAG 60
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
1 MetGlySerSerGlyLeuLeuSerLeuLeuValLeuPheValLeuLeuAlaAsnValGln 20
QY 61 GAACCTGGCGACGCTGAAGGATCTCTGGCAAGCGGTGTCCTCCAAATCAAAAGTGAATGC 120
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
21 GlyProGlyLeuThrAspTrpLeuPheProArgCysProLysIleArgGluGluCys 40
QY 121 GAAGTGGGAAGATAGACACGTGTACCAACCCAGAGATTGCCAGAAAACATGAGTGT 180
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
41 GluPheGlnGluArgAspValCysThrLysAspArgGlnCysGlnAspAsnLysLysCys 60
QY 181 TGCCGTTTCAGCGTGGGAAGAAATGTTTACACTTCAGAAAGGATATATGAGTATGCCA 240
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
61 CysValPheSerCysGlyLysLysCysLeuAspLeuLysGlnAspValCysGluMetPro 80
QY 241 CAGGAGGCTGCCCTCGCTGCTCCATACACACACTGGTGTACATATAAAACAACTAAG 300
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
81 LysGluThrGlyProCysLeuAlaTyrPheLeuHisTrpTrpTyrAspLysLysAspAsn 100
QY 301 ATCTGCTCCGAATTCATCTATGCGCGTGGCCAGGGGAACAATAACAATTCCTCAACTGAA 360
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
101 ThrCysSerMetPheValTyrGlyCysGlnGlyAsnAsnAsnAsnPheGlnSerLys 120
QY 361 GCTATCTCTGCTGGTCACTGCAAA 384
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
121 AlaAsnCysLeuAsnThrCysLys 128
```

RESULT 15

ID ABP69809 standard; protein; 86 AA.

AC ABP69809;

DT 20-JAN-2003 (first entry)

DE Human polypeptide SEQ ID NO 1856.

XX Human; genome mapping; gene therapy; food supplement; virus; fungus;
KW cell-proliferative disorder; neurodegenerative disease; bacterial;
KW Parkinson's disease; Alzheimer's disease; autoimmune disease;
KW multiple sclerosis; diabetes; genetic disorder; wound; burn; infection;
KW arthritis; cytosolic; immunomodulator; nontropic; neuroprotective;
KW antiparkinsonian; antidiabetic; immunosuppressive; dermatological;
KW haemostatic; vulnerrary; fungicide; antibacterial; virucide; protozoacide;
KW antiarthritic.

OS Homo sapiens.

PN WO2002070539-A2.

XX 12-SEP-2002.

XX 05-MAR-2002; 2002WO-US0005095.

XX 05-MAR-2001; 2001US-00799451.

XX (HYSE-) HYSEQ INC.

XX Tang YT, Zhou P, Goodrich RW, Auandi V, Zhang J, Zhao QA, Ren F;
PI Xue AJ, Yang Y, Ma Y, Yamazaki V, Chen R, Wang Z, Ghosh M;
PI Wehrman T, Wang J, Wang D, Drmanac RT;

XX WPI; 2002-759812/82.

DR N-PSDB; AB212026.

XX New polynucleotides comprising sequences assembled from expressed
PT sequence tags (ESTs), useful for treating cell-proliferative,
PT neurodegenerative, autoimmune, genetic, myeloid or lymphoid, or platelet
PT or coagulation disorders.

XX

PS Claim 9; SEQ ID NO 1856; 1012pp + Sequence Listing; English.

XX The invention relates to an isolated polynucleotide (I) comprising a
CC nucleotide sequence selected from any of 948 sequences (AB211119-
CC AB212066) or their mature protein coding portion, active domain coding
CC protein or complementary sequences. The polynucleotides are useful for
CC identifying expressed genes or for physical mapping of human genome. The
CC encoded polypeptides (ABP69802-ABP69849) are useful as molecular weight
CC markers, as a food supplement, for generating antibodies, in medical
CC imaging, screening and diagnostic assays and for treating cell-
CC proliferative disorders (cancer), neurodegenerative diseases (Parkinson's
CC or Alzheimer's disease), autoimmune diseases (multiple sclerosis,
CC diabetes, lupus) genetic disorders, myeloid or lymphoid disorders,
CC platelet or coagulation disorders, wound, burns, incision, ulcers, liver
CC or lung fibrosis, infections (bacterial, viral, fungal, parasitic),
CC arthritis, etc. Note: The sequence data for this patent did not form part
CC of the printed specification, but was obtained in electronic format
CC directly from WIPO at ftp.wipo.int/pub/published_pct_sequences

XX Sequence 86 AA;

Alignment Scores:

Pred. No.: 3.58e-34 Length: 86
Score: 412.00 Matches: 74
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 53.93% Indels: 0
DB: 5 Gaps: 0

US-10-807-204-11 (1-396) x ABP69809 (1-86)

QY 1 ATGGGACTCTCAGGACTTCTGCCAATCTGTCATTCATCTTTGGGGGACATCCAG 60

Db 1 MetGlyLeuSerGlyLeuLeuProIleLeuValProPheIleLeuLeuGlyAspIleGln 20

QY 61 GAACCTGGCGACGCTGAAGGATCTCTGGCAAGCGGTGTCCTCCAAATCAAAAGTGAATGC 120

Db 21 GluProGlyHisAlaGluGlyIleLeuGlyLysProCysProLysValGluCys 40

QY 121 GAAGTGGGAAGATAGACACGTGTACCAACCCAGAGATTGCCAGAAAACATGAGTGT 180

Db 41 GluValGluGluIleAspGlnCysThrLysProArgAspCysProGluAsnMetLysCys 60

QY 181 TGCCGTTTCAGCGTGGGAAGAAATGTTTACACTTCAGAAAGTGAATGC 222

Db 61 CysProPheSerArgGlyLysLysCysLeuAspPheArgLys 74

RESULT 16

ABU26667

ID ABU26667 standard; protein; 86 AA.

XX AC ABU26667;

XX DT 01-MAY-2003 (first entry)

XX Human protein modification + maintenance molecule protein SEQ ID No 21.

XX Cytostatic; antiarteriosclerotic; anti-HIV; anti-allergic; anticonvulsant;
KW cerebroprotective; antiparkinsonian; nontropic; anti-inflammatory;
KW antiulcer; hepatotropic; gynaecological; antibacterial; virucide;
KW protozoacide; antiparasitic; cell proliferative disease; PMOD;
KW protein modification and maintenance molecule; immunogenic fragment;
KW cancer; autoimmune; inflammatory disease; neurological disorder;
KW gastrointestinal; developmental; vesicle trafficking disorder; infection;
KW protein-protein interaction; drug-target interaction;
KW gene expression profile; human.

XX OS Homo sapiens.

XX WO2003000844-A2.

XX 03-JAN-2003.

XX

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PF 18-JUN-2002; 2002WO-US019360.
XX
XX 22-JUN-2001; 2001US-0300508P.
XX 06-JUL-2001; 2001US-0302445P.
XX 13-JUL-2001; 2001US-0305405P.
XX 09-AUG-2001; 2001US-0311442P.
XX 24-AUG-2001; 2001US-0314821P.
XX 29-AUG-2001; 2001US-0315922P.
XX 03-MAY-2002; 2002US-0378205P.
XX
XX (INCY-) INCYTE GENOMICS INC.
XX
XX Gandhi AR, Kable AE, Swarnakar A, Hafalia AJA, Tran B, Duggan BM;
XX Warren BA, Ison CH, Honchell CD, Nguyen DB, Lu DAM, Lee EA, Yue H;
XX Forsythe IJ, Barroso I, Ramkumar J, Griffin JA, Li JX, Yang J,
XX Thangavelu K, Gietzen KJ, Ding L, Baughn MR, Borowsky ML, Yao MG;
XX Wallia NK, Mason PM, Gururajan R, Lee S, Becha SA, Tran SY,
XX Elliott VS, Luo W, Sprague WW, Tang YT, Lu Y, Zabarjadian Y;
XX
XX WPI; 2003-184039/18.
XX N-PSDB; ABB23220.
XX
XX New isolated human PMOD polypeptide and polynucleotide, useful for
XX diagnosing, treating and preventing diseases or conditions associated
XX with the aberrant PMOD expression, e.g. cancer, AIDS, atherosclerosis and
XX infections.
XX
XX Claim 76; Page 196; 225pp; English.
XX
XX The invention relates to an isolated polypeptide comprising: any of 28
XX sequences of 48-1256 amino acids; a natural amino acid sequence at least
XX 90% identical to the 28 amino acid sequences, 94% identical to a sequence
XX of 703 or 267 amino acids, 96% identical to a sequence of 414 amino
XX acids, or 97% identical to a sequence of 242 amino acids, all given in
XX the specification; or a biologically active or immunogenic fragment of
XX the isolated polypeptide. The polypeptides and polynucleotides are useful
XX in diagnosing, treating and preventing diseases or conditions associated
XX with the decreased expression of protein modification and maintenance
XX molecules (PMOD), such as cell proliferative diseases (e.g. cancer,
XX atherosclerosis), autoimmune/inflammatory diseases (e.g. AIDS,
XX allergies), neurological disorders (e.g. stroke, Parkinson's disease,
XX epilepsy), gastrointestinal (e.g. ulcer, cirrhosis), reproductive (e.g.
XX endometriosis), developmental, vesicle trafficking disorders, and
XX infections (e.g. bacterial, viral, parasitic, protozoal). These are also
XX useful in assessing the effects of exogenous compounds on the expression
XX of nucleic acid and amino acid sequences of PMOD. The PMOD or its
XX fragments are useful in screening compounds for effectiveness as agonist
XX or antagonist of the polypeptides, or in altering the expression of the
XX target polynucleotide and compounds that specifically bind to or modulate
XX the activity of the polypeptide. The microarray is useful in monitoring
XX or measuring protein-protein interactions, drug-target interactions, and
XX gene expression profiles. This sequence represents a human PMOD protein
XX of the invention
XX
XX SQ Sequence 86 AA;
XX
XX Alignment Scores:
XX Pred. No.: 3.58e-34 Length: 86
XX Score: 412.00 Matches: 74
XX Percent Similarity: 100.00% Conservative: 0
XX Best Local Similarity: 100.00% Mismatches: 0
XX Query Match: 53.93% Indels: 0
XX DB: 6 Gaps: 0
XX
XX US-10-807-204-11 (1-396) x ABJ26667 (1-86)
XX
XX 1 ATGGGACTCTCAGGACTTCTGCCAATCTGTGTACCATTCATCTTTGGGGACATCCAG 60
XX |||||
XX 1 MetGlyLeuSerGlyLeuLeuProIleuValProPheIleuLeuGlyAspIleGln 20
XX
XX 61 GAACCTGGGACGCTGAAGGATCTCTGGCAGCGGTGTCCCAAAATCAAAAGTGAATGC 120
XX |||||
XX 21 GluProGlyHisAlaGluGlyIleLeuGlyProCysProIleuLeuValGluCys 40
XX |||||
```

```
QY 121 GAAATGGAGAAATAGACCAAGTGTACCAAAACCCAGAGATTGCCAGAAAACATGAAGTGT 180
DB 41 GluValGluGluLeuLeuAspGlnCysThrLysProArgAspCysProGluAsnMetLysCys 60
QY 181 TGCCCGTTCAGCGTCGTAAGAAATGTTTAGACTTCAGAAAG 222
DB 61 CysProPheSerArgGlyLysLysCysLeuAspPheArgLys 74
RESULT 17
ABBI2236
ID ABBI2236 standard; peptide; 101 AA.
XX
XX AC ABB12236;
XX
XX DT 11-JAN-2002 (first entry)
XX
XX DE Human eppin-1 homologue, SEQ ID NO:2606.
XX
XX KW Human; cytokine; cell proliferation; cell differentiation; growth factor;
KW haematopoiesis regulation; tissue growth; immunomodulator; activin;
KW inhibin; chemotaxis; chemokinesis; thrombolysis; oncogenesis;
KW proliferation; metastasis; cancer; tumour; haematopoietic disorder;
KW myeloid cell disorder; lymphoid cell disorder; asthma; arthritis;
KW chronic inflammatory condition; proliferative retinopathy;
KW atherosclerosis; coronary heart disease; arterial ischaemia;
KW bone disorder; osteoporosis; vascular growth disorder;
KW tissue regeneration; wound healing; infection; immune disorder;
KW cell culture; drug screening; gene therapy; antiinflammatory;
KW antiasthmatic; antiarthritic; haemostatic; antiarteriosclerotic;
KW cytostatic; osteopathic; vasotropic; cardiant; virucide; antibacterial;
KW antifungal; vulnery; antiulcer.
XX
XX OS Homo sapiens.
XX
XX PN WO200157188-A2.
XX
XX PD 09-AUG-2001.
XX
XX PF 05-FEB-2001; 2001WO-US003800.
XX
XX PR 03-FEB-2000; 2000US-00496914.
XX 27-APR-2000; 2000US-00560875.
XX
XX PA (HYSE-) HYSEQ INC.
XX
XX FI Tang YT, Liu C, Drmanac RT;
XX
XX DR WPI; 2001-457740/49.
XX N-PSDB; ABA09480.
XX
XX PT Human proteins and DNA encoding sequences useful for preventing, treating
XX or ameliorating a medical condition in a mammalian subject e.g. arthritis
XX and cancer.
XX
XX PS Claim 20; Page 318; 1963pp; English.
XX
XX CC Sequences ABB10981-ABB12330 represent 1350 novel human polypeptides, and
XX sequences ABA08225-ABA09574 represent nucleic acids encoding them. The
XX invention also relates to vectors and recombinant host cells comprising a
XX nucleotide of the invention, methods of producing the novel polypeptides,
XX antibodies against the polypeptides, methods of detecting the nucleotides
XX or polypeptides in a sample, and methods of identifying compounds which
XX bind to polypeptides of the invention. Although novel, many of the
XX polypeptides of the invention have homology to known proteins, thereby
XX giving an insight into their probable biological activities, and hence
XX potential therapeutic applications. The polypeptides of the invention may
XX have various activities, including cytokine, cell proliferation or cell
XX differentiation activities; stem cell growth factor activity;
XX haematopoiesis regulatory activity; tissue growth activity;
XX immunomodulatory activity; activin or inhibin-related activities;
XX chemotactic or chemokinetic activities; haemostatic, thrombotic or
XX thrombolytic activities; receptor or ligand activities; or may be
```

CC involved in oncogenesis, cancer cell proliferation or metastasis.
 CC Depending on their biological activities, polypeptides and nucleotides of
 CC the invention are useful for preventing, treating or ameliorating medical
 CC conditions, e.g., by protein or gene therapy. Such conditions include
 CC cancers, haematopoietic disorders (e.g., myeloid or lymphoid cell
 CC disorders), chronic inflammatory conditions (e.g., asthma or arthritis),
 CC proliferative retinopathy, atherosclerosis, coronary heart disease,
 CC arterial ischaemia, bone disorders (e.g., osteoporosis), and abnormal
 CC vascular growth. Polypeptides involved with tissue regeneration and
 CC repair (or nucleic acids encoding them) may be used to promote wound
 CC healing (e.g., of burns, incisions and ulcers), while those with
 CC immunomodulatory activities may be used in the treatment of viral,
 CC bacterial and fungal infections in addition to immune disorders.
 CC Polypeptides with growth factor activity may be used in cell cultures to
 CC promote cell growth. For example, such polypeptides may be used to
 CC manipulate stem cells in culture to give rise to neuroepithelial cells
 CC that can be used to augment or replace cells damaged by illness,
 CC autoimmune disease or accidental damage. The polypeptides and nucleotides
 CC may also be used in the diagnosis of the above conditions, and in drug
 CC screening techniques. The present sequence represents a novel human
 CC polypeptide of the invention
 XX
 SQ Sequence 101 AA;

Alignment Scores:
 Pred. No.: 3,7e-34 Length: 101
 Score: 412.00 Matches: 74
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 53.93% Indels: 0
 DB: 4 Gaps: 0

US-10-807-204-11 (1-396) x ABB12236 (1-101)

QY 1 ATFGAGCTCTAGGACTTCTGCGCAATCTGTGACCATTCCTTTTGGGGACATCCAG 60
 Db |||||
 16 MetGlyLeuSerGlyLeuLeuProIleLeuValProPheIleLeuLeuGlyAspIleGln 35
 QY 61 GAACCTGGCGCGCTGAGGCAATCTTGGCAAGCGGTGCCAAATCAAAGTGAATGC 120
 Db |||||
 36 GluProGlyHisAlaGluGlyIleLeuGlyProCysProGlyIleLeuValGluCys 55
 QY 121 CAAGTGGAGAAATAGACAGGTGTACCAAAACCAGAGATTGCCAGAAAACATGAAGTGT 180
 Db |||||
 56 GluValGluGluLeuAspGlnCysThrLysProArgAspCysProGluAsnMetLysCys 75
 QY 181 TGCCCGTTCAGCCGTGGAAAGAAATGTTTAGACTTCAGAAAG 222
 Db |||||
 76 CysProPheSerArgGlyLysLysCysLeuAspPheArgLys 89

RESULT 18

ID AAE27094
 XX AAE27094 standard; protein; 117 AA.

AC AAE27094;

DT 13-DEC-2002 (first entry)

XX Human secreted protein #1.

XX Human; immunodeficiency; X-linked agammaglobulinaemia; septic shock;
 KW autoimmune disorder; rheumatoid arthritis; multiple sclerosis; cancer;
 KW Grave's disease; diabetes mellitus; haematopoietic disorder; stroke;
 KW respiratory disorder; asthma; allergy; gastrointestinal disorder;
 KW inflammatory bowel disease; neurodegenerative disorder; hepatitis;
 KW Parkinson's disease; Alzheimer's disease; cardiovascular disorder;
 KW atherosclerosis; myocarditis; renal disorder; fungicide; virucide;
 KW hyperproliferative disorder; acute glomerulonephritis; tonsillitis;
 KW respiratory disorder; rhinitis; sinusitis; neurological disease;
 KW endocrine disorder; Addison's disease; reproductive system disorder;
 KW endometriosis; vasotropic; vulnery; cytoskatic; nootropic; cardiant;
 KW anti-HIV; tranquilliser; gout; antiparasitic.

OS Homo sapiens.
 XX
 PN US2002077287-A1.
 XX
 XX 20-JUN-2002.
 PD
 XX
 XX 11-MAY-2001; 2001US-00852659.
 PF
 XX
 PR 11-SEP-1998; 98US-00152060.

XX (RUBE/) RUBEN S M.
 PA (ROSE/) RUBEN C A.
 PA (LIYY/) LI Y.
 PA (ZENG/) ZENG Z.
 PA (KYAW/) KYAW H.
 PA (FISC/) FISCHER C L.
 PA (LIHH/) LI H.
 PA (SOPP/) SOPPET D R.
 PA (GENT/) GENTZ R L.
 PA (WEIY/) WEI Y.
 PA (MOOR/) MOORE P A.
 PA (YOUN/) YOUNG P E.
 PA (GREE/) GREENE J M.
 PA (FERR/) FERRIE A M.

XX Ruben SM, Rosen CA, Li Y, Zeng Z, Kyaw H, Fischer CL, Li H;
 PI Soppet DR, Gentz RL, Wei Y, Moore PA, Young PE, Greene JM;
 PI Ferrie AM;

XX WPI; 2002-598780/64.

PT Novel human secreted polypeptides and polynucleotides for diagnosing,
 PT preventing, treating immune, hyperproliferative, cardiovascular,
 PT neurological, reproductive disorders and identifying modulators of
 PT therapeutic use.

XX Disclosure; Page 16; 209pp; English.

CC AAD44636-AAD44676 represent cDNAs corresponding to 28 human secreted
 CC protein genes, and AAE26959-AAE26999 represent the proteins they encode.
 CC AAE27000-AAE27025 represent human secreted protein fragments or their
 CC variants. The secreted proteins and genes are useful for preventing,
 CC treating or ameliorating medical conditions, e.g., by protein or gene
 CC therapy. Specific uses are described for each of the 28 genes, based on
 CC the tissues in which they are most highly expressed and include
 CC developing products for the diagnosis or treatment of immunodeficiencies,
 CC e.g., X-linked agammaglobulinaemia, B cell immunodeficiencies, severe
 CC combined immunodeficiencies, autoimmune disorders e.g., systemic lupus
 CC erythematosus, rheumatoid arthritis, multiple sclerosis, autoimmune
 CC thyroiditis, autoimmune haemolytic anaemia, Goodpasture's syndrome,
 CC Grave's disease, diabetes mellitus, dermatitis, inflammatory conditions
 CC including septic shock, sepsis, reperfusion injury, inflammatory bowel
 CC disease, Crohn's disease, haematopoietic disorders, respiratory disorders
 CC e.g., asthma and allergy, gastrointestinal disorders e.g., inflammatory
 CC bowel disease), cancers e.g., gastric, ovarian, lung, liver, bladder and
 CC breast), central nervous system (CNS) disorders e.g., Parkinson's
 CC injury and/or stroke, neurodegenerative disorders e.g., Alzheimer's
 CC disease and Alzheimer's disease, AIDS-related dementia and prion disease,
 CC cardiovascular disorders e.g., myocarditis, arrhythmias, atherosclerosis,
 CC inflammatory disorders e.g., hepatitis, gout, trauma, pancreatitis
 CC sarcoidosis and allogenic transplant rejection, blood-related disorder
 CC (thrombosis, arterial thrombosis, atherosclerosis), hyperproliferative
 CC disorders, respiratory disorders e.g. rhinitis, sinusitis, tonsillitis,
 CC lung cancer, allergic disorders, pneumonitis, renal disorders, e.g. acute
 CC glomerulonephritis, neurological diseases, liver disorders, endocrine
 CC disorders e.g., hyperthyroidism, Addison's disease, hyperpituitarism,
 CC infectious diseases and reproductive system disorders e.g. endometriosis.
 CC The present sequence represents a human secreted protein of the invention

SQ Sequence 117 AA;

Alignment Scores: 8.57e-32 Length: 117
 Pred. No.:

	Score:	389.50	Matches:	65	
	Percent Similarity:	77.00%	Conservative:	12	
	Best Local Similarity:	65.00%	Mismatches:	22	
	Query Match:	50.98%	Indels:	1	
	DB:	5	Gaps:	1	
US-10-807-204-11 (1-396) x AAE27094 (1-117)					
Qy	85	CTTGGCAACCGGTGTCGCCAAATCAAAGTGGAATGCGAAGTGGAGAATAAGACCAGTGT	144		
Dd	14	LeuGlyArg--CysProLysIleargGluGluCysGluPheGlnGluArgaspValCys	32		
Qy	145	ACCAAACCCAGAGATTGCCAGAAACAATGAAGTAGTTGCCGCTTCAGCCGTGGGAAAGAAA	204		
Dd	33	ThrLysAspArgGlnCysGlnAspAsnLysCysCysValPheSerCysGlyLysLys	52		
Qy	205	TGTTTAGACTTCAGAAAGCATATGCAGTAGTATGCACAGGAGGTGGCCCTGCTGGCC	264		
Dd	53	CysLeuAspLeuLysGlnAspValCysGluMetProLysGluThrGlyProCysLeuAla	72		
Qy	265	TCCATACCACTGGTGGTACATAAAAAAATAAGATCTGCTCCGAATTTCATCTATGGC	324		
Dd	73	TyrPheLeuHisTrpTrpTyrAspLysLysAspAsnThrCysSerMetPheValTyrGly	92		
Qy	325	GTTTGCAGGGGAACAATTAACAATTCCTCAAGCTATCTGCTGGTCACTGCAAA	384		
Dd	93	GlyCysGlnGlyAsnAsnAsnPheGlnSerLysAlaAsnCysLeuAsnThrCysLys	112		
RESULT 19					
ID	AAE27165				
XX	AAE27165 standard; protein; 117 AA.				
XX	AAE27165;				
DT	13-DEC-2002 (first entry)				
DE	Human gene 24 encoded secreted protein fragment #1.				
KW	Human; secreted protein; autoimmune disease; hyperproliferative disorder;				
KW	rheumatoid arthritis; neoplasm; cerebrovascular disorder; angiogenesis;				
KW	cerebral ischaemia; cardiovascular disorder; nervous system disorder;				
KW	cardiac arrest; Alzheimer's disease; ocular disorder; wound healing;				
KW	infection; corneal infection; skin aging; food additive; preservative;				
KW	tissue regeneration; immunosuppressive; antiproliferative; cytostatic;				
KW	cardiant; vasotropic; cerebroprotective; neurotropic; neuroprotective;				
KW	antibacterial; virucide; fungicide; ophthalmological; gene therapy;				
XX	vulnerary.				
OS	Homo sapiens.				
PN	US2002076756-A1.				
XX	20-JUN-2002.				
XX	XX				
Pf	11-MAY-2001; 2001US-00853161.				
XX	XX				
PR	02-FEB-2001; 2001US-0265583P.				
XX	(RUBE/) RUBEN S M.				
PA	(ROSE/) ROSEN C A.				
PA	(LIYY/) LI Y.				
PA	(ZENG/) ZENG Z.				
PA	(KYAW/) KYAW H.				
PA	(FISC/) FISCHER C L.				
PA	(LIHH/) LI H.				
PA	(SOPP/) SOPPET D R.				
PA	(GENT/) GENTZ R L.				
PA	(WEIV/) WEI Y.				
PA	(MOOR/) MOORE P A.				
PA	(YOUN/) YOUNG P E.				
PA	(GREEN/) GREENE J M.				
PA	(FERR/) FERRIE A M.				
XX	XX				
PI	Ruben SM, Rosen CA, Li Y, Zeng Z, Kyaw H, Fischer CL, Li H;				
PI	Soppet DR, Gentz RL, Wei Y, Moore PA, Young PE, Greene JM;				
PI	Ferrie AM;				
XX	XX				
DR	WPI; 2002-574454/61.				
XX	XX				
PT	New nucleic acid molecules encoding 28 human secreted proteins, useful				
PT	for diagnosing, preventing, treating or ameliorating medical conditions				
XX	and as food additives or preservatives.				
PS	Disclosure; Page 17; 20pp; English.				
XX	AD44854-AD44984 represent cDNAs corresponding to 28 human secreted				
CC	protein genes, and AAE27097-AAE27137 represent the proteins they encode.				
CC	AAE27138-AAE27164 represent human secreted protein fragments. The genes				
CC	and their corresponding secreted proteins are useful for preventing,				
CC	treating or ameliorating medical conditions, e.g., by protein or gene				
CC	therapy. Secreted protein sequences of the invention are useful for the				
CC	diagnosis or treatment of disorders such as autoimmune diseases (e.g.				
CC	rheumatoid arthritis), hyperproliferative disorders (e.g. neoplasms of				
CC	the breast or liver), cerebrovascular disorders (e.g. cerebral ischaemia,				
CC	angiogenesis), cardiovascular disorders (e.g. cardiac arrest), nervous				
CC	system disorders (e.g. Alzheimer's disease), infections caused by fungi,				
CC	bacteria and viruses and ocular disorders (e.g. corneal infection). The				
CC	polypeptides can also be used to aid wound healing and epithelial cell				
CC	proliferation, to prevent skin aging due to sunburn, to maintain organs				
CC	before transplantation, for supporting cell culture of primary tissues,				
CC	to regenerate tissues and in chemotaxis. They can also be used as food				
CC	additives or preservative to increase or decrease storage capabilities,				
CC	fat content, lipid, protein, carbohydrate, vitamins, minerals, cofactors				
CC	and other nutritional components. The present sequence represents a human				
CC	secreted protein fragment referred to in the disclosure of the invention				
XX	XX				
SQ	Sequence 117 AA;				
Alignment Scores:					
Pred. No.:	8,57e-32	Length:	117		
Score:	389.50	Matches:	65		
Percent Similarity:	77.00%	Conservative:	12		
Best Local Similarity:	65.00%	Mismatches:	22		
Query Match:	50.98%	Indels:	1		
DB:	5	Gaps:	1		
US-10-807-204-11 (1-396) x AAE27165 (1-117)					
Qy	85	CTTGGCAACCGGTGTCGCCAAATCAAAGTGGAATGCGAAGTGGAGAATAAGACCAGTGT	144		
Dd	14	LeuGlyArg--CysProLysIleargGluGluCysGluPheGlnGluArgaspValCys	32		
Qy	145	ACCAAACCCAGAGATTGCCAGAAACAATGAAGTAGTTGCCGCTTCAGCCGTGGGAAAGAAA	204		
Dd	33	ThrLysAspArgGlnCysGlnAspAsnLysCysCysValPheSerCysGlyLysLys	52		
Qy	205				

DE Human secreted protein gene 24, protein #4.

XX Secreted protein; immunodeficiency; multiple sclerosis;

XX severe combined immunodeficiency; autoimmune disorder; cancer;

KW rheumatoid arthritis; diabetes mellitus; haematopoietic disorder;

KW inflammatory condition; septic shock; inflammatory bowel disease;

KW Crohn's disease; respiratory disorder; asthma; allergy; stroke;

KW gastrointestinal disorder; central nervous system disorder;

KW ischaemic brain injury; neurodegenerative disorder; Parkinson's disease;

KW Alzheimer's disease; cardiovascular disorder; atherosclerosis;

KW blood-related disorder; thrombosis; atherosclerosis; renal disorder;

KW hyperproliferative disorder; acute glomerulonephritis; Addison's disease;

KW endocrine disorder; liver disease; reproductive system disorder;

KW endometriosis; infectious disease; pancreatic disorder; vaccine;

KW wound repair; angiogenesis; lymphatic disorder; hair loss; body weight;

XX body height; hair colour; human.

XX Homo sapiens.

OS US2002172994-A1.

PN 21-NOV-2002.

XX 11-MAY-2001; 2001US-00852797.

XX 14-MAR-1997; 97US-0040710P.

PR 14-MAR-1997; 97US-0040762P.

PR 30-MAY-1997; 97US-0048100P.

PR 30-MAY-1997; 97US-0048189P.

PR 30-MAY-1997; 97US-0048357P.

PR 30-MAY-1997; 97US-0050934P.

PR 06-JUN-1997; 97US-0048970P.

PR 05-SEP-1997; 97US-0057765P.

PR 19-DEC-1997; 97US-0068368P.

PR 12-MAR-1998; 98WO-US004858.

PR 11-SEP-1998; 98US-00152060.

PR 02-FEB-2001; 2001US-0265583P.

XX (RUBEN S M.

PA (ROSE/) ROSEN C A.

PA (LIYI/) LI Y.

PA (ZENG/) ZENG Z.

PA (KYAW/) KYAW H.

PA (FISC/) FISCHER C L.

PA (LIH/) LI H.

PA (SOPP/) SOPPET D R.

PA (GENT/) GENTZ R L.

PA (WEI/) WEI Y.

PA (MOOR/) MOORE P A.

PA (YOUN/) YOUNG P E.

PA (GREE/) GREENE J M.

PA (FERR/) FERRIE A M.

XX Ruben SM, Rosen CA, Li Y, Zeng Z, Kyaw H, Fischer CL, Li H;

PI Soppet DR, Gentz RL, Wei Y, Moore PA, Young PE, Greene JM;

PI Ferrie AM;

XX WPI: 2003-310989/30.

XX New human secreted polypeptides and polynucleotides for diagnosing,

PT prognosing, preventing and treating immune, hyperproliferative, liver,

PT kidney, reproductive disorders and for identifying modulators of

PT therapeutic use.

XX Disclosure; Page 16; 209pp; English.

XX The invention relates to an isolated polypeptide comprising an amino acid

CC sequence at least 95% identical to sequence of 28 human secreted

CC proteins, their fragment, polypeptide domain, epitope, secreted form,

CC variant, allelic variant, or species homologue, or the encoded sequence

CC included in ATCC 97921 and 97922. Also included are the encoding nucleic

CC acids, recombinant vectors, host cells, antibodies, and genes. The

CC proteins and nucleic acids are useful for diagnosing, preventing,

CC

CC treating, prognosing or ameliorating a medical condition e.g.

CC immunodeficiencies (e.g. X-linked agammaglobulinemia, B cell

CC immunodeficiencies, severe combined immunodeficiencies), autoimmune

CC disorders (e.g. systemic erythematosus, rheumatoid arthritis, multiple

CC sclerosis, autoimmune thyroiditis, autoimmune haemolytic anaemia,

CC Goodpasture's syndrome, Grave's disease, diabetes mellitus, dermatitis),

CC haematopoietic disorders, inflammatory conditions (e.g. septic shock,

CC sepsis, reperfusion injury, inflammatory bowel disease, Crohn's disease),

CC respiratory disorders (e.g. asthma and allergy), gastrointestinal

CC disorders, cancers (e.g. gastric, ovarian, lung, bladder, liver and

CC breast), central nervous system (CNS) disorders (e.g. ischaemic brain

CC injury and/or stroke, traumatic brain injury), neurodegenerative

CC disorders (e.g. Parkinson's disease and Alzheimer's disease, AIDS-related

CC dementia, and prion disease), cardiovascular disorders (e.g. atherosclerosis, myocarditis, cardiovascular disease, and cardiopulmonary

CC bypass complications), inflammation (e.g. hepatitis, gout, trauma,

CC pancreatitis, sarcoidosis, dermatitis, allergic transplant rejection),

CC blood-related disorders (thrombosis, arterial thrombosis),

CC hyperproliferative disorders, renal disorders (e.g. acute

CC glomerulonephritis), endocrine disorders (e.g. Addison's disease,

CC hyperthyroidism, hyperpituitarism), liver diseases and disorders,

CC reproductive system disorders (e.g. endometriosis), infectious diseases,

CC and pancreatic disorders. Many other diseases and disorders are listed in

CC the specification. They also useful as a vaccine adjuvant. Further they

CC are useful to enhance or inhibit complement mediated cell lysis, for

CC stimulating wound and tissue repair, angiogenesis, and the repair of

CC vascular or lymphatic diseases or disorders. They are also useful to

CC prevent hair loss, to modulate mammalian characteristics such as body

CC height, weight, hair colour, and to increase or decrease storage

CC capabilities, fat content, lipid, protein, carbohydrate, vitamins,

CC minerals, cofactors or other nutritional components. The proteins are

CC also useful for identifying binding partners. The present sequence

CC represents a secreted protein of the invention

XX SQ Sequence 117 AA;

Alignment Scores:

Pred. No.: 8.57e-32 Length: 117

Score: 389.50 Matches: 65

Percent Similarity: 77.00% Conservative: 12

Best Local Similarity: 65.00% Mismatches: 22

Query Match: 50.98% Indels: 1

DB: 6 Gaps: 1

US-10-807-204-11 (1-396) x ABU65038 (1-117)

QY 85 CTTGGCAAGCCGTGTCCTCAAAATCAAGTGGAAATGCGAAGTGGAGAAATAGACCACTGT 144

DB 14 LeuGlyArg---CysProLysIleArgGluGluCysGluPheGlnGluArgAspValCys 32

QY 145 ACCAAACCCAGAGATTGCCAGAAACATGAAGTGTTCGCCCTTCAGCCGTGGAAGAAA 204

DB 33 ThrLysAspArgGlnCysGlnAspAsnLysLysCysCysValPheSerCysGlyLysLys 52

QY 205 TGTTTAGACTTCAGAAAGATATATGTCAGTATGCCACAGGAGCTGGCCCTCTGCGCC 264

DB 53 CysLeuAspLeuLysGlnAspValCysGluMetProLysGluThrGlyProCysLeuAla 72

QY 265 TCCATACCACTGTGTGGTACAAATAAATACTAAGATCTGCTCGAATTCATCTATGCG 324

DB 73 TyrPheLeuHisTrpIrrPyrAspLysLysAspAsnThrCysSerMetPheValTyrGly 92

QY 325 GGTTCGCCAGGGGAACAATAACAACTTCCAAACTGAAGCTATCTGTGTGTCACCTGCAA 384

DB 93 GlyCysGlnGlyAsnAsnAsnAsnPheGlnSerLysAlaAsnCysLeuAsnThrCysLys 112

RESULT 21

ADG89847

ID ADG89847 standard; protein; 117 AA.

XX

AC ADG89847;

XX

DT 11-MAR-2004 (first entry)

DE Human secreted protein #2.
 XX Human; immunodeficiency; X-linked agammaglobulinaemia; septic shock;
 KW autoimmune disorder; rheumatoid arthritis; multiple sclerosis; cancer;
 KW Grave's disease; diabetes mellitus; haematopoietic disorder; stroke;
 KW respiratory disorder; asthma; allergy; gastrointestinal disorder;
 KW inflammatory bowel disease; neurodegenerative disorder; hepatitis;
 KW Parkinson's disease; Alzheimer's disease; cardiovascular disorder;
 KW atherosclerosis; myocarditis; renal disorder; fungicide; virucide;
 KW hyperproliferative disorder; acute glomerulonephritis; tonsillitis;
 KW respiratory disorder; rhinitis; sinusitis; neurological disease;
 KW endocrine disorder; Addison's disease; reproductive system disorder;
 KW endometriosis; vasotrophic; vulnery; cytotatic; nootropic; cardiant;
 KW anti-HIV; tranquilliser; gout; antiparasitic.
 XX Homo sapiens.
 XX US2002077287-A1.
 XX 20-JUN-2002.
 XX 11-MAY-2001; 2001US-00852659.
 XX 11-SEP-1998; 98US-00152060.
 XX (RUBE/) RUBEN S M.
 XX (ROSE/) ROSEN C A.
 XX (LIYV/) LI Y.
 XX (ZENG/) ZENG Z.
 XX (KYAW/) KYAW H.
 XX (FISC/) FISCHER C L.
 XX (LIH/) LI H.
 XX (SOPP/) SOPP D R.
 XX (GENT/) GENTZ R L.
 XX (WEI/) WEI Y.
 XX (MOOR/) MOORE P A.
 XX (YOUN/) YOUNG P E.
 XX (GREE/) GREENE J M.
 XX (FERR/) FERRIE A M.
 XX Ruben SM, Rosen CA, Li Y, Zeng Z, Kyaw H, Fischer CL, Li H;
 PI Soppet DR, Gentz RL, Wei Y, Moore PA, Young PE, Greene JM;
 PI Ferrie AM;
 XX WPI; 2002-598780/64.
 XX Novel human secreted polypeptides and polynucleotides for diagnosing,
 PT preventing, treating immune, hyperproliferative, cardiovascular, of
 PT neurological, reproductive disorders and identifying modulators of
 PT therapeutic use.
 XX Disclosure; Page 16; 209pp; English.
 XX AAD44636-AAD44676 represent cDNAs corresponding to 28 human secreted
 CC protein genes, and AAE26959-AAE26999 represent the proteins they encode.
 CC AAE27000-AAE27025 represent human secreted protein fragments or their
 CC variants. The secreted proteins and genes are useful for preventing,
 CC treating or ameliorating medical conditions e.g. by protein or gene
 CC therapy. Specific uses are described for each of the 28 genes, based on
 CC the tissues in which they are most highly expressed and include
 CC developing products for the diagnosis or treatment of immunodeficiencies,
 CC e.g., X-linked agammaglobulinaemia, B cell immunodeficiencies, severe
 CC combined immunodeficiencies, autoimmune disorders e.g., systemic lupus
 CC erythematosus, rheumatoid arthritis, multiple sclerosis, autoimmune
 CC thyroiditis, autoimmune haemolytic anaemia, Goodpasture's syndrome,
 CC Grave's disease, diabetes mellitus, dermatitis, inflammatory conditions
 CC including septic shock, sepsis, reperfusion injury, inflammatory bowel
 CC disease, Crohn's disease, haematopoietic disorders, respiratory disorders
 CC e.g., asthma and allergy, gastrointestinal disorders e.g., inflammatory
 CC bowel disease, cancers e.g., gastric, ovarian, lung, liver, bladder and
 CC breast), central nervous system (CNS) disorders e.g., ischaemic brain
 CC injury and/or stroke, neurodegenerative disorders e.g., Parkinson's
 CC disease and Alzheimer's disease, AIDS-related dementia and prion disease,

CC cardiovascular disorders e.g., myocarditis, arrhythmias, atherosclerosis,
 CC inflammatory disorders e.g., hepatitis, gout, trauma, pancreatitis,
 CC sarcoidosis and allogeneic transplant rejection, blood-related disorder
 CC (thrombosis, arterial thrombosis, atherosclerosis), hyperproliferative
 CC disorders, respiratory disorders e.g. rhinitis, sinusitis, tonsillitis,
 CC lung cancer, allergic disorders, pneumonitis, renal disorders, endocrine
 CC glomerulonephritis, neurological diseases, liver disorders, endocrine
 CC disorders e.g., hyperthyroidism, Addison's disease, hyperpituitarism,
 CC infectious diseases and reproductive system disorders e.g. endometriosis.
 CC The present sequence represents a human secreted protein of the invention
 XX
 XX Sequence 102 AA;
 Alignment Scores: 1.19e-31 Length: 102
 Pred. NO.: 388.00 Matches: 63
 Score: 77.08% Conservative: 11
 Percent Similarity: 65.62% Mismatches: 22
 Best Local Similarity: 50.79% Indels: 0
 Query Match: 5 Gaps: 0
 DB:
 US-10-807-204-11 (1-396) x AAE27095 (1-102)
 QY 97 TGTCCTCCAAATCAAGTGGATGCGAAGTGGAGAAATAGACAGTGTACCAACCCAGA 156
 DB 2 CysProlylsileArgGluGluCysGluPheGlnGluArgAspValCysThrLysAspArg 21
 QY 157 GATTGCCCAAGAAACATGAAGTGTGGCCGTTGACCGTGGAGAAAGAAATGTTAGACTTC 216
 DB 22 GlnCysGlnAspAsnLysLysCysValPheSerCysGlyLysLysCysLeuAspLeu 41
 QY 217 AGAAAGGATATATGAGTATGCCACAGAGGCTGGCCCTGGCTCCATACCACAC 276
 DB 42 LysGlnAspValCysGluMetProLysGluThrGlyProCysLeuAlaTyrPheLeuHis 61
 QY 277 TGGTGGTACATAAAACCTAAGATCTGCTCCGAATTCATCTATGGGGTGGCAGGG 336
 DB 62 TrpTrpTyrAspLysLysAspAsnThrCysSerMetPheValTyrGlyGlyCysGlnGly 81
 QY 337 AACATAACAACTTCCAAACTGAAGCTATCTGTCTGGTCACTGCACCA 384
 DB 82 AsnAsnAsnAsnPheGlnSerLysAlaAsnCysLeuAsnThrCysLys 97
 RESULT 23
 AAE28009
 ID AAE28009 standard; protein; 102 AA.
 XX
 XX AAE28009;
 AC AAE28009;
 XX
 XX 13-DEC-2002 (first entry)
 DT
 XX
 XX Human gene 24 encoded secreted protein fragment #2.
 DE
 XX
 KW Human; secreted protein; autoimmune disease; hyperproliferative disorder;
 KW rheumatoid arthritis; neoplasm; cerebrovascular disorder; angiogenesis;
 KW cerebral ischaemia; cardiovascular disorder; nervous system disorder;
 KW cardiac arrest; Alzheimer's disease; ocular disorder; wound healing;
 KW infection; corneal infection; skin aging; food additive; preservative;
 KW tissue regeneration; immunosuppressive; antiproliferative; cytostatic;
 KW cardiant; vasotrophic; cerebroprotective; nootropic; neuroprotective;
 KW antibacterial; virucide; fungicide; ophthalmological; gene therapy;
 KW vulnery.
 XX
 OS Homo sapiens.
 XX
 XX US2002076756-A1.
 PN
 XX
 PD 20-JUN-2002.
 XX
 XX 11-MAY-2001; 2001US-00853161.
 PF
 XX 02-FEB-2001; 2001US-0265583P.
 XX
 XX

PA (RUBE//) RUBEN S M.
PA (ROSE//) ROSEN C A.
PA (LIY//) LI Y.
PA (ZENG//) ZENG Z.
PA (KYAW//) KYAW H.
PA (FISC//) FISCHER C L.
PA (LIHH//) LI H.
PA (SOPP//) SOPPET D R.
PA (GENT//) GENTZ R L.
PA (WEIY//) WEI Y.
PA (MOOR//) MOORE P A.
PA (YOUN//) YOUNG P E.
PA (GREE//) GREENE J M.
PA (FERR//) FERRIE A M.

PI Ruben SM, Rosen CA, Li Y, Zeng Z, Kyaw H, Fischer CL, Li H;
PI Soppet DR, Gentz RL, Wei Y, Moore PA, Young PE, Greene JM;
PI Ferrie AM;

XX WPI; 2002-574454/61.

XX New nucleic acid molecules encoding 28 human secreted proteins, useful
PT for diagnosing, preventing, treating or ameliorating medical conditions
PT and as food additives or preservatives.

XX Disclosure; Page 17; 209pp; English.

XX AAD44854-AAD44984 represent cDNAs corresponding to 28 human secreted
CC protein genes, and AAE27097-AAE27137 represent the proteins they encode.
CC AAE27138-AAE27164 represent human secreted protein fragments. The genes
CC and their corresponding secreted proteins are useful for preventing,
CC treating or ameliorating medical conditions, e.g., by protein or gene
CC therapy. Secreted protein sequences of the invention are useful for the
CC diagnosis or treatment of disorders such as autoimmune diseases (e.g.
CC rheumatoid arthritis), hyperproliferative disorders (e.g. neoplasms of
CC the breast or liver), cerebrovascular disorders (e.g. cerebral ischaemia,
CC angioneurosis), cardiovascular disorders (e.g. cardiac arrest), nervous
CC system disorders (e.g. Alzheimer's disease), infections caused by fungi,
CC bacteria and viruses and ocular disorders (e.g. corneal infection). The
CC polypeptides can also be used to aid wound healing and epithelial cell
CC proliferation, to prevent skin aging due to sunburn, to maintain organs
CC before transplantation, for supporting cell culture of primary tissues,
CC to regenerate tissues and in chemotaxis. They can also be used as food
CC additives or preservative to increase or decrease storage capabilities,
CC fat content, lipid, protein, carbohydrate, vitamins, minerals, cofactors
CC and other nutritional components. The present sequence represents a human
CC secreted protein fragment referred to in the disclosure of the invention
XX
SQ Sequence 102 AA;

Alignment Scores:
Pred. No.: 1.19e-31 Length: 102
Score: 388.00 Matches: 63
Percent Similarity: 77.08% Conservative: 11
Best Local Similarity: 65.62% Mismatches: 22
Query Match: 50.79% Indels: 0
DB: 5 Gaps: 0

US-10-807-204-11 (1-396) x AAE28009 (1-102)

Qy 97 TGTCCCAAAATCAAAAGTGGATGCGAGTGGAGAAATAGACAGTACCAAAACCAGA 156
Db 2 CysProlysisLeaArgGluGluCysGluPheGlnGluArgAspValCysThrLysAspArg 21

Qy 157 GATTGCCAGAAAACATGAAGTGTGGCCGTTGACCGGTGGAAGAAATGTTTACATTC 216
Db 22 GlnCysGlnAspAsnLysLysCysCysValPheSerCysGlyLysLysCysLeuAspLeu 41

Qy 217 AGAAGATATATGCAGTATGCCACAGGAGCTGGCCCTCGCTCCATACACAC 276
Db 42 LysGlnAspValCysGluMetProLysGluThrGlyProCysLeuAlaTyrrPheLeuHis 61

Qy 277 TGGTGGTACAATAAAAAAACTAAGATCTGCTCCGAATTTCATCTATGCGCGGTGCCAGGGG 336

Db 62 TrpTrpTyraAspLysLysAspAsnThrCysSerMetPheValTyrrGlyGlyCysGlnGly 81

Qy 337 AACATAAACACTTCCAAACTGAAGCTATCTGTCTGCTACCTGCACAA 384
Db 82 AsnAsnAsnAsnPheGlnSerLysAlaAsnCysLeuAsnThrCysLys 97

RESULT 24
ABU65039
ID ABU65039 standard; peptide; 102 AA.
XX AC ABU65039;
XX AC
DT 15-MAY-2003 (first entry)
DE Human secreted protein gene 24, protein #3.
XX KW
XX KW Secreted protein; immunodeficiency; multiple sclerosis;
KW severe combined immunodeficiency; autoimmune disorder; cancer;
KW rheumatoid arthritis; diabetes mellitus; haematopoietic disorder;
KW inflammatory condition; septic shock; inflammatory bowel disease;
KW Crohn's disease; respiratory disorder; asthma; allergy; stroke;
KW gastrointestinal disorder; central nervous system disorder;
KW ischaemic brain injury; neurodegenerative disorder; Parkinson's disease;
KW Alzheimer's disease; cardiovascular disorder; atherosclerosis;
KW blood-related disorder; thrombosis; acute glomerulonephritis; renal disorder;
KW hyperproliferative disorder; liver disease; reproductive system disorder;
KW endocrine disorder; infectious disease; pancreatic disorder; vaccine;
KW wound repair; angiogenesis; lymphatic disorder; hair loss; body weight;
XX body height; hair colour; human.
OS Homo sapiens.
XX
XX US2002172994-A1.
XX 21-NOV-2002.

XX 11-MAY-2001; 2001US-00852797.

XX 14-MAR-1997; 97US-0040710P.
PR 14-MAR-1997; 97US-0040762P.
PR 30-MAY-1997; 97US-0048100P.
PR 30-MAY-1997; 97US-0048189P.
PR 30-MAY-1997; 97US-0048357P.
PR 30-MAY-1997; 97US-0050934P.
PR 06-JUN-1997; 97US-0048970P.
PR 05-SEP-1997; 97US-0057765P.
PR 19-DEC-1997; 97US-0068368P.
PR 12-MAR-1998; 98WO-US004858.
PR 11-SEP-1998; 98US-00152060.
PR 02-FEB-2001; 2001US-0265583P.

XX (RUBE//) RUBEN S M.
XX (ROSE//) ROSEN C A.
PA (LIY//) LI Y.
PA (ZENG//) ZENG Z.
PA (KYAW//) KYAW H.
PA (FISC//) FISCHER C L.
PA (LIHH//) LI H.
PA (SOPP//) SOPPET D R.
PA (GENT//) GENTZ R L.
PA (WEIY//) WEI Y.
PA (MOOR//) MOORE P A.
PA (YOUN//) YOUNG P E.
PA (GREE//) GREENE J M.
PA (FERR//) FERRIE A M.

XX Ruben SM, Rosen CA, Li Y, Zeng Z, Kyaw H, Fischer CL, Li H;
PI Soppet DR, Gentz RL, Wei Y, Moore PA, Young PE, Greene JM;
PI Ferrie AM;
XX
XX WPI; 2003-310989/30.

XX New human secreted polypeptides and polynucleotides for diagnosing,
 PT prognosing, preventing and treating immune, hyperproliferative, liver,
 PT kidney, reproductive disorders and for identifying modulators of
 PT therapeutic use.
 XX
 XX Disclosure; Page 16; 209pp; English.
 XX
 XX The invention relates to an isolated polypeptide comprising an amino acid
 CC sequence at least 95% identical to sequence of 28 human secreted
 CC proteins, their fragment, polypeptide domain, epitope, secreted form,
 CC variant, allelic variant, or species homologue, or the encoded sequence
 CC included in ATCC 9721 and 9722. Also included are the encoding nucleic
 CC acids, recombinant vectors, host cells, antibodies, and genes. The
 CC proteins and nucleic acids are useful for diagnosing, preventing,
 CC treating, prognosing or ameliorating a medical condition e.g.
 CC immunodeficiencies (e.g. X-linked agammaglobulinemia, B cell
 CC immunodeficiencies, severe combined immunodeficiencies), autoimmune
 CC disorders (e.g. systemic erythematous, rheumatoid arthritis, multiple
 CC sclerosis, autoimmune thyroiditis, autoimmune haemolytic anaemia,
 CC Goodpasture's syndrome, Grave's disease, diabetes mellitus, dermatitis),
 CC haematopoietic disorders, inflammatory conditions (e.g. septic shock,
 CC sepsis, reperfusion injury, inflammatory bowel disease, Crohn's disease),
 CC respiratory disorders (e.g. asthma and allergy), gastrointestinal
 CC disorders, cancers (e.g. gastric, ovarian, lung, bladder, liver and
 CC breast), central nervous system (CNS) disorders (e.g. ischaemic brain
 CC injury and/or stroke, traumatic brain injury), neurodegenerative
 CC disorders (e.g. Parkinson's disease and Alzheimer's disease, AIDS-related
 CC dementia, and prion disease), cardiovascular disorders (e.g.
 CC atherosclerosis, myocarditis, cardiovascular disease, and cardiopulmonary
 CC bypass complications), inflammation (e.g. hepatitis, gout, trauma,
 CC pancreatitis, sarcoidosis, dermatitis, allogeneic transplant rejection),
 CC blood-related disorders (thrombosis, arterial thrombosis),
 CC hyperproliferative disorders, renal disorders (e.g. acute
 CC glomerulonephritis), endocrine disorders (e.g. Addison's disease,
 CC hyperthyroidism, hypothyroidism), liver diseases and disorders,
 CC reproductive system disorders (e.g. endometriosis), infectious diseases,
 CC and pancreatic disorders. Many other diseases and disorders are listed in
 CC the specification. They also useful as a vaccine adjuvant. Further they
 CC are useful to enhance or inhibit complement mediated cell lysis, for
 CC stimulating wound and tissue repair, angiogenesis, and the repair of
 CC vascular or lymphatic diseases or disorders. They are also useful to
 CC prevent hair loss, to modulate mammalian characteristics such as body
 CC height, weight, hair colour, and to increase or decrease storage
 CC capabilities, fat content, lipid, protein, carbohydrate, vitamins,
 CC minerals, cofactors or other nutritional components. The proteins are
 CC also useful for identifying binding partners. The present sequence
 CC represents a secreted protein of the invention
 XX
 SQ Sequence 102 AA;

Alignment Scores:
 Pred. No.: 1.19e-31 Length: 102
 Score: 388.00 Matches: 63
 Percent Similarity: 77.08% Conservative: 11
 Best Local Similarity: 65.62% Mismatches: 22
 Query Match: 50.79% Indels: 0
 DB: Gaps: 0

US-10-807-204-11 (1-396) x ABU65039 (1-102)

QY 97 TGTCCCAAAATCAAGTGAAGTGGAGAAATAGACAGGTGTACCAAAACCAGA 156
 Db 2 CysProlylIleargGluGluCysGluPheGlnGluargaspValCysThrlylasparg 21
 QY 157 GATTGTCAGAAACACATGAAGTGTTCGCCGTTTCAGCCGTGGAAAGAAATGTTAGACTTC 216
 Db 22 GlnCysGlnAspAsnlylCysCysValPheSerCysGlyLyslylCysLeuAspLeu 41
 QY 217 AGAAGGATATATGCAGTATGCCACAGGAGGCTGCGCCCTGCTGCCTCCATACACAC 276
 Db 42 LysGlnAspValCysGluMetProlylGluThrGlyProCysLeuAlaTyrPheLeuHis 61

QY 277 TGTGTGTACATTAATAAACTAAGATCTGCTCCGAATTCATCTATGCGGTGCGAGGG 336
 Db 62 TrpTrpTyrAspLysLysAspAsnThrCysSerMetPheValTyrGlyGlyCysGlnGly 81
 QY 337 AACAAATAACAACTTCCAAACTGAAGCTATCTGCTGCTGCTACCTGCAAA 384
 Db 82 AsnAsnAsnAsnPheGlnSerLysAlaAsnCysLeuAsnThrCysLys 97
 RESULT 25
 ADG89848
 ID ADG89848 standard; protein; 102 AA.
 XX AC ADG89848;
 XX DT 11-MAR-2004 (first entry)
 XX DE Human secreted protein gene 24 protein #6.
 XX KW Secreted protein; gene therapy; neural disorder; immune system disorders;
 KW muscular disorder; reproductive disorder; gastrointestinal disorder;
 KW pulmonary disorder; cardiovascular disorder; renal disorder;
 KW proliferative disorder; cancer; systemic lupus erythematosus;
 KW rheumatoid arthritis; multiple sclerosis; thyroiditis; anaemia;
 KW Grave's disease; diabetes; hepatitis; asthma; allergy; nephritis;
 KW Parkinson's disease; Alzheimer's disease; atherosclerosis;
 KW myocardial infarction; AIDS; infection; human.
 XX OS Homo sapiens.
 XX PN US2003225009-A1.
 XX PD 04-DEC-2003.
 XX PF 30-JAN-2002; 2002US-00058993.
 XX PR 14-MAR-1997; 97US-0040710P.
 PR 14-MAR-1997; 97US-0040762P.
 PR 30-MAY-1997; 97US-0048100P.
 PR 30-MAY-1997; 97US-0048189P.
 PR 30-MAY-1997; 97US-0048357P.
 PR 30-MAY-1997; 97US-0050934P.
 PR 06-JUN-1997; 97US-0048970P.
 PR 05-SEP-1997; 97US-0057765P.
 PR 19-DEC-1997; 97US-0068368P.
 PR 12-MAR-1998; 98WO-US004858.
 PR 11-SEP-1998; 98US-00152060.
 PR 02-FEB-2001; 2001US-0265583P.
 PR 11-MAY-2001; 2001US-00852859.
 PR 11-MAY-2001; 2001US-00852797.
 PR 11-MAY-2001; 2001US-00853161.
 XX (ROSE/) ROSEN C A.
 PA (RUBE/) RUBEN S M.
 PA (LIYY/) LI Y.
 PA (ZENG/) ZENG Z.
 PA (KYAW/) KYAW H.
 PA (FISC/) FISCHER C L.
 PA (LIHH/) LI H.
 PA (SOPP/) SOPPET D R.
 PA (GENT/) GENTZ R L.
 PA (WEIY/) WEI Y.
 PA (MOOR/) MOORE P A.
 PA (YOUN/) YOUNG P E.
 PA (GREE/) GREENE J M.
 PA (FERR/) FERRIE A M.
 PA (HAST/) HASTINGS G A.
 XX Rosen CA, Ruben SM, Li Y, Zeng Z, Kyaw H, Fischer CL, Li H;
 PI Soppet DR, Gentz RL, Wei Y, Moore PA, Young PE, Greene JM;
 PI Ferrie AM, Hastings GA;
 XX WPI; 2004-042167/04.
 XX

PT New polypeptides and nucleic acid molecules for diagnosing, preventing or
PT treating diseases associated with aberrant expression or activity of the
PT polypeptide, e.g. cancer, asthma, AIDS, Parkinson's disease or diabetes.
XX
XX
PS Disclosure; SEQ ID NO 121; 320pp; English.

CC The invention relates to an isolated nucleic acid molecule encoding a
CC secreted protein that is at least 95% identical to a polynucleotide
CC fragment of any of the nucleotide sequences listed in table 1A of the
CC specification, which is hybridisable to the nucleotide sequences, a
CC polynucleotide encoding a polypeptide (or a polypeptide fragment, domain
CC or epitope of any of the amino acid sequences) listed in table 1A of the
CC specification, a polynucleotide which is an (allelic) variant of the
CC nucleotide sequences listed in the specification, a polynucleotide which
CC encodes a species homologue of the above amino acid sequences, a
CC polynucleotide capable of hybridising under stringent conditions to any
CC of the above polynucleotides, where the polynucleotide does not hybridise
CC under stringent conditions to a nucleic acid molecule having a nucleotide
CC sequence of only A or T residues. Also included are a recombinant vector
CC comprising the above nucleic acid molecule, making a recombinant host
CC cell comprising the above nucleic acid molecule, an isolated polypeptide
CC comprising a sequence that is at least 95% identical to the polypeptide
CC (or its fragment, domain, epitope, secreted form, (allelic) variant or
CC homologue) encoded by the above nucleic acid molecule, an isolated
CC antibody that binds specifically to the above polypeptide, a recombinant
CC host cell produced by the above method and that expresses the above
CC polypeptide, making an isolated polypeptide, preventing, treating or
CC ameliorating a medical condition, diagnosing a pathological condition or
CC a susceptibility to a pathological condition in a subject, identifying a
CC binding partner to the above polypeptide, the gene corresponding to the
CC cDNA sequence given in the specification, and identifying an activity in
CC a biological assay. The nucleic acid molecule and polypeptide are useful
CC in diagnosing, preventing, prognosing or treating diseases or disorders
CC associated with aberrant expression and/or activity of the above
CC polypeptide, such as neural disorders, immune system disorders, muscular
CC disorders, reproductive disorders, gastrointestinal disorders, pulmonary
CC disorders, cardiovascular disorders, renal disorders, proliferative
CC disorders and/or cancers. In particular, these diseases are systemic
CC lupus erythematosus, rheumatoid arthritis, multiple sclerosis, as
CC thyroiditis, anaemia, Grave's disease, diabetes, hepatitis, asthma,
CC allergies, nephritis, Parkinson's disease, Alzheimer's disease,
CC atherosclerosis, myocardial infarction, AIDS and infections. The methods
CC may be used for identifying agonists and antagonists of the
CC polynucleotide and polypeptide. The present sequence is a protein from
CC one of the 28 disclosed secreted protein genes, it is not clear whether
CC this is an alternative expressed protein or a fragment of one of the
CC claimed proteins.

XX
SQ Sequence 102 AA;

Alignment Scores:
Pred. No.: 1.19e-31 Length: 102
Score: 388.00 Matches: 63
Percent Similarity: 77.08% Conservative: 11
Best Local Similarity: 65.62% Mismatches: 22
Query Match: 50.79% Indels: 0
DB: 8 Gaps: 0

US-10-807-204-11 (1-396) x ADG98848 (1-102)

QY 97 TGTCCCAAAATCAAGTGGATGCGAAGTGGAGAAATAGACAGTGATCCAAACCCAGA 156
DB 2 CysProlysisileArgGluGluCysGluPheGlnGluArgSpValCysThrLysAspArg 21
QY 157 GATTGCCAGAACATGATGTTGCGCGTTCAGCCGTGGAAGAAATGTTTACATTC 216
DB 22 GlnCysGlnAspAenLysLysCysCysValPheSerCysGlyLysLysCysLeuAspLeu 41
QY 217 AGAAGATATATGATGTCACAGAGGCTGCGCCCTGCGCTCATACACAC 276
DB 42 LysGlnAspValCysGluMetProLysGluThrGlyProCysLeuAlaTyPheLeuHis 61
QY 277 TGGTGGTACATAAAAAAACTAAGATCTGCTCCGAATTCATCTATGCGGGTTGCCAGGGG 336

Db 62 TifTfTyAspLysLysAspAenThrCysSerMetPheValTyGlyGlyCysGlnGly 81
QY 337 AACAAATCAACTTCGAACTGAAGCTATCTGTCTGCTACCTGCAGAA 384
Db 82 AsnAsnAsnAsnPheGlnSerLysAlaAsnCysLeuAsnThrCysLys 97
RESULT 26
ADA19813
ID ADA19813 standard; protein; 134 AA.
XX
AC ADA19813;
XX
DT 20-NOV-2003 (first entry)
TX Mouse EPPIN protein SEQ ID NO:14.
DE
XX
KW DJ11; Kunitz-type protease inhibitor domain; antiinflammatory;
KW antiallergic; thrombolytic; anticoagulant; cardiant; vasotropic;
KW antibacterial; immunosuppressive; antirheumatic; antiarthritic;
KW nephrotropic; antipsoriatic; vulnery; protease inhibitor; gene therapy;
KW acute pancreatitis; pulmonary injury; allergy-induced protease release;
KW deep vein thrombosis; myocardial infarction; shock; septic shock;
KW hyperfibrinolytic haemorrhage; inflammatory disorder; emphysema;
KW idiopathic pulmonary fibrosis; rheumatoid arthritis; glomerulonephritis;
KW chronic inflammatory bowel disease; psoriasis; EPPIN.

XX Mus musculus.

XX WO2003070770-A2.

XX 28-AUG-2003.

XX 18-FEB-2003; 2003WO-EP001629.

XX 21-FEB-2002; 2002US-0358683P.

XX (GENE-) GENEPROT INC.

XX Bougueleret L, Bairoch A, Niknejad A;

XX WPI; 2003-663849/62.

XX New engineered human Kunitz-type protease inhibitor for diagnosing,
PT preventing or treating conditions associated with excessive proteinase
PT activity, e.g. inflammation, pulmonary injuries, myocardial infarction or
PT hemorrhage.

XX Disclosure; Fig 1; 87pp; English.

XX The present invention describes an isolated, purified or recombinant DJ11
CC polypeptide comprising a Kunitz-type protease inhibitor domain or its
CC biologically active portion. The polypeptide comprises at least 98 %
CC identity to residues 77-127 of a 131 amino acid sequence (S1, see
CC ADA19800), or to residues 52-102 of a 106 amino acid sequence (S2, see
CC ADA19801). DJ11 has antiinflammatory, antiallergic, thrombolytic,
CC anticoagulant, cardiant, vasotropic, antibacterial, immunosuppressive,
CC antirheumatic, antiarthritic, nephrotropic, antipsoriatic and vulnery
CC activities, and can be used as a protease inhibitor and in gene therapy.
CC Composition and methods from the present invention can be used in
CC diagnosing, preventing or treating conditions associated with excessive
CC proteinase activity, such as acute pancreatitis, pulmonary injury,
CC allergy-induced protease release, deep vein thrombosis, myocardial
CC infarction, shock (including septic shock), hyperfibrinolytic
CC haemorrhage, and especially, inflammatory disorders (e.g. emphysema,
CC idiopathic pulmonary fibrosis, rheumatoid arthritis, glomerulonephritis,
CC chronic inflammatory bowel disease or psoriasis). The DJ11 proteins may
CC be used in preserving platelet function, organ preservation or in wound
CC healing. The polynucleotide sequence encoding DJ11 may be used as
CC hybridisation probes, in chromosome and gene mapping, in the generation
CC of antisense RNA and DNA, and as targets for pharmaceutical intervention.
CC The present sequence represents a mouse EPPIN protein given in comparison
CC with DJ11 proteins in the exemplification of the present invention.

```
XX SQ Sequence 134 AA;
Alignment Scores:
Pred. No.: 2,058-31 Length: 134
Score: 386.00 Matches: 66
Percent Similarity: 70.54% Conservative: 25
Best Local Similarity: 51.16% Mismatches: 38
Query Match: 50.52% Indels: 0
DB: Gaps: 0

US-10-807-204-11 (1-396) x ADA19813 (1-134)
QY 1 ATGGACTCTCAGGACTTCTGCAATCTCTGGTATCCATTCATCTTTTGGGGGACATCCAG 60
DB 1 MetLysLeuSerGlyPheValSerIleLeuValLeuPheGlyLeuLeuAaArgValGln 20
QY 61 GAACCTGGGACGCTGAAGGCATCTTGGCAAGCCGTGTCCCAAAATCAAAAGTGAATGC 120
DB 21 GlyProSerLeuAaAspLeuLeuPheProArgArgCysProArgPheArgGluCys 40
QY 121 GAAGTGGAGAAATAGACAGGTGTACCAACCCAGAGATTGCCAGAAACATGAAGTGT 180
DB 41 GluHisGlnGluArgAspLeuCysThrArgAspArgCysProLysLysGluLysCys 60
QY 181 TGCCCGTTCAGCGCTGCGAAGAAATGTTTAGACTTCAGAAAGATATATGAGTATGCCA 240
DB 61 CysValPheAsnCysGlyLysLysCysLeuAaAsnProGlnAspIleCysSerLeuPro 80
QY 241 CAGGAGGTGGCCCTGCTGCTGCCATCCACACTGGTGTTGATCAATAAATAAACTAAG 300
DB 81 LysAspSerGlyTyrcysMetAlaTyrcysPheArgArgGlyTrpPheAsnLysGluAsnSer 100
QY 301 ATCTGCTCGAATTCATCTATCGCGTTCAGGGGACACATTAACAATCTCCAACTGAA 360
DB 101 ThrCysGlnValPheIleTyrcysGlyGlyCysGlnGlyAsnAsnAsnPheGlnSerGln 120
QY 361 GCTATCTGTCTGCTCACCTGCAAAAAA 387
DB 121 SerIleCysGlnAsnAlaCysGluLys 129

RESULT 27
ADA19804
ID ADA19804 standard; protein; 43 AA.
XX AC ADA19804;
XX DT 20-NOV-2003 (first entry)
XX DE Engineered human DJ11 partial amino acid sequence SEQ ID NO:5.
XX DW
XX KW DJ11; Kunitz-type protease inhibitor domain; antiinflammatory;
XX KW antiallergic; thrombolytic; anticoagulant; cardiant; vasotropic;
XX KW antibacterial; immunosuppressive; antirheumatic; antiarthritic;
XX KW nephrotropic; antipsoriatic; vulnary; protease inhibitor; gene therapy;
XX KW acute pancreatitis; pulmonary injury; allergy-induced protease release;
XX KW deep vein thrombosis; myocardial infarction; shock; septic shock;
XX KW hyperfibrinolytic haemorrhage; inflammatory disorder; emphysema;
XX KW idiopathic pulmonary fibrosis; rheumatoid arthritis; glomerulonephritis;
XX KW chronic inflammatory bowel disease; psoriasis.
XX OS Synthetic.
XX OS Homo sapiens.
XX PN WO2003070770-A2.
XX PD 28-AUG-2003.
XX PF 18-FEB-2003; 2003WO-EP001629.
XX PR 21-FEB-2002; 2002US-0358683P.
XX PA (GENE-) GENEPROT INC.
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XX Bouqueleret L, Bairoch A, Niknejad A;
XX WPI; 2003-663849/62.
XX New engineered human Kunitz-type protease inhibitor for diagnosing.
XX PT preventing or treating conditions associated with excessive proteinase
XX PT activity, e.g. inflammation, pulmonary injuries, myocardial infarction or
XX PT hemorrhage.
XX PS Disclosure; Page 79; 87pp; English.
XX The present invention describes an isolated, purified or recombinant DJ11
XX polypeptide comprising a Kunitz-type protease inhibitor domain or its
XX biologically active portion. The polypeptide comprises at least 98 %
XX identity to residues 77-127 of a 131 amino acid sequence (S1, see
XX ADA19800), or to residues 52-102 of a 106 amino acid sequence (S2, see
XX ADA19801). DJ11 has antiinflammatory, antiallergic, thrombolytic,
XX anticoagulant, cardiant, vasotropic, antibacterial, immunosuppressive,
XX antirheumatic, antiarthritic, nephrotropic, antipsoriatic and vulnary
XX activities, and can be used as a protease inhibitor and in gene therapy.
XX Composition and methods from the present invention can be used in
XX diagnosing, preventing or treating conditions associated with excessive
XX proteinase activity, such as acute pancreatitis, pulmonary injury
XX allergy-induced protease release, deep vein thrombosis, myocardial
XX infarction, shock (including septic shock), hyperfibrinolytic
XX haemorrhage, and especially, inflammatory disorders (e.g. emphysema,
XX idiopathic pulmonary fibrosis, rheumatoid arthritis, glomerulonephritis,
XX chronic inflammatory bowel disease or psoriasis). The DJ11 proteins may
XX be used in preserving platelet function, organ preservation or in wound
XX healing. The polynucleotide sequence encoding DJ11 may be used as
XX hybridisation probes, in chromosome and gene mapping, in the generation
XX of antisense RNA and DNA, and as targets for pharmaceutical intervention.
XX The present sequence represents a partial engineered human DJ11 protein
XX amino acid sequence from the present invention.
XX SQ Sequence 43 AA;
Alignment Scores:
Pred. No.: 9,968-18 Length: 43
Score: 254.00 Matches: 43
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 33.25% Indels: 0
DB: Gaps: 0
US-10-807-204-11 (1-396) x ADA19804 (1-43)
QY 94 CCGTGTCCCAAAATCAAAAGTGAATGCGAAGTGAAGAAATAGACCAGTGTACCAACCC 153
DB 1 ProCysProLysIleLysValGluCysGluValGluIleAspGlnCysThrLysPro 20
QY 154 AGAGATTGCCAGAAACATGAAGTGTGCGGTTCAGCCGTGGAAGAAATGTTTAGAC 213
DB 21 ArgAspCysProGluAsnMetLysCysCysProPheSerArgGlyLysLysCysLeuAa 40
QY 214 TTCAGAAAG 222
DB 41 PheArgLys 43
RESULT 28
AAE13093
ID AAE13093 standard; peptide; 64 AA.
XX AC AAE13093;
XX DT 28-JAN-2002 (first entry)
XX DE Human serine proteinase inhibitor BTL.009 C-terminal peptide.
XX KW Human; BTL.009 protein; serine proteinase inhibitor; cytostatic;
XX KW nephrotropic; idiopathic pulmonary fibrosis; cystic fibrosis; emphysema;
XX KW rheumatoid arthritis; adult respiratory distress syndrome; angioplasty;
```


RESULT 30	
AAE13084	
ID	AAE13084 standard; peptide; 58 AA.
XX	
AC	AAE13084;
XX	
DT	28-JAN-2002 (first entry)
XX	
DE	Human serine proteinase inhibitor BTL.009 peptide.
XX	
KW	Human; BTL.009 protein; serine proteinase inhibitor; cytostatic;
KW	nephrotropic; idiopathic pulmonary fibrosis; cystic fibrosis; emphysema;
KW	rheumatoid arthritis; adult respiratory distress syndrome; angiolasty;
KW	blood coagulation; glomerulonephritis; prophylactic; platelet activation;
KW	neutrophil; monocyte; granulocyte; organ failure; inflammatory disease;
KW	elastase inhibitor; chymotrypsin inhibitor; lung injury; vascular injury;
KW	therapeutic.
XX	
OS	Homo sapiens.
XX	
XX	US6294648-B1.
PN	
XX	
PD	25-SEP-2001.
XX	
XX	20-JUL-1999; 99US-00358569.
XX	
PR	20-JUL-1999; 99US-00358569.
XX	
PA	(FARB) BAYER CORP.
XX	
PI	Delaria K, Roczniak S, Davies C;
XX	
XX	WPI; 2001-662224/76.
DR	
XX	New isolated protein for inhibiting human serine protease activity in the
PT	treatment of e.g. emphysema and adult respiratory distress syndrome.
XX	
PS	Claim 1; Col 15-16; 16pp; English.
XX	
CC	The invention relates to human BTL.009 protein, a serine proteinase
CC	inhibitor of the Kunitz family that exhibits greater potency towards
CC	neutral serine proteinases. BTL.009 protein is found to inhibit leukocyte
CC	elastase, chymotrypsin-like protease and trypsin-like protease. BTL.009
CC	protein is useful for treating emphysema, idiopathic pulmonary fibrosis,
CC	adult respiratory distress syndrome, cystic fibrosis, rheumatoid
CC	arthritis, organ failure, glomerulonephritis, other inflammatory diseases
CC	and diseases involving lung and vascular injury. BTL.009 is also useful
CC	for preventing neutrophil and monocyte activation and formation of active
CC	oxygen species during the oxidative burst of stimulated granulocytes.
CC	BTL.009 is useful for reducing platelet activation and blood coagulation
CC	and for the prophylactic or therapeutic treatment of patients undergoing
CC	angioplasty. The present sequence is human serine proteinase inhibitor
CC	BTL.009 peptide corresponding to Kunitz domain used in the
CC	exemplification of the invention. Note: The present sequence shown in
CC	column 14 and sequence listing of the specification lacks 3 amino acid
CC	residues at the C-terminal end
XX	
SQ	Sequence 58 AA;
Alignment Scores:	
Pred. No.:	8, 07e-16
Score:	236.00
Percent Similarity:	80.36%
Best Local Similarity:	66.07%
Query Match:	30.89%
DB:	4
US-10-807-204-11 (1-396) x AAE13084 (1-58)	
QY	217 AGAAGGATATGTCAGTATGCCACAGGAGGTCGCCCTGCTGCCTCCATACACAC 276
DB	1 LysGlnAspValCysGluMetProLysGluThrGlyProCysLeuAlaTrpLeuHis 20

QY	277	TGTTGGTACAAATAAAAACTAAGATCTGCTCCGAATTCATCTATGCGGTTGCCAGGG	336
DB	21	TrpTrpTyraSpLysLysAspAsnThrCysSerMetPheValTrGlyGlyCysGlnGly	40
QY	337	AACAATAACAACCTTCCAAACTGAAGCTATCTGCTGCTGCCTCACCTGCAAA	384
DB	41	AsnAsnAsnAsnPheGlnSerLysAlaAsnCysLeuAsnThrCysLys	56

RESULT 31

AAE60630

ID

AAE60630 standard; protein; 58 AA.

XX

AAE60630;

AC

27-APR-2001 (first entry)

DT

Kunitz domain, SEQ ID NO:8, used to identify BTL.010 protein.

XX

Human BTL.010; neutral serine protease inhibitor; elastase inhibitor;

XX

proteinase-3 inhibitor; Kunitz domain; emphysema;

XX

idiopathic pulmonary fibrosis; adult respiratory distress syndrome;

XX

cystic fibrosis; rheumatoid arthritis; organ failure; glomerulonephritis;

XX

platelet activation; blood coagulation; neutrophil activation;

XX

monocyte activation; angiolasty; inflammatory disease; lung injury;

XX

vascular injury; nephrotropic; antirheumatic; antiarthritic.

XX

Unidentified.

OS

US6180607-B1.

XX

30-JAN-2001.

PN

05-AUG-1999; 99US-00369494.

XX

05-AUG-1999; 99US-00369494.

PR

(DAVI/) DAVIES C.

XX

(CHEN/) CHEN D.

PA

(ROCH/) ROCZNIAK S.

XX	Davies C, Chen D, Roczniak S;
XX	WPI; 2001-190860/19.
XX	Novel serine proteinase inhibitor of the Kunitz family, BTL.010 useful
XX	for treating emphysema, cystic fibrosis, adult respiratory distress
XX	syndrome, rheumatoid arthritis, organ failure and glomerulonephritis.
XX	Disclosure: Col 6; 17pp; English.
XX	The invention relates to a novel human serine protease inhibitor of the
XX	Kunitz family, BTL.010 (fragments given in AAB60623, AAB60631 and
XX	AAB60634). The BTL.010 protein is thought to preferentially inhibit
XX	neutral serine proteases such as elastase and proteinase-3, relative to
XX	trypsin-like and chymotrypsin-like proteases. A substantial proportion of
XX	the BTL.010 protein Kunitz domain (AAB60631) was identified via homology
XX	searching in the GenBank high throughput genomic (HTG) DNA sequence
XX	database using the Kunitz domain sequences AAB60630, and was confirmed as
XX	being novel using the Kunitz domain sequences AAB60632, and AAB60633.
XX	This sequence information was extended to provide a larger region of
XX	BTL.010 protein sequence data (AAB60634) by identifying an open reading
XX	frame (ORF) which comprised DNA encoding the BTL.010 Kunitz domain
XX	fragment in a 399 bp fragment of human genomic DNA (AAF59750),
XX	corresponding to bases 16016-16414 of GenBank accession number AC004846.
XX	The entire BTL.010 Kunitz domain sequence (AAB60623) was obtained from
XX	the BTL.010 ORF-encoded sequence. The BTL.010 protein, and pharmaceutical
XX	compositions comprising it, may be used for inhibiting protease activity,
XX	particularly that of leukocyte elastase, in the prevention, treatment or
XX	amelioration of medical conditions such as emphysema, idiopathic
XX	pulmonary fibrosis, adult respiratory distress syndrome, cystic fibrosis,
XX	rheumatoid arthritis, organ failure or glomerulonephritis. BTL.010
XX	compositions of the invention modulate at least one physiological

CC condition such as platelet activation, blood coagulation, neutrophil
CC activation, or monocyte activation. BTL010 is also useful for the
CC prophylactic or therapeutic treatment of patients undergoing angioplasty,
CC and for the treatment of inflammatory diseases and diseases involving
CC lung and vascular injury. The present sequence represents a Kunitz domain
CC sequence used to identify the BTL010 protein
XX
XX
SQ Sequence 58 AA;

Alignment Scores:
Pred. No.: 8.07e-16 Length: 58
Score: 236.00 Matches: 37
Percent Similarity: 80.36% Conservative: 8
Best Local Similarity: 66.07% Mismatches: 11
Query Match: 30.89% Indels: 0
DB: 4 Gaps: 0

US-10-807-204-11 (1-396) x AAB60630 (1-58)

QY 217 AGAAGGATATATGCAGTATGCCAGGAGGCTGCCCTGCCTCCATACCACAC 276
Db 1 LysGlnAspValCysGluMetProLysGluThrGlyProCysLeuAlaTyrPheLeuHis 20
QY 277 TGGTGGTACAAATAAAACAACTAAGATCTGCTCCGAATTCATCTATGGCGGTTGCCAGGG 336
Db 21 TrpTrpTyrAspLysLysAspAsnThrCysSerMetPheValTyrGlyGlyCysGlnGly 40
QY 337 AACATAACACTTCCAACTGAAGCTATCTGTGTGCTACCTGCACAA 384
Db 41 AsnAsnAsnAsnPheGlnSerLysAlaAsnCysLeuAsnThrCysLys 56

RESULT 32

ID ADF41997
AD ADF41997 standard; protein; 58 AA.

XX
AC ADF41997;

DT 12-FEB-2004 (first entry)

DE Human CAB37 Kunitz domain peptide.

XX albumin fusion; Kunitz domain; cytostatic; haemostatic;

KW hereditary angioedema; cancer; bleeding; gene therapy; human; CAB37.

XX Homo sapiens.

OS WO2003066824-A2.

FN 14-AUG-2003.

PD 07-FEB-2003; 2003WO-US003616.

PF 07-FEB-2002; 2002US-0355547P.

XX (AVET) AVENTIS BEHRING GMBH.

PA (AVET) AVENTIS BEHRING LLC.

PA (DELZ) DELTA BIOTECHNOLOGY LTD.

PA (DYAX-) DYAX CORP.

XX Hauser H, Weimer T, Romberg V, Kee SM, Sleep D, Ladner RC;

PI Ley AC;

XX WPI; 2003-731497/69.

XX Albumin fusion protein comprising a Kunitz domain peptide and an albumin,
PT useful for preparing a composition for treating a patient with hereditary
PT angioedema or angioedema-related disease, cancer or bleeding disorder.

XX Disclosure; Page 20; 110pp; English.

XX The invention relates to a novel albumin fusion protein comprising a
CC Kunitz domain peptide or its fragment or variant and an albumin or its
CC fragment or variant. The fusion protein of the invention demonstrates

CC cytostatic and haemostatic activities and may be useful for preparing a
CC composition for treating a patient with hereditary angioedema, an
CC angioedema-related disease, cancer, a cancer-related disease or a
CC bleeding disorder, as well as during gene therapy procedures. The current
CC sequence is that of the human Kunitz domain peptide of the invention.

XX SQ Sequence 58 AA;

Alignment Scores:
Pred. No.: 8.07e-16 Length: 58
Score: 236.00 Matches: 37
Percent Similarity: 80.36% Conservative: 8
Best Local Similarity: 66.07% Mismatches: 11
Query Match: 30.89% Indels: 0
DB: 7 Gaps: 0

US-10-807-204-11 (1-396) x ADF41997 (1-58)

QY 217 AGAAGGATATATGCAGTATGCCAGGAGGCTGCCCTGCCTCCATACCACAC 276

Db 1 LysGlnAspValCysGluMetProLysGluThrGlyProCysLeuAlaTyrPheLeuHis 20

QY 277 TGGTGGTACAAATAAAACAACTAAGATCTGCTCCGAATTCATCTATGGCGGTTGCCAGGG 336

Db 21 TrpTrpTyrAspLysLysAspAsnThrCysSerMetPheValTyrGlyGlyCysGlnGly 40

QY 337 AACATAACACTTCCAACTGAAGCTATCTGTGTGCTACCTGCACAA 384

Db 41 AsnAsnAsnAsnPheGlnSerLysAlaAsnCysLeuAsnThrCysLys 56

RESULT 33

ID ADF41997
AD ADF41997 standard; peptide; 58 AA.

XX
AC ADF41997;

DT 06-MAY-2004 (first entry)

DE Human Kunitz domain (KD) peptide.

XX BTL010 protein; serine proteinase inhibitor; Kunitz domain; emphysema;

KW idiopathic pulmonary fibrosis; adult respiratory distress syndrome;

KW cystic fibrosis; rheumatoid arthritis; organ failure; glomerulonephritis;

KW inflammatory disease; oxidative burst; platelet activation;

KW blood coagulation; gene therapy; human; KD.

XX Homo sapiens.

OS US6689582-B1.

FN 10-FEB-2004.

PD 12-MAY-2000; 2000US-00569670.

PF 05-AUG-1999; 99US-00369494.

XX (FARB) BAYER PHARM CORP.

XX Davies C, Chen D, Roczniak S;

PI WPI; 2004-141424/14.

XX New isolated polynucleotide encoding BTL010 serine proteinase, useful
PT for treating e.g. emphysema, idiopathic pulmonary fibrosis, adult
PT respiratory distress syndrome, cystic fibrosis, rheumatoid arthritis or
PT glomerulonephritis.

XX Disclosure; SEQ ID NO 8; 17pp; English.

XX The invention relates to BTL010, a human serine proteinase inhibitor of

CC the Kunitz family and its corresponding nucleic acid sequence. The

CC sequences of the invention are useful for treating diseases, e.g.

CC emphysema, idiopathic pulmonary fibrosis, adult respiratory distress


```
Percent Similarity: 78.43%      Conservative: 5
Best Local Similarity: 68.63%      Mismatches: 11
Query Match: 28.66%      Indels: 0
DB: 5      Gaps: 0

US-10-807-204-11 (1-396) x AAE27025 (1-51)
QY 229 TGCAGTATGCCACAGAGGCTGGCCCTGCTGCCTCCATACACACTGGTGGTACAAAT 288
Db 1 CysGluMetProLysGluThrGlyProCysLeuAlaTyrPheLeuHisTrpTrpTrpAsp 20
QY 289 AAAAAAATAAGATCTGTCGAATTCATCTATGCGGTTCGCGGGAACAAATACAAAC 348
Db 21 LysLysAspAsnThrCysSerMetPheValTyrGlyGlyCysGlnGlyAsnAsnAsn 40
QY 349 TTCCAAACTGAAGCTATCTGCTGCTCACCTGC 381
Db 41 PheGlnSerLysAlaAsnCysLeuAsnThrCys 51

RESULT 37
AAE27163
ID AAE27163 standard; protein; 51 AA.
XX
AC AAE27163;
XX
DT 13-DEC-2002 (first entry)
XX
DE Human gene 24 encoded secreted protein fragment kunitz-type domain.
XX
KW Human; secreted protein; autoimmune disease; hyperproliferative disorder;
KW rheumatoid arthritis; neoplasm; cerebrovascular disorder; angiogenesis;
KW cerebral ischaemia; cardiovascular disorder; nervous system disorder;
KW cardiac arrest; Alzheimer's disease; ocular disorder; wound healing;
KW infection; corneal infection; skin aging; food additive; preservative;
KW tissue regeneration; immunosuppressive; antiproliferative; cytostatic;
KW cardiant; vasotropic; cerebroprotective; nootropic; neuroprotective;
KW antibacterial; virucide; fungicide; ophthalmological; gene therapy;
KW vulnary.
XX
OS Homo sapiens.
XX
PN US2002076756-A1.
XX
PD 20-JUN-2002...
XX
PF 11-MAY-2001; 2001US-00853161.
XX
PR 02-FEB-2001; 2001US-0265583P.
XX
PA (RUBE/) RUBEN S M.
PA (ROSE/) ROSEN C A.
PA (LIYY/) LI Y.
PA (ZENG/) ZENG Z.
PA (KYAW/) KYAW H.
PA (FISC/) FISCHER C L.
PA (LIHH/) LI H.
PA (SOPP/) SOPPET D R.
PA (GENT/) GENTZ R L.
PA (WEIY/) WEI Y.
PA (MOOR/) MOORE P A.
PA (YOUN/) YOUNG P E.
PA (GREE/) GREENE J M.
PA (FERR/) FERRIE A M.
XX
PI Ruben SM, Rosen CA, Li Y, Zeng Z, Kyaw H, Fischer CL, Li H;
PI Soppet DR, Gentz RL, Wei Y, Moore PA, Young PE, Greene JM;
PI Ferrie AM;
XX
DR WPI; 2002-574454/61.
XX
PT New nucleic acid molecules encoding 28 human secreted proteins, useful
PT for diagnosing, preventing, treating or ameliorating medical conditions
PT and as food additives or preservatives.
```

```
XX Disclosure; Page 16; 209pp; English.
XX
CC AAD4854-AAD44984 represent CDNA's corresponding to 28 human secreted
CC protein genes, and AAE27097-AAE27137 represent the proteins they encode.
CC AAE27138-AAE27164 represent human secreted protein fragments. The genes
CC and their corresponding medical conditions, e.g., by protein or gene
CC treating or ameliorating medical conditions, e.g., by protein or gene
CC diagnosis or treatment of disorders such as autoimmune diseases (e.g.
CC rheumatoid arthritis), hyperproliferative disorders (e.g. neoplasms of
CC the breast or liver), cerebrovascular disorders (e.g. cerebral ischaemia,
CC angiogenesis), cardiovascular disorders (e.g. cardiac arrest), nervous
CC system disorders (e.g. Alzheimer's disease), infections caused by fungi,
CC bacteria and viruses and ocular disorders (e.g. corneal infection). The
CC polypeptides can also be used to aid wound healing and epithelial cell
CC proliferation, to prevent skin aging due to sunburn, to maintain organs
CC before transplantation, for supporting cell culture of primary tissues,
CC to regenerate tissues and in chemotaxis. They can also be used as food
CC additives or preservative to increase or decrease storage capabilities,
CC fat content, lipid, protein, carbohydrate, vitamins, minerals, cofactors
CC and other nutritional components. The present sequence represents a human
CC secreted protein fragment kunitz-type domain referred to in the
CC disclosure of the invention
XX
SQ Sequence 51 AA;

Alignment Scores:
Pred. No.: 4,69e-14      Length: 51
Score: 219.00      Matches: 35
Percent Similarity: 78.43%      Conservative: 5
Best Local Similarity: 68.63%      Mismatches: 11
Query Match: 28.66%      Indels: 0
DB: 5      Gaps: 0

US-10-807-204-11 (1-396) x AAE27163 (1-51)
QY 229 TGCAGTATGCCACAGAGGCTGGCCCTGCTGCCTCCATACACACTGGTGGTACAAAT 288
Db 1 CysGluMetProLysGluThrGlyProCysLeuAlaTyrPheLeuHisTrpTrpTrpAsp 20
QY 289 AAAAAAATAAGATCTGTCGAATTCATCTATGCGGTTCGCGGGAACAAATACAAAC 348
Db 21 LysLysAspAsnThrCysSerMetPheValTyrGlyGlyCysGlnGlyAsnAsnAsn 40
QY 349 TTCCAAACTGAAGCTATCTGCTGCTCACCTGC 381
Db 41 PheGlnSerLysAlaAsnCysLeuAsnThrCys 51

RESULT 38
ADG89845
ID ADG89845 standard; protein; 51 AA.
XX
AC ADG89845;
XX
DT 11-MAR-2004 (first entry)
XX
DE Human secreted protein gene 24 protein #3.
XX
KW Secreted protein; gene therapy; neural disorder; immune system disorders;
KW muscular disorder; reproductive disorder; gastrointestinal disorder;
KW pulmonary disorder; cardiovascular disorder; renal disorder;
KW proliferative disorder; cancer; systemic lupus erythematosus;
KW rheumatoid arthritis; multiple sclerosis; thyroiditis; anaemia;
KW Grave's disease; diabetes; hepatitis; asthma; allergy; nephritis;
KW Parkinson's disease; Alzheimer's disease; atherosclerosis;
KW myocardial infarction; AIDS; infection; human.
XX
OS Homo sapiens.
XX
PN US2003225009-A1.
XX
PD 04-DEC-2003.
```

XX PF 30-JAN-2002; 2002US-00058993.

PR 14-MAR-1997; 97US-0040710P.

PR 14-MAR-1997; 97US-0040762P.

PR 30-MAY-1997; 97US-0048100P.

PR 30-MAY-1997; 97US-0048189P.

PR 30-MAY-1997; 97US-0048357P.

PR 30-MAY-1997; 97US-0050934P.

PR 06-JUN-1997; 97US-0048970P.

PR 05-SEP-1997; 97US-0057765P.

PR 19-DEC-1997; 97US-0068368P.

PR 12-MAR-1998; 98WO-US004858.

PR 11-SEP-1998; 98US-00152060.

PR 02-FEB-2001; 2001US-0245583P.

PR 11-MAY-2001; 2001US-00852859.

PR 11-MAY-2001; 2001US-00852797.

PR 11-MAY-2001; 2001US-00853161.

XX (ROSE/) ROSEN C A.

PA (RUBE/) RUBEN S M.

PA (LIYY/) LI Y.

PA (ZENG/) ZENG Z.

PA (KYAW/) KYAW H.

PA (FISC/) FISCHER C L.

PA (LIHH/) LI H.

PA (SOPP/) SOPPET D R.

PA (GENT/) GENTZ R L.

PA (WEIY/) WEI Y.

PA (MOOR/) MOORE P A.

PA (YOUN/) YOUNG P E.

PA (GREE/) GREENE J M.

PA (FERR/) FERRIE A M.

PA (HAST/) HASTINGS G A.

XX Rosen CA, Ruben SM, Li Y, Zeng Z, Kyaw H, Fischer CL, Li H;

PI Soppet DR, Gentz RL, Wei Y, Moore PA, Young PE, Greene JM;

PI Ferrie AM, Hastings GA;

XX WPI; 2004-042167/04.

XX New polypeptides and nucleic acid molecules for diagnosing, preventing or

XX treating diseases associated with aberrant expression or activity of the

XX polypeptide, e.g. cancer, asthma, AIDS, Parkinson's disease or diabetes.

XX Disclosure; SEQ ID NO 118; 320pp; English.

XX The invention relates to an isolated nucleic acid molecule encoding a

XX secreted protein that is at least 95% identical to a polynucleotide

XX fragment of any of the nucleotide sequences listed in table 1A of the

XX specification, which is hybridisable to the nucleotide sequences, a

XX polynucleotide encoding a polypeptide (or a polypeptide fragment, domain

XX or epitope of any of the amino acid sequences) listed in table 1A of the

XX specification, a polynucleotide which is an (allelic) variant of the

XX nucleotide sequences listed in the specification, a polynucleotide which

XX encodes a species homologue of the above amino acid sequences, a

XX polynucleotide capable of hybridising under stringent conditions to any

XX of the above polynucleotides, where the polynucleotide does not hybridise

XX under stringent conditions to a nucleic acid molecule having a nucleotide

XX sequence of only A or T residues. Also included are a recombinant vector

XX comprising the above nucleic acid molecule, making a recombinant host

XX cell comprising the above nucleic acid molecule, an isolated polypeptide

XX (or its fragment, domain, epitope, secreted form, (allelic) variant or

XX homologue) encoded by the above nucleic acid molecule, an isolated

XX antibody that binds specifically to the above polypeptide, a recombinant

XX host cell produced by the above method and that expresses the above

XX polypeptide, making an isolated polypeptide, preventing, treating or

XX ameliorating a medical condition, diagnosing a pathological condition or

XX a susceptibility to a pathological condition in a subject, identifying a

XX binding partner to the above polypeptide, the gene corresponding to the

XX cDNA sequence given in the specification, and identifying an activity in

XX a biological assay. The nucleic acid molecule and polypeptide are useful

in diagnosing, preventing, prognosing or treating diseases or disorders

associated with aberrant expression and/or activity of the above

polypeptide, such as neural disorders, immune system disorders, muscular

disorders, reproductive disorders, gastrointestinal disorders, pulmonary

disorders, cardiovascular disorders, renal disorders, proliferative

disorders and/or cancers. In particular, these diseases are systemic

lupus erythematosus, rheumatoid arthritis, multiple sclerosis,

thyroiditis, anaemia, Grave's disease, diabetes, hepatitis, asthma,

allergies, nephritis, Parkinson's disease, Alzheimer's disease,

atherosclerosis, myocardial infarction, AIDS and infections. The methods

may be used for identifying agonists and antagonists of the

polynucleotide and polypeptide. The present sequence is a protein from

one of the 28 disclosed secreted protein genes, it is not clear whether

this is an alternative expressed protein or a fragment of one of the

claimed proteins.

XX

SQ Sequence 51 AA;

Alignment Scores:

Pred. No.: 4.69e-14 Length: 51

Score: 219.00 Matches: 35

Percent Similarity: 78.43% Conservative: 5

Best Local Similarity: 68.63% Mismatches: 11

Query Match: 28.66% Indels: 0

DB: 8 Gaps: 0

US-10-807-204-11 (1-396) x ADG89845 (1-51)

Qy 229 TGCAGTATGCCACAGGAGGCTGGCCCTGGCTGCCCTCCATACCACACTGGTGTAACAAT 288

Db 1 CysGluMetProLysGluThrGlyProCysLeuAlaTyrPheLeuHisTrrpTyrAsp 20

Qy 289 AAAAAAATAAGATCTGCTCCGAATTCATCTATGGCGGTGCCAGGGGAACAATAACAAC 348

Db 21 LysLysAspAsnThrCysSerMetPheValTyrGlyGlyCysGlnGlyAsnAsnAsnAsn 40

Qy 349 TTCCAAACTGAAGCTATCTGCTGGTCACCTGC 381

Db 41 PheGlnSerLysAlaAsnCysLeuAsnThrCys 51

RESULT 39

AAR62523

ID AAR62523 standard; peptide; 560 AA.

XX AAR62523;

AC AAR62523;

XX

DT 25-MAR-2003 (revised)

DT 06-JUN-1995 (first entry)

XX

DE Hookworm anticoagulant.

XX

KW Hookworm; anticoagulant; serine protease-inhibitor; blood loss; vaccine;

KW vascular disease therapy.

XX

OS Ancyllostoma caninum.

XX

FN WO9425000-A1.

XX

PD 10-NOV-1994.

XX

PF 29-APR-1994; 94WO-US004707.

XX

PR 30-APR-1993; 93US-00055988.

XX

PA (UYUA) UNIV YALE.

XX

PI Cappello M, Hotez PJ, Richards FE, Hawdon JM;

XX

DR WPI; 1994-357862/44.

XX

XX Anticoagulant protein isolated from Ancyllostoma hookworm - useful to

XX prevent blood loss during infection, as vaccine and to treat vascular

XX disorders.

XX PS Disclosure; Page 27-29; 39pp; English.

XX CC An anticoagulant was isolated from extracts of adult hookworm (Ancylostoma caninum). Preliminary sequencing identified 2 internal peptide fragments (AAR62521-22). The protein sequence of the anticoagulant, predicted from a 2.3 kb clone isolated from a cDNA library of adult hookworm, is given in AAR62523. The protein sequence exhibited homology to the pancreatic trypsin-inhibitor (AAR62524), green mamba venom (AAR62525) and tissue factor pathway inhibitors (AAR62526-8), suggesting the anticoagulant to be a Kunitz-type serine protease-inhibitor. (Updated on 25-MAR-2003 to correct PN field.)

XX SQ Sequence 560 AA;

Alignment Scores:

Pred. No.:	5,128-10	Length:	560
Score:	182.50	Matches:	46
Percent Similarity:	41.94%	Conservative:	19
Best Local Similarity:	29.68%	Mismatches:	57
Query Match:	23.89%	Indels:	33
DB:	2	Gaps:	3

US-10-807-204-11 (1-396) x AAR62523 (1-560)

QY 20 TGCCAACTCTGTACCAATTCATCTCTTTGGGGGACATCCAGGAACCTGGGCACGCTGAAG 79

DB 166 CysLysSerPhePheGlyCysGlyGlyAenGlyAenAenPheMetThrLysAla 185

QY 80 GCATCTTTGGCAAGCGGTGTCCTCAAA---ATCAAGTGGATGCGAATGCGAAGAAATAG 136

DB 186 LysCysMet--GlutThrCysSerLysHisIleLysProGluThrGluGlnAsePValCys 205

QY 137 ACCAGTGTACCAACCCAGAGATGCCAGAAAACATGAAGTGTGCGCGTTC---AGCC 193

DB 205 exGlnProIleLysAlaGlyProCysMetAlaMetLeuLysArgTyrAlaTyrAsePhe 225

QY 194 GTGGAAAGAAATGTTAGACTTC----- 216

DB 225 ysLysLysArgCysValGlnPheIleTyrGlyGlyCysLysGlyAenLysAenAenPheG 245

QY 217 -----AGAAAGGATA 226

DB 245 LuSerMetGluGluCysThrArgThrCysLysLysAlaValProGluProGluGlnAseP 265

QY 227 TATGCAGTATGCACAGGAGGCTGCCCTGCTGCTCCATACACACACTGGTGTACA 286

DB 265 hrCysSerGlnProIleGluValGlyProCysLysAlaMetLeuLysArgTyrAlaTyrA 285

QY 287 ATAAAAAACTAAGATCTCTCGAATTCATCTATGGCGGTGCGAGGGGAACAATAACA 346

DB 285 sPAsnLysLysAenLysCysValArgPheIleTyrGlyGlyCysLysGlyAenLysAenA 305

QY 347 ACTTCCAACTGAAGCTACTCTCTGGTGCACCTGCAAAAAA 387

DB 305 snPheGluSerMetGluGluCysThrTyrThrCysLysLys 318

RESULT 40

ABB71150

ID ABB71150 standard; protein; 2858 AA.

XX AC ABB71150;

XX DT 26-MAR-2002 (first entry)

XX DE Drosophila melanogaster polypeptide SEQ ID NO 40242.

XX KW Drosophila; developmental biology; cell signalling; insecticide; pharmaceutical.

XX OS Drosophila melanogaster.

XX PN WO200171042-A2.

XX PD 27-SEP-2001.

XX PR 23-MAR-2001; 2001WO-US009231.

XX PR 23-MAR-2000; 2000US-0191637P.

XX PR 11-JUL-2000; 2000US-00614150.

XX PA (PEKE) PE CORP NY.

XX PI Venter JC, Adams M, Li PWD, Myers EW;

XX DR WPI; 2001-656860/75.

XX DR N-PSDB; ABL15253.

XX PT New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signaling and cell-cell interactions.

XX PS Disclosure; SEQ ID NO 40242; 21pp + Sequence Listing; English.

XX CC The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention is useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins (ABBS7737-ABBS72072). The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences

XX SQ Sequence 2858 AA;

Alignment Scores:

Pred. No.:	1,04e-09	Length:	2858
Score:	181.00	Matches:	36
Percent Similarity:	42.98%	Conservative:	13
Best Local Similarity:	31.58%	Mismatches:	35
Query Match:	23.69%	Indels:	30
DB:	4	Gaps:	3

US-10-807-204-11 (1-396) x ABB71150 (1-2858)

QY 136 GACCAAGTGTACCAACCCAGCA-----GATTCCCCAGAAAACATGAAGTGTGCCCG 186

DB 1748 AsparGysAlaLeuProLysGlnThrGlyAspCysSerGlyLysLeuAlaLysTrpHis 1767

QY 187 TTCAGCCGTGA---AGAAATGTTAGACTTC----- 216

DB 1768 PheSerGluSerGluLysArgCysValProPheTyrTyrSerGlyCysGlyAenLys 1787

QY 217 -----AGAAAGGAT 225

DB 1788 AsnAenPheProThrLeuGluSerCysGluAsePHisCysProArgGlnValAlaLysAseP 1807

QY 226 ATATGCAGTATGCCACAGAGGCTGGCCCTGCTGCTCCATACACACTGGTGTAC 285

DB 1808 IleCysGluIleProAlaGluValGlyGlyCysAlaAenTyrValThrSerTrpTyrTyr 1827

QY 286 AATAAAAACTAAGATCTGCTCCGATTCATCTATGCGCGTTCGCCAGGGAACAATAAC 345

DB 1828 AspThrGlnAsePHisGlnAlaCysArgGlnPheTyrTyrGlyCysGlyAenGluAen 1847

QY 346 AACTTCCAACTGAAGCTATCTGTGCTGCTGCACCTGCAAAAAA 387

DB 1848 ArgPheProThrGluGluSerCysLeuAlaArgCysAsePArg 1861

RESULT 41

ABB58064

ID ABB58064 standard; protein; 3060 AA.

XX AC ABB58064;

CC	differentiation factor)-associated serum protein (GASP)	
XX	Sequence 571 AA;	
SQ	Sequence 571 AA;	
Alignment Scores:		
Pred. No.:	8.31e-10	Length: 571
Score:	180.50	Matches: 35
Percent Similarity:	42.73%	Conservative: 12
Best Local Similarity:	31.82%	Mismatches: 34
Query Match:	23.63%	Indels: 29
DB:	7	Gaps: 3
US-10-807-204-11 (1-396) x AAE39498 (1-571)		
QY	139 CAGTGTACCAACCC-----AGAGATTGCCAGAAACATG-----	174
Db	322 GluCysLeuLysProProAspSerGluAspCysGlyGluGlnThrArgTrpHisPhe	341
QY	175 -----AAGTGTGCCGTCAGCCGTGGAAG-----	201
Db	342 AspAlaGlnAlaAsnAsnCysLeuThrPheThrPheGlyHisCysHisAsnLeuAsn	361
QY	202 -----AAATGTTTAGACTTCAGAAAGATATATGC	231
Db	362 HisPheGluThrTyrGluAlaCysMetLeuAlaCysMetSerGlyProLeuAlaThrCys	381
QY	232 AGTATGCCACAGAGGCTGGCCCTCGCTCCATACACACACTGGTGGTACAAATAA	291
Db	382 SerLeuProAlaLeuGlnGlyProCysLysAlaTyrValProArgTrpAlaTyrAsnSer	401
QY	292 AAAACTAAGATCTGCTCCGAATTCATCTATGCGCGTTCACGGGAAACAATAACAACCTTC	351
Db	402 GlnThrGlyLeuCysGlnSerPheValTyrGlyGlyCysGluGlyAsnGlyAsnAsnPhe	421
QY	352 CAAACTGAAGCTATCTGCTGCTACCTGC	381
Db	422 GluSerArgGluAlaCysGluGluSerCys	431
RESULT 43		
AAE39459		
ID	AAE39459 standard; protein; 571 AA.	
XX	AAE39459;	
DT	18-DEC-2003 (first entry)	
XX	Mouse GDF-associated serum protein (GASP)1 protein.	
XX	Mouse; GDF-associated serum protein; GASP; amphotrophic lateral sclerosis; growth and differentiation factor; GDF; chronic glucocorticoid therapy; familial periodic paralysis; paroxysmal myoglobinuria; muscular disorder; progressive dystrophic ophthalmoplegia; adipose tissue disorder; frailty; bone degenerative disorder; congenital myopathy; Eaton-Lambert syndrome; muscular dystrophy; congestive obstructive pulmonary disease; cachexia; carpal tunnel syndrome; premature gonadal failure; vitamin D deficiency; nutritional deficiency; osteoarthritis; hyperparathyroidism; sarcopaenia; androgen suppression; myasthenia gravis; hyperglycaemia; organ atrophy; metabolic disorder; metabolic syndrome; anorexia nervosa; osteoporosis; myotonia; neuroprotective; obesity; immunomodulator; diabetes.	
XX	Mus sp.	
XX	Key	Location/Qualifiers
FT	Domain	105..170
FT	/note= "Follistatin domain"	
XX	US2003162714-A1.	
XX	28-AUG-2003.	
XX	21-FEB-2003; 2003US-00369736.	
XX	21-FEB-2002; 2002US-0357845P.	
PR	20-DEC-2002; 2002US-0434644P.	
XX	(AMHP) WYETH.	
XX	Hill JJ, Wolfman NM;	
XX	WPI; 2003-756055/71.	
DR	N-PSDB; AAD59923.	
XX	Composition containing growth and differentiation factor-associated serum protein-1, useful for treating e.g. muscular dystrophy or diabetes, also for diagnosis.	
PT	Disclosure; Fig 6C; Opp; English.	
XX	The present invention relates to the use of a protein GDF (growth and differentiation factor)-associated serum protein (GASP) 1 comprising at least one follistatin domain to modulate the level or activity of growth and differentiation factor (GDF) -8. Administration of GASP1 is used to modulate GDF-8 for treatment of muscular disorders such as muscular dystrophy (benign X-linked, limb-girdle, facioscapulohumeral, myotonic, distal, oculopharyngeal, Duchenne or Fukuyama-type congenital), progressive dystrophic ophthalmoplegia, amphotrophic lateral sclerosis, congestive obstructive pulmonary disease, congenital myopathy (myotonia), familial periodic paralysis, paroxysmal myoglobinuria, myasthenia gravis, Eaton-Lambert syndrome, secondary myasthenia, organ atrophy, frailty, carpal tunnel syndrome, paroxysmal muscle atrophy, sarcopaenia, cachexia and other muscle wasting syndromes such as diabetes types 1 or 2, impaired muscle, metabolic disorders such as diabetes types 1 or 2, impaired glucose tolerance, hyperglycaemia, metabolic syndrome, insulin resistance induced by trauma and obesity, adipose tissue disorder such as obesity, and bone degenerative conditions such as osteoporosis, osteopaenia, osteoarthritis, low bone mass due to chronic glucocorticoid therapy, premature gonadal failure, vitamin D deficiency, androgen suppression, secondary hyperparathyroidism, nutritional deficiencies and anorexia nervosa. The present sequence is mouse GDF (growth and differentiation factor)-associated serum protein (GASP)	
XX	Sequence 571 AA;	
Alignment Scores:		
Pred. No.:	8.31e-10	Length: 571
Score:	180.50	Matches: 35
Percent Similarity:	42.73%	Conservative: 12
Best Local Similarity:	31.82%	Mismatches: 34
Query Match:	23.63%	Indels: 29
DB:	7	Gaps: 3
US-10-807-204-11 (1-396) x AAE39459 (1-571)		
QY	139 CAGTGTACCAACCC-----AGAGATTGCCAGAAACATG-----	174
Db	322 GluCysLeuLysProProAspSerGluAspCysGlyGluGlnThrArgTrpHisPhe	341
QY	175 -----AAGTGTGCCGTCAGCCGTGGAAG-----	201
Db	342 AspAlaGlnAlaAsnAsnCysLeuThrPheThrPheGlyHisCysHisAsnLeuAsn	361
QY	202 -----AAATGTTTAGACTTCAGAAAGATATATGC	231
Db	362 HisPheGluThrTyrGluAlaCysMetLeuAlaCysMetSerGlyProLeuAlaThrCys	381
QY	232 AGTATGCCACAGAGGCTGGCCCTCGCTCCATACACACACTGGTGGTACAAATAA	291
Db	382 SerLeuProAlaLeuGlnGlyProCysLysAlaTyrValProArgTrpAlaTyrAsnSer	401
QY	292 AAAACTAAGATCTGCTCCGAATTCATCTATGCGCGTTCACGGGAAACAATAACAACCTTC	351
Db	402 GlnThrGlyLeuCysGlnSerPheValTyrGlyGlyCysGluGlyAsnGlyAsnAsnPhe	421
QY	352 CAAACTGAAGCTATCTGCTGCTACCTGC	381
Db	422 GluSerArgGluAlaCysGluGluSerCys	431

PT preventing or treating conditions associated with excessive proteinase
PT activity, e.g. inflammation, pulmonary injuries, myocardial infarction or
PT hemorrhage.

XX Disclosure; Page 80; 87pp; English.

XX The present invention describes an isolated, purified or recombinant DJ11
CC polypeptide comprising a Kunitz-type protease inhibitor domain or its
CC biologically active portion. The polypeptide comprises at least 98 %
CC identity to residues 77-127 of a 131 amino acid sequence (S1, see
CC ADA19800), or to residues 52-102 of a 106 amino acid sequence (S2, see
CC ADA19801). DJ11 has antiinflammatory, antibacterial, thrombolytic,
CC anticoagulant, cardiatic, vasotropic, antipneumatic, immunosuppressive,
CC antirheumatic, antiarthritic, nephrotropic, antipsoriatic and vulnary
CC activities, and can be used as a protease inhibitor and in gene therapy.
CC Composition and methods from the present invention can be used in
CC diagnosing, preventing or treating conditions associated with excessive
CC proteinase activity, such as acute pancreatitis, pulmonary injury,
CC allergy-induced protease release, deep vein thrombosis, myocardial
CC infarction, shock (including septic shock), hyperfibrinolytic
CC haemorrhage, and especially, inflammatory disorders (e.g. emphysema,
CC idiopathic pulmonary fibrosis, rheumatoid arthritis, glomerulonephritis,
CC chronic inflammatory bowel disease or psoriasis). The DJ11 proteins may
CC be used in preserving platelet function, organ preservation or in wound
CC healing. The polynucleotide sequence encoding DJ11 may be used as
CC hybridisation probes, in chromosome and gene mapping, in the generation
CC of antisense RNA and DNA, and as targets for pharmaceutical intervention.
CC The present sequence represents a partial engineered human DJ11 protein
CC amino acid sequence from the present invention.

XX Sequence 33 AA;

Alignment Scores:
Pred. No.: 5.08e-10 Length: 33
Score: 180.00 Matches: 32
Percent Similarity: 96.97% Conservatives: 0
Best Local Similarity: 96.97% Mismatches: 1
Query Match: 23.56% Indels: 0
DB: 7 Gaps: 0

US-10-807-204-11 (1-396) x ADA19806 (1-33)

QY 295 ACTAAGATCTGCTCCGAATTCATCTATGCGGTGCCAGGGGAACAATAACACTTCCAA 354
Db 1 ThrLysIleCysSerGluPheIleTyRGlyGlySerGlnGlyAsnAsnAenPheGln 20

QY 355 ACTGAAGCTATCTGCTGTCACCTGCACCAAAAATACCAT 393

Db 21 ThrGluAlaIleCysLeuValThrCysLysLysTyRHis 33

RESULT 46

ADA19809

ID ADA19809 standard; peptide; 33 AA.

XX ADA19809;

XX 20-NOV-2003 (first entry)

DE Engineered human DJ11 partial amino acid sequence SEQ ID NO:10.

XX DJ11; Kunitz-type protease inhibitor domain; antiinflammatory;
KW antiarthritic; thrombolytic; anticoagulant; cardiatic; vasotropic;
KW antibacterial; immunosuppressive; antirheumatic; antipneumatic;
KW nephrotropic; antipsoriatic; vulnary; protease inhibitor; gene therapy;
KW acute pancreatitis; pulmonary injury; allergy-induced protease release;
KW deep vein thrombosis; myocardial infarction; shock; septic shock;
KW hyperfibrinolytic haemorrhage; inflammatory disorder; emphysema;
KW idiopathic pulmonary fibrosis; rheumatoid arthritis; glomerulonephritis;
KW chronic inflammatory bowel disease; psoriasis.

XX Synthetic.

OS Homo sapiens.

XX

PN WO2003070770-A2.

XX 28-AUG-2003.

XX 18-FEB-2003; 2003WO-EP001629.

XX 21-FEB-2002; 2002US-0358683P.

XX (GENE-) GENEPROT INC.

XX Bougueleret L, Bairoch A, Niknejad A;

XX WPI; 2003-663849/62.

XX New engineered human Kunitz-type protease inhibitor for diagnosing,
PT preventing or treating conditions associated with excessive proteinase
PT activity, e.g. inflammation, pulmonary injuries, myocardial infarction or
PT hemorrhage.

XX Disclosure; Page 82-83; 87pp; English.

XX The present invention describes an isolated, purified or recombinant DJ11
CC polypeptide comprising a Kunitz-type protease inhibitor domain or its
CC biologically active portion. The polypeptide comprises at least 98 %
CC identity to residues 77-127 of a 131 amino acid sequence (S1, see
CC ADA19800), or to residues 52-102 of a 106 amino acid sequence (S2, see
CC ADA19801). DJ11 has antiinflammatory, antibacterial, thrombolytic,
CC anticoagulant, cardiatic, vasotropic, antipneumatic, immunosuppressive,
CC antirheumatic, antiarthritic, nephrotropic, antipsoriatic and vulnary
CC activities, and can be used as a protease inhibitor and in gene therapy.
CC Composition and methods from the present invention can be used in
CC diagnosing, preventing or treating conditions associated with excessive
CC proteinase activity, such as acute pancreatitis, pulmonary injury,
CC allergy-induced protease release, deep vein thrombosis, myocardial
CC infarction, shock (including septic shock), hyperfibrinolytic
CC haemorrhage, and especially, inflammatory disorders (e.g. emphysema,
CC idiopathic pulmonary fibrosis, rheumatoid arthritis, glomerulonephritis,
CC chronic inflammatory bowel disease or psoriasis). The DJ11 proteins may
CC be used in preserving platelet function, organ preservation or in wound
CC healing. The polynucleotide sequence encoding DJ11 may be used as
CC hybridisation probes, in chromosome and gene mapping, in the generation
CC of antisense RNA and DNA, and as targets for pharmaceutical intervention.
CC The present sequence represents a partial engineered human DJ11 protein
CC amino acid sequence from the present invention.

XX Sequence 33 AA;

Alignment Scores:
Pred. No.: 5.08e-10 Length: 33
Score: 180.00 Matches: 32
Percent Similarity: 96.97% Conservatives: 0
Best Local Similarity: 96.97% Mismatches: 1
Query Match: 23.56% Indels: 0
DB: 7 Gaps: 0

US-10-807-204-11 (1-396) x ADA19809 (1-33)

QY 295 ACTAAGATCTGCTCCGAATTCATCTATGCGGTGCCAGGGGAACAATAACACTTCCAA 354
Db 1 ThrLysIleCysSerGluPheIleTyRGlyGlySerGlnGlyAsnAsnAenPheGln 20

QY 355 ACTGAAGCTATCTGCTGTCACCTGCACCAAAAATACCAT 393

Db 21 ThrGluAlaIleCysLeuValThrCysLysLysTyRHis 33

RESULT 47

AAR99146

ID AAR99146 standard; protein; 58 AA.

XX AAR99146;

XX 12-FEB-1997 (first entry)

XX

DE Aprotinin-like Kunitz domain.
XX Aprotinin; Kunitz domain; human neutrophil elastase; hNE;
KW connective tissue; alpha 1 protease inhibitor; API; neutrophil;
KW alaph antitrypsin; respiratory disorder; cystic fibrosis;
KW smokers emphysema.
XX Synthetic.
XX WO9620278-A2.
XX 04-JUL-1996.
XX 15-DEC-1995; 95WO-US016349.
XX 16-DEC-1994; 94US-00358160.
XX (PROT-) PROTEIN ENG CORP.
XX Ley AC, Ladner RC, Guterman SK, Roberts BL, Markland W, Kent RB;
XX WPI; 1996-321851/32.
XX New engineered inhibitors of human neutrophil elastase - contg. aprotinin
PT -like Kunitz domain for treating, e.g. cystic fibrosis or other
PT respiratory disorders.
XX Example 23; Page 47; 105pp; English.
XX Genetically engineered human derived Kunitz domains can be used to
CC inhibit human neutrophil elastase, an enzyme involved in the elimination
CC of pathogens and the restructuring of connective tissue. In cases of
CC reduction of the circulating alpha-1-protease inhibitor (API or alpha
CC antitrypsin), or the inactivation of API by oxidation (smokers
CC emphysema), extensive destruction of the lung tissue may result from
CC uncontrolled elastolytic activity of human neutrophil elastase. Other
CC respiratory disorders such as cystic fibrosis are thought to be caused by
CC human neutrophil elastase release by neutrophils. The genetically
CC engineered human derived Kunitz domains can be used to treat such
CC respiratory disorders. See AAR99146-R99211
XX
SQ Sequence 58 AA;

Alignment Scores:
Pred. No.: 1.18e-09 Length: 58
Score: 177.00 Matches: 21
Percent Similarity: 65.43% Conservative: 5
Best Local Similarity: 56.36% Mismatches: 19
Query Match: 23.17% Indels: 0
DB: 2 Gaps: 0

US-10-807-204-11 (1-396) x AAR99146 (1-58)
Qy 217 AGAAGGNATATGACGATATCCACAGAGGCTGCGCCCTCGCTCCATACCAAC 276
Db 1 ArgProAepPheCysLeuLeuProAlaGluThrGlyProCysArgAlaMetIleProArg 20
Qy 277 TGGTGGTACATAAATAAATAAGTCTGCTCCGNAATTCATCTATGGCGGTGCCAGGG 336
Db 21 PheTyTyAsnAlaLysSerGlyLysCysGluProPheIleTyTGlyGlyCysGlyGly 40
Qy 337 AACCAATACAACTTCCAACTGAAGCTATCTGCTGGTGCACCTGC 381
Db 41 AsnAlaAsnAnPheLysThrGluGluGluCysArgArgThrCys 55

RESULT 48
AAE13096
ID AAE13096 standard; peptide; 43 AA.
XX
XX AAE13096;
XX
XX 28-JAN-2002 (first entry)
XX

DE Human serine proteinase inhibitor BTL.009 peptide fragment #2.
XX
XX Human: BTL.009 protein; serine proteinase inhibitor; cytostatic;
KW nephrotropic; idiopathic pulmonary fibrosis; cystic fibrosis; emphysema;
KW rheumatoid arthritis; adult respiratory distress syndrome; angiodiastasy;
KW blood coagulation; glomerulonephritis; prophylactic; platelet activation;
KW neutrophil; monocyte; granulocyte; organ failure; inflammatory disease;
KW elastase inhibitor; chymotrypsin inhibitor; lung injury; vascular injury;
KW therapeutic.
XX
XX Homo sapiens.
OS
XX US6294648-B1.
FN
XX 25-SEP-2001.
PD
XX 20-JUL-1999; 99US-00358569.
PF
XX 20-JUL-1999; 99US-00358569.
PR
XX (FARB) BAYER CORP.
PA
XX Delaria K, Roczniaak S, Davies C;
PI WPI; 2001-662224/76.
XX
XX New isolated protein for inhibiting human serine protease activity in the
PT treatment of e.g. emphysema and adult respiratory distress syndrome.
XX
XX Disclosure; Col 5-6; 16pp; English.
PS
XX The invention relates to human BTL.009 protein, a serine proteinase
CC inhibitor of the Kunitz family that exhibits greater potency towards
CC neutral serine proteinases. BTL.009 protein is found to inhibit leukocyte
CC elastase, chymotrypsin-like protease and trypsin-like protease. BTL.009
CC protein is useful for treating emphysema, idiopathic pulmonary fibrosis,
CC adult respiratory distress syndrome, cystic fibrosis, rheumatoid
CC arthritis, organ failure, glomerulonephritis, other inflammatory diseases
CC and diseases involving lung and vascular injury. BTL.009 is also useful
CC for preventing neutrophil and monocyte activation and formation of active
CC oxygen species during the oxidative burst of stimulated granulocytes.
CC BTL.009 is useful for reducing platelet activation and blood coagulation
CC and for the prophylactic or therapeutic treatment of patients undergoing
CC angioplasty. The present sequence is human serine proteinase inhibitor
CC BTL.009 peptide fragment related to the invention
XX
SQ Sequence 43 AA;

Alignment Scores:
Pred. No.: 1.79e-09 Length: 43
Score: 175.00 Matches: 29
Percent Similarity: 78.57% Conservative: 4
Best Local Similarity: 69.05% Mismatches: 9
Query Match: 22.91% Indels: 0
DB: 4 Gaps: 0

US-10-807-204-11 (1-396) x AAE13096 (1-43)
Qy 259 CTGGCCCTCCATACACACTGCTGGTACATAAATAAATAAGATCTGCTCGAATTCATC 318
Db 1 LeuAlaTyPheLeuHisTrpTrpTyAspLysLysAspAsnThrCysSerMetPheVal 20
Qy 319 TATGGCGGTGCCAGGGGAACAATAACAACCTCCAACTCAAGCTATCTGCTGGTCACC 378
Db 21 TyTGlyGlyCysGlnGlyAsnAsnAsnAsnAsnAsnAsnAsnAsnAsnAsnAsnAsn 40
Qy 379 TGCAAA 384
Db 41 CysLys 42

RESULT 49
AAE13092
ID AAE13092 standard; peptide; 54 AA.


```
Db      ||| ||| ||| ::: ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
1 ArgProAspPheCysGlnLeuGlyTyrSerAlaGlyProCysValAlaMetPheProArg 20
QY      277 TGGTGGTACAAATAAAAAAATAAGATCTGCTCCGNAATTCATCTATGGCGGTGCCAGGGG 336
        ::::: ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      21 TyrPheTyrAsnGlyThrSerMetAlaCysGluThrPheValTyrGlyGlyCysMetGly 40
        ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY      337 AACAAATAACAACTTCCAAACTGAAGCTATCTGTCTGTGGTCACCTGCANA 384
        ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      41 AsnGlyAsnAsnPheValThrGluLysAspCysLeuGlnThrCysArg 56
        ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
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GenCore version 5.1.6
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(without alignments)
2749.863 Million cell updates/sec

Title: US-10-807-204-11

Perfect score: 764

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Ygapop 10.0 , Ygapext 0.5
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Delop 6.0 , Delext 7.0

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Maximum Match 100%

Listing first 50 summaries

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-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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3	236	30.9	58	3	US-09-369-49A-8
4	233	30.9	58	4	US-09-569-670-8
5	233	30.5	54	3	US-09-358-569D-8
6	231	30.2	55	3	US-09-358-569D-1
7	186	24.3	66	1	US-08-358-160-113
8	186	24.3	79	6	5466783-7
9	186	24.3	79	6	5466783-7
10	177	23.2	58	1	US-08-358-160-71
11	175	22.9	43	3	US-09-358-569D-13
12	175	22.9	54	3	US-09-358-569D-9

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15	173	22.6	58	1	US-08-358-160-18
16	169	22.1	77	6	5466783-4
17	169	22.1	77	6	5466783-4
18	168	22.0	86	4	US-09-910-430-8
19	167	21.9	58	1	US-08-358-160-10
20	167	21.9	58	1	US-08-358-160-11
21	166	21.7	58	1	US-07-664-989B-48
22	166	21.7	58	1	US-07-664-989B-51
23	166	21.7	58	1	US-08-358-160-1
24	166	21.7	58	1	US-08-358-160-15
25	166	21.7	58	1	US-08-358-160-26
26	166	21.7	58	1	US-08-358-160-27
27	165	21.6	62	1	US-07-664-989B-49
28	165	21.6	58	1	US-08-358-160-24
29	164	21.5	58	1	US-08-358-160-9
30	164	21.5	61	2	US-08-829-876-211
31	164	21.5	61	2	US-08-829-876-214
32	164	21.5	61	3	US-09-234-874A-211
33	164	21.5	61	3	US-09-234-874A-214
34	164	21.5	61	4	US-09-234-873A-211
35	164	21.5	61	4	US-09-234-873A-214
36	163	21.3	58	1	US-07-664-989B-84
37	163	21.3	58	1	US-08-358-160-12
38	163	21.3	58	1	US-08-358-160-61
39	163	21.3	58	1	US-08-463-155A-56
40	163	21.3	58	1	US-08-463-432B-56
41	163	21.3	58	3	US-08-676-124-69
42	163	21.3	58	3	US-09-414-878-69
43	163	21.3	58	3	US-09-240-136-69
44	163	21.3	58	4	US-09-638-770A-69
45	163	21.3	61	2	US-08-829-876-180
46	163	21.3	61	2	US-08-829-876-218
47	163	21.3	61	3	US-09-234-874A-180
48	163	21.3	61	3	US-09-234-874A-218
49	163	21.3	61	4	US-09-234-873A-180
50	163	21.3	61	4	US-09-234-873A-218

ALIGNMENTS

RESULT 1
US-09-152-060-75
; Sequence 75, Application US/09152060
; Patent No. 6448230
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 28 Human Secreted Proteins
; FILE REFERENCE: P2003P1.US
; CURRENT APPLICATION NUMBER: US/09/152.060
; CURRENT FILING DATE: 1998-09-11
; EARLIER APPLICATION NUMBER: PCT/US98/04858
; EARLIER FILING DATE: 1998-03-12
; EARLIER APPLICATION NUMBER: 60/040,762
; EARLIER FILING DATE: 1997-03-14
; EARLIER APPLICATION NUMBER: 60/040,710
; EARLIER FILING DATE: 1997-03-14
; EARLIER APPLICATION NUMBER: 60/050,934
; EARLIER FILING DATE: 1997-05-30
; EARLIER APPLICATION NUMBER: 60/048,100
; EARLIER FILING DATE: 1997-05-30
; EARLIER APPLICATION NUMBER: 60/048,357
; EARLIER FILING DATE: 1997-05-30
; EARLIER APPLICATION NUMBER: 60/048,189
; EARLIER FILING DATE: 1997-05-30
; EARLIER APPLICATION NUMBER: 60/057,765
; EARLIER FILING DATE: 1997-09-05
; EARLIER APPLICATION NUMBER: 60/048,970
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/068,368
; EARLIER FILING DATE: 1997-12-19
; NUMBER OF SEQ ID NOS: 118

Sequence 123, Appl
Sequence 17, Appl
Sequence 18, Appl
Patent No. 5466783
Sequence 8, Appl
Sequence 10, Appl
Sequence 11, Appl
Sequence 48, Appl
Sequence 51, Appl
Sequence 1, Appl
Sequence 15, Appl
Sequence 26, Appl
Sequence 27, Appl
Sequence 49, Appl
Sequence 24, Appl
Sequence 9, Appl
Sequence 211, Appl
Sequence 214, Appl
Sequence 211, Appl
Sequence 214, Appl
Sequence 214, Appl
Sequence 84, Appl
Sequence 12, Appl
Sequence 56, Appl
Sequence 56, Appl
Sequence 69, Appl
Sequence 69, Appl
Sequence 69, Appl
Sequence 180, Appl
Sequence 218, Appl
Sequence 180, Appl
Sequence 218, Appl
Sequence 180, Appl
Sequence 218, Appl

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; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 75
; LENGTH: 133
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-152-060-75

Alignment Scores:
Pred. No.: 5,4e-41 Length: 133
Score: 455.00 Matches: 77
Percent Similarity: 74.22% Conservative: 18
Best Local Similarity: 60.16% Mismatches: 33
Query Match: 59.55% Indels: 0
DB: 4 Gaps: 0

US-10-807-204-11 (1-396) x US-09-152-060-75 (1-133)
Qy 1 ATGGACTCTCAGGACTTCTGCCAATCTGTGATGACATTCATCTTTGGGGACATCCAG 60
Db 1 MetGlySerSerGlyLeuLeuSerLeuLeuValLeuPheValLeuLeuAlaAsnValGln 20

Qy 61 GAACCTGGGACGCTGAAGGATCTTGGCAAGCGGTGTCCTCCAAATCAAAGTGAATGC 120
Db 21 GlyProGlyLeuThrAspTrpLeuPheProArgArgCysProLysIleArgGluGluCys 40

Qy 121 GNACTGGAGAAATAGACCAGTGTACCAAAACCCAGAGATTGCCAGAAACATCAAGTGT 180
Db 41 GluPheGlnGluArgPheValCysThrLysAspArgGlnCysGlnAspAsnLysLysCys 60

Qy 181 TGCCCGTTTACCGCTGCAAGAAATGTTAGACTTTCAGAAAGGATATATGTCAGTATGCCA 240
Db 61 CysValPheSerCysGlyLysLysCysLeuAspLysGlnAspValCysGluMetPro 80

Qy 241 CAGGAGCGTGGCCCTGCTGCTCCATACCACTGGTGGTACATAAAACCTAAG 300
Db 81 LysGluThrGlyProCysLeuAlaTyrPheLeuHisTrpTrpTyrAspLysLysAspAsn 100

Qy 301 ATCTGCTCCGAATTCANCTATGGGGTTCAGGGGACATACAACTCCCAACTGAA 360
Db 101 ThrCysSerMetPheValTyrGlyCysGlnGlyAsnAsnAsnPheGlnSerLys 120

Qy 361 GCTATCTGCTGGTCACTGCATA 384
Db 121 AlaAsnCysLeuAsnThrCysLys 128

RESULT 2
US-09-358-569D-10
; Sequence 10, Application US/09358569D
; Patent No. 6294648
; GENERAL INFORMATION:
; APPLICANT: Delaria, Kathy
; APPLICANT: Rocznia, Steve
; TITLE OF INVENTION: Protein Having Proteinase Inhibitor Activity
; FILE REFERENCE: MSB-7259
; CURRENT APPLICATION NUMBER: US/09/358,569D
; CURRENT FILING DATE: 1999-07-20
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 10
; LENGTH: 64
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Extension of
; OTHER INFORMATION: Seq Id 1
US-09-358-569D-10

Alignment Scores:
Pred. No.: 5.32e-18 Length: 64
Score: 242.00 Matches: 38
Percent Similarity: 79.31% Conservative: 8
Best Local Similarity: 65.52% Mismatches: 12

; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 75
; LENGTH: 133
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-807-204-11 (1-396) x US-09-358-569D-10 (1-64)

Qy 211 GACTTCAGAAAGGATATATGCAGTATGCCACAGAGGCTGGCCCTCCCTCCATCCATA 270
Db 1 AspLeuLysGlnAspValCysGluMetProLysGluThrGlyProCysLeuAlaTyrPhe 20

Qy 271 CCACACTGGTGGTACATAAAAAAATAAGATCTGCTCCGAATTCATCTATGGCGGTGC 330
Db 21 LeuHisTrpTrpTyrAspLysLysAspAsnThrCysSerMetPheValTyrGlyGlyCys 40

Qy 331 CAGGGGACAAATAACACTTCCAACTGAGAGCTATCTGTCTGGTCACTGCATAA 384
Db 41 GlnGlyAsnAsnAsnAsnPheGlnSerLysAlaAsnCysLeuAsnThrCysLys 58

RESULT 3
US-09-369-494-8
; Sequence 8, Application US/09369494
; Patent No. 618607
; GENERAL INFORMATION:
; APPLICANT: Davies, Christopher
; APPLICANT: Chen, Dadong
; APPLICANT: Rocznia, Steve
; TITLE OF INVENTION: Protein Having Proteinase Inhibitor Activity
; FILE REFERENCE: MSB-7260
; CURRENT APPLICATION NUMBER: US/09/369,494
; CURRENT FILING DATE: 1999-08-05
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 8
; LENGTH: 58
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:fragment from
; OTHER INFORMATION: computer database
US-09-369-494-8

Alignment Scores:
Pred. No.: 2.32e-17 Length: 58
Score: 236.00 Matches: 37
Percent Similarity: 80.36% Conservative: 8
Best Local Similarity: 66.07% Mismatches: 11
Query Match: 30.89% Indels: 0
DB: 3 Gaps: 0

US-10-807-204-11 (1-396) x US-09-369-494-8 (1-58)
Qy 217 AGAAGGATATATGCAGTATGCCACAGAGGCTGGCCCTCCCTCCATACACAC 276
Db 1 LysGlnAspValCysGluMetProLysGluThrGlyProCysLeuAlaTyrPheLeuHis 20

Qy 277 TGGTGGTACATAAAAAAATAAGATCTGCTCCGAATTCATCTATGGCGGTGCACGGG 336
Db 21 TrpTrpTyrAspLysLysAspAsnThrCysSerMetPheValTyrGlyGlyCysGlnGly 40

Qy 337 AACATAACAACTTCCAACTGAAGCTATCTGTCTGGTCACTGCATAA 384
Db 41 AsnAsnAsnAsnPheGlnSerLysAlaAsnCysLeuAsnThrCysLys 56

RESULT 4
US-09-569-670-8
; Sequence 8, Application US/09569670
; Patent No. 6689582
; GENERAL INFORMATION:
; APPLICANT: Davies, Christopher
; APPLICANT: Chen, Dadong
; APPLICANT: Rocznia, Steve
; TITLE OF INVENTION: Protein Having Proteinase Inhibitor Activity
; FILE REFERENCE: MSB-7260
; CURRENT APPLICATION NUMBER: US/09/569,670
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; CURRENT FILING DATE: 2000-05-12
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 8
; LENGTH: 58
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:fragment from
; OTHER INFORMATION: computer database
US-09-569-670-8

Alignment Scores:
Pred. No.: 2,32e-17 Length: 58
Score: 236.00 Matches: 37
Percent Similarity: 80.36% Conservative: 8
Best Local Similarity: 66.07% Mismatches: 11
Query Match: 30.89% Indels: 0
DB: 4 Gaps: 0

US-10-807-204-11 (1-396) x US-09-569-670-8 (1-58)
QY 217 AGAAGGATATATGCAGTATGCCAGGAGCTGCCCTGGCTCCATACCACAC 276
Db 1 LysGlnAspValCysGluMetProLysGluThrGlyProCysLeuAlaTy:PheLeuHis 20
QY 277 TGGTGGTACATAAAAAAAGTATCTGCTCCGAATTCATCTATGGCGGTTGCCAGGGG 336
Db 21 TrpTrpTyAspLysAspAsnThrCysSerMetPheValTyGlyGlyCysGlnGly 40
QY 337 AACATAACAATTCCTCAAGCTATCTGTCTGGTCACCTGC 384
Db 41 AsnAsnAsnAsnPheGlnSerLysAlaAsnCysLeuAsnThrCysLys 56

RESULT 5
US-09-358-569D-8
; Sequence 8, Application US/09358569D
; Patent No. 6294648
; GENERAL INFORMATION:
; APPLICANT: Delaria, Kathy
; APPLICANT: Rocznia, Steve
; APPLICANT: Davies, Christopher
; TITLE OF INVENTION: Protein Having Proteinase Inhibitor Activity
; FILE REFERENCE: MSB-7259
; CURRENT APPLICATION NUMBER: US/09/358,569D
; CURRENT FILING DATE: 1999-07-20
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 8
; LENGTH: 54
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:derived from
; OTHER INFORMATION: EST sequence database
US-09-358-569D-8

Alignment Scores:
Pred. No.: 4.8e-17 Length: 54
Score: 233.00 Matches: 37
Percent Similarity: 79.63% Conservative: 6
Best Local Similarity: 68.52% Mismatches: 11
Query Match: 30.50% Indels: 0
DB: 3 Gaps: 0

US-10-807-204-11 (1-396) x US-09-358-569D-8 (1-54)
QY 223 GATATATGAGTATGCCAGGAGCTGCCCTGGCTCCATACCACACTGGTGG 282
Db 1 AspValCysGluMetProLysGluThrGlyProCysLeuAlaTy:PheLeuHisTrpTrp 20
QY 283 TACAATAAAAAAAGTATCTGCTCCGAATTCATCTATGGCGGTTGCCAGGGGAACAT 342
Db 1 LysGlnAspValCysGluMetProLysGluThrGlyProCysLeuAlaTy:PheLeuHis 20
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Db 21 TyrAspLysLysAspAsnThrCysSerMetPheValTyGlyGlyCysGlnGlyAsnAsn 40
QY 343 AACAACTCCAAACTGAAGCTATCTGTCTGTACCTGCACAA 384
Db 41 AsnAsnPheGlnSerLysAlaAsnCysLeuAsnThrCysLys 54

RESULT 6
US-09-358-569D-1
; Sequence 1, Application US/09358569D
; Patent No. 6294648
; GENERAL INFORMATION:
; APPLICANT: Delaria, Kathy
; APPLICANT: Rocznia, Steve
; APPLICANT: Davies, Christopher
; TITLE OF INVENTION: Protein Having Proteinase Inhibitor Activity
; FILE REFERENCE: MSB-7259
; CURRENT APPLICATION NUMBER: US/09/358,569D
; CURRENT FILING DATE: 1999-07-20
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 55
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:derived from
; OTHER INFORMATION: EST sequence database
US-09-358-569D-1

Alignment Scores:
Pred. No.: 7.95e-17 Length: 55
Score: 231.00 Matches: 36
Percent Similarity: 80.00% Conservative: 8
Best Local Similarity: 65.45% Mismatches: 11
Query Match: 30.24% Indels: 0
DB: 3 Gaps: 0

US-10-807-204-11 (1-396) x US-09-358-569D-1 (1-55)
QY 217 AGAAGGATATATGCAGTATGCCAGGAGCTGCCCTGGCTCCATACCACAC 276
Db 1 LysGlnAspValCysGluMetProLysGluThrGlyProCysLeuAlaTy:PheLeuHis 20
QY 277 TGGTGGTACATAAAAAAAGTATCTGCTCCGAATTCATCTATGGCGGTTGCCAGGGG 336
Db 21 TrpTrpTyAspLysLysAspAsnThrCysSerMetPheValTyGlyGlyCysGlnGly 40
QY 337 AACATAACAATTCCTCAAGCTATCTGTCTGGTCACCTGC 381
Db 41 AsnAsnAsnAsnPheGlnSerLysAlaAsnCysLeuAsnThrCys 55

RESULT 7
US-08-160-113
; Sequence 113, Application US/08358160
; Patent No. 5663143
; GENERAL INFORMATION:
; APPLICANT: LEY, Arthur C.
; APPLICANT: LADNER, Robert C.
; APPLICANT: GUTERMAN, Sonia K.
; APPLICANT: ROBERTS, Bruce L.
; APPLICANT: MARKLAND, William
; APPLICANT: KENT, Rachel B.
; TITLE OF INVENTION: ENGINEERED HUMAN-DERIVED KUNITZ
; TITLE OF INVENTION: DOMAINS THAT INHIBIT HUMAN NEUTROPHIL ELASTASE
; NUMBER OF SEQUENCES: 234
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W. Suite 300
; CITY: Washington
; STATE: District of Columbia
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
```


Db 44 AsnLysAsnAenPheLysAlaGluCysValArgAlaCysArg 59

RESULT 10

US-08-358-160-71

Sequence 71, Application US/08358160

Patent No. 5663143

GENERAL INFORMATION:

APPLICANT: LEY, Arthur C.

APPLICANT: LADNER, Robert C.

APPLICANT: GUTERMAN, Sonia K.

APPLICANT: ROBERTS, Bruce L.

APPLICANT: MARKLAND, William

APPLICANT: KENT, Rachel B.

TITLE OF INVENTION: ENGINEERED HUMAN-DERIVED KUNITZ

TITLE OF INVENTION: DOMAINS THAT INHIBIT HUMAN NEUTROPHIL ELASTASE

NUMBER OF SEQUENCES: 234

CORRESPONDENCE ADDRESS:

ADDRESSEE: BROWDY AND NEIMARK

STREET: 419 Seventh Street, N.W. Suite 300

CITY: Washington

STATE: District of Columbia

COUNTRY: USA

ZIP: 20004

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent In Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/358,160

FILING DATE: 16-DEC-1994

CLASSIFICATION: 514

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/133,031

FILING DATE: 13-OCT-1993

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/009,319

FILING DATE: 26-JAN-1993

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/664,989

FILING DATE: 01-MAR-1991

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/487,063

FILING DATE: 02-MAR-1990

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/240,160

FILING DATE: 02-SEP-1988

ATTORNEY/AGENT INFORMATION:

NAME: Cooper, Iver P.

REGISTRATION NUMBER: 28,005

REFERENCE/DOCKET NUMBER: LEY=1

TELECOMMUNICATION INFORMATION:

TELEPHONE: 202-628-5197

TELEFAX: 202-737-3528

TELEX: 248633

INFORMATION FOR SEQ ID NO: 71:

SEQUENCE CHARACTERISTICS:

LENGTH: 58 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-358-160-71

Alignment Scores:

Pred. No.: 5,71e-11 Length: 58

Score: 177.00 Matches: 31

Percent Similarity: 65.45% Conservative: 5

Best Local Similarity: 56.36% Mismatches: 19

Query Match: 23.17% Indels: 0

DB: 1 Gaps: 0

US-10-807-204-11 (1-396) x US-08-358-160-71 (1-58)

217 AGAAGGATATATGCAGTATGCCACAGAGGCTGGCCCTCCCTCCATACCACAC 276

1 ArgProAspPheCysLeuLeuProAlaGluThrGlyProCysArgAlaMetIleProArg 20

277 TGGTGGTACATAAAAACTAAGATCTGCTCCGAATTCATCTATGGCGGTGGCCAGGGG 336

21 PheTyrTyrAenAlaLysSerGlyLysCysGluProPheIleTyrGlyCysGlyGly 40

337 AACATAACAACTTCCAACTGAAGCTATCTGTCTGTGTCACCTGC 381

41 AsnAlaAenAenPheLysThrGluGluCysArgArgThrCys 55

RESULT 11

US-09-358-569D-13

Sequence 13, Application US/09358569D

Patent No. 6294648

GENERAL INFORMATION:

APPLICANT: Delaria, Kathy

APPLICANT: Rocznik, Steve

APPLICANT: Davies, Christopher

TITLE OF INVENTION: Protein Having Proteinase Inhibitor Activity

FILE REFERENCE: MSB-7259

CURRENT APPLICATION NUMBER: US/09/358,569D

CURRENT FILING DATE: 1999-07-20

NUMBER OF SEQ ID NOS: 15

SOFTWARE: Patent In Ver. 2.0

SEQ ID NO 13

LENGTH: 43

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Description of Artificial Sequence: Artificial

OTHER INFORMATION: sequence derived from EST database

US-09-358-569D-13

Alignment Scores:

Pred. No.: 8.7e-11 Length: 43

Score: 175.00 Matches: 29

Percent Similarity: 78.57% Conservative: 4

Best Local Similarity: 69.05% Mismatches: 9

Query Match: 22.91% Indels: 0

DB: 3 Gaps: 0

US-10-807-204-11 (1-396) x US-09-358-569D-13 (1-43)

259 CTGGCTCCATACACACTGGTGTAACAATAAAAACTAGATCTGCTCCGAATTCATC 318

1 LeuAlaTyrPheLeuHisTyrTyrAspLysAspAenThrCysSerMetPheVal 20

319 TATGCGGTGGCAGGGGAACAATAACAACTTCCAACTGAAGCTATCTGTCTGTGTCACC 378

21 TyrGlyGlyCysGlnGlyAenAenAenAenPheGlnSerLysAlaAenCysLeuAenThr 40

379 TGCAAA 384

41 CysLys 42

RESULT 12

US-09-358-569D-9

Sequence 9, Application US/09358569D

Patent No. 6294648

GENERAL INFORMATION:

APPLICANT: Delaria, Kathy

APPLICANT: Rocznik, Steve

APPLICANT: Davies, Christopher

TITLE OF INVENTION: Protein Having Proteinase Inhibitor Activity

FILE REFERENCE: MSB-7259

CURRENT APPLICATION NUMBER: US/09/358,569D

CURRENT FILING DATE: 1999-07-20

NUMBER OF SEQ ID NOS: 15

SOFTWARE: Patent In Ver. 2.0

SEQ ID NO 9

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; LENGTH: 54
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:derived from
; OTHER INFORMATION: EST sequence database
US-09-358-569D-9

Alignment Scores:
Pred. No.: 9.23e-11 Length: 54
Score: 175.00 Matches: 27
Percent Similarity: 68.52% Conservative: 10
Best Local Similarity: 50.00% Mismatches: 17
Query Match: 22.91% Indels: 0
DB: 3 Gaps: 0

US-10-807-204-11 (1-396) x US-09-358-569D-9 (1-54)
Qy 223 GATATATGCAGTATGCCACAGGAGCTGGCCCTGCCTGCCTCCATACACACTGGTGG 282
Db 1 AspleuCysGlnLeuProGlnAlaArgGlyProCysLysAlaAlaLeuLeuArgTyrPhe 20
Qy 283 TACAATAAAAACTAAGATCTGCTCGAATTCATCTATGCGGTGCGAGGGGAACAAT 342
Db 21 TyrAsnSerThrSerAsnAlaCysGluProPheThrTyrGlyGlyCysGlnGlyAsnAsn 40
Qy 343 AACAACTTCCAACTGAAGCTATCTGCTGCTGCACCTGCATA 384
Db 41 AsnAsnPheGluThrThrGluMetCysLeuArgIleCysGlu 54

RESULT 13
US-08-358-160-123
; Sequence 123, Application US/08358160
; Patent No. 5663143
; GENERAL INFORMATION:
; APPLICANT: LEY, Arthur C.
; APPLICANT: LADNER, Robert C.
; APPLICANT: GUTERMAN, Sonia K.
; APPLICANT: ROBERTS, Bruce L.
; APPLICANT: MARKLAND, William
; APPLICANT: KENT, Rachel B.
; TITLE OF INVENTION: ENGINEERED HUMAN-DERIVED KUNITZ
; TITLE OF INVENTION: DOMAINS THAT INHIBIT HUMAN NEUTROPHIL ELASTASE
; NUMBER OF SEQUENCES: 234
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W. Suite 300
; CITY: Washington
; STATE: District of Columbia
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/358,160
; FILING DATE: 16-DEC-1994
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/133,031
; FILING DATE: 13-OCT-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/009,319
; FILING DATE: 26-JAN-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/664,989
; FILING DATE: 01-MAR-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/487,063
; FILING DATE: 02-MAR-1990
; PRIOR APPLICATION DATA:
```

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; APPLICATION NUMBER: US 07/240,160
; FILING DATE: 02-SEP-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Cooper, Iver P.
; REGISTRATION NUMBER: 28,005
; REFERENCE/DOCKET NUMBER: LEY=1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; TELEX: 248633
; INFORMATION FOR SEQ ID NO: 123:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 67 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-358-160-123

Alignment Scores:
Pred. No.: 9.77e-11 Length: 67
Score: 175.00 Matches: 27
Percent Similarity: 68.52% Conservative: 10
Best Local Similarity: 50.00% Mismatches: 17
Query Match: 22.91% Indels: 0
DB: 1 Gaps: 0

US-10-807-204-11 (1-396) x US-08-358-160-123 (1-67)
Qy 223 GATATATGCAGTATGCCACAGGAGCTGGCCCTGCCTGCCTCCATACACACTGGTGG 282
Db 6 AspleuCysGlnLeuProGlnAlaArgGlyProCysLysAlaAlaLeuLeuArgTyrPhe 25
Qy 283 TACAATAAAAACTAAGATCTGCTCGAATTCATCTATGCGGTGCGAGGGGAACAAT 342
Db 26 TyrAsnSerThrSerAsnAlaCysGluProPheThrTyrGlyGlyCysGlnGlyAsnAsn 45
Qy 343 AACAACTTCCAACTGAAGCTATCTGCTGCTGCACCTGCATA 384
Db 46 AsnAsnPheGluThrThrGluMetCysLeuArgIleCysGlu 59

RESULT 14
US-08-358-160-17
; Sequence 17, Application US/08358160
; Patent No. 5663143
; GENERAL INFORMATION:
; APPLICANT: LEY, Arthur C.
; APPLICANT: LADNER, Robert C.
; APPLICANT: GUTERMAN, Sonia K.
; APPLICANT: ROBERTS, Bruce L.
; APPLICANT: MARKLAND, William
; APPLICANT: KENT, Rachel B.
; TITLE OF INVENTION: ENGINEERED HUMAN-DERIVED KUNITZ
; TITLE OF INVENTION: DOMAINS THAT INHIBIT HUMAN NEUTROPHIL ELASTASE
; NUMBER OF SEQUENCES: 234
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W. Suite 300
; CITY: Washington
; STATE: District of Columbia
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/358,160
; FILING DATE: 16-DEC-1994
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/133,031
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; FILING DATE: 13-OCT-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/009,319
; FILING DATE: 26-JAN-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/664,989
; FILING DATE: 01-MAR-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/487,063
; FILING DATE: 02-MAR-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/240,160
; FILING DATE: 02-SEP-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Cooper, Iver P.
; REGISTRATION NUMBER: 28,005
; REFERENCE/DOCKET NUMBER: LEY=1
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; TELEX: 248633
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 58 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-358-160-17

Alignment Scores:
Pred. No.: 1.55e-10 Length: 58
Score: 173.00 Matches: 28
Percent Similarity: 62.50% Conservative: 7
Best Local Similarity: 50.00% Mismatches: 21
Query Match: 22.64% Indels: 0
DB: 1 Gaps: 0

US-10-807-204-11 (1-396) x US-08-358-160-17 (1-58)
QY 217 AGAAGGATATATGCAGTATGCCAGGAGGCTGCGCTGCCCTCCATACACAC 276
Db 1 ArgProAspPheCysGlnLeuGlyTyrSerAlaGlyProCysAlaMetPheProArg 20
QY 277 TGGTGGTACAATAAATAAAGTATCGTCCGAATTCATCTATGGGGTGGCCAGGG 336
Db 21 TyrPheTyrAsnGlyThrSerMetAlaCysGluThrPheValTyrGlyCysMetGly 40
QY 337 AACATAACAACCTCCAACTGAAGCTATCTGTCTGGTCACCTGCAAA 384
Db 41 AsnGlyAsnAsnPheValThrGluLysAspCysLeuGlnThrCysArg 56

RESULT 15
US-08-358-160-18
; Sequence 18, Application US/08358160
; Patent No. 5663143
; GENERAL INFORMATION:
; APPLICANT: LEY, Arthur C.
; APPLICANT: LADNER, Robert C.
; APPLICANT: GUTERMAN, Sonia K.
; APPLICANT: ROBERTS, Bruce L.
; APPLICANT: MARKLAND, William
; APPLICANT: KENT, Rachel B.
; TITLE OF INVENTION: ENGINEERED HUMAN-DERIVED KUNITZ
; NUMBER OF SEQUENCES: 234
; CORRESPONDENCE ADDRESS:
; ADDRESS: 419 Seventh Street, N.W. Suite 300
; CITY: Washington
; STATE: District of Columbia
; COUNTRY: USA
; ZIP: 20004

; FILING DATE: 13-OCT-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/009,319
; FILING DATE: 26-JAN-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/664,989
; FILING DATE: 01-MAR-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/487,063
; FILING DATE: 02-MAR-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/240,160
; FILING DATE: 02-SEP-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Cooper, Iver P.
; REGISTRATION NUMBER: 28,005
; REFERENCE/DOCKET NUMBER: LEY=1
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; TELEX: 248633
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 58 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-358-160-17

Alignment Scores:
Pred. No.: 1.55e-10 Length: 58
Score: 173.00 Matches: 28
Percent Similarity: 62.50% Conservative: 7
Best Local Similarity: 50.00% Mismatches: 21
Query Match: 22.64% Indels: 0
DB: 1 Gaps: 0

US-10-807-204-11 (1-396) x US-08-358-160-17 (1-58)
QY 217 AGAAGGATATATGCAGTATGCCAGGAGGCTGCGCTGCCCTCCATACACAC 276
Db 1 ArgProAspPheCysGlnLeuGlyTyrSerAlaGlyProCysAlaMetPheProArg 20
QY 277 TGGTGGTACAATAAATAAAGTATCGTCCGAATTCATCTATGGGGTGGCCAGGG 336
Db 21 TyrPheTyrAsnGlyThrSerMetAlaCysGluThrPheValTyrGlyCysMetGly 40
QY 337 AACATAACAACCTCCAACTGAAGCTATCTGTCTGGTCACCTGCAAA 384
Db 41 AsnGlyAsnAsnPheValThrGluLysAspCysLeuGlnThrCysArg 56

RESULT 16
5466783-4
; Patent No. 5466783
; APPLICANT: Wun, Tze-Chien, Kretzmer, Kuniko K.; Broze,
; George J. Jr.
; TITLE OF INVENTION: HUMAN TISSUE FACTOR INHIBITOR
; NUMBER OF SEQUENCES: 26
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/93,285
; FILING DATE: 15-JUL-1993
```


RESULT 21
US-07-664-989B-48
; Sequence 48, Application US/07664989B
; Patent No. 5223409
; GENERAL INFORMATION:
; APPLICANT: Ladner, Robert Charles
; APPLICANT: Guterma, Sonia Kosow
; APPLICANT: Roberts, Bruce Lindsey
; APPLICANT: Markland, William
; APPLICANT: Ley, Arthur Charles
; APPLICANT: Kent, Rachel Baribault
; TITLE OF INVENTION: Directed Evolution of No. 5223409el
; NUMBER OF SEQUENCES: 121
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Browdy and Neimark
; STREET: 419 Seventh Street, N.W.
; CITY: Suite 300
; STATE: DC
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WORDPERFECT 4.2
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/664, 989B
; FILING DATE: 19910301
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US89/03731
; FILING DATE: 01-SEP-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/240,160
; FILING DATE: 02-SEP-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Cooper, Iver P.
; REGISTRATION NUMBER: 28005
; REFERENCE/DOCKET NUMBER: LADNER 7
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; INFORMATION FOR SEQ ID NO: 48:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 58 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-07-664-989B-48
Alignment Scores:
Pred. No.: 8.89e-10 Length: 58
Score: 166.00 Matches: 26
Percent Similarity: 61.82% Conservative: 8
Best Local Similarity: 47.27% Mismatches: 21
Query Match: 21.73% Indels: 0
DB: 1 Gaps: 0
US-10-807-204-11 (1-396) x US-07-664-989B-48 (1-58)
Qy 217 AGAAGATATATGAGTATGCCAGAGGCTGCGCCCTCGCTCCATACACAC 276
Db 1 ArgProaspPheCysLeuGluProProTyrThrGlyProCysValAlaMetPheProArg 20
Qy 277 TGGTGGTACATATAAACTAAGATCTGCTCCGAATTCATCTATGGCGTTGCCAGGG 336
Db 21 TyrPheTyrAsnAlaLysAlaGlyLeuCysGlnThrPheValTyrGlyGlyCysMetGly 40

Qy 337 AACAAATAACAACCTCCAACTGAAGCTATCTGTCTGTGTCACCTGC 381
Db 41 AsnGlyAsnAsnPhelysSerAlaGluAspCysMetArgThrCys 55
RESULT 22
US-07-664-989B-51
; Sequence 51, Application US/07664989B
; Patent No. 5223409
; GENERAL INFORMATION:
; APPLICANT: Ladner, Robert Charles
; APPLICANT: Guterma, Sonia Kosow
; APPLICANT: Roberts, Bruce Lindsey
; APPLICANT: Markland, William
; APPLICANT: Ley, Arthur Charles
; APPLICANT: Kent, Rachel Baribault
; TITLE OF INVENTION: Directed Evolution of No. 5223409el
; NUMBER OF SEQUENCES: 121
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Browdy and Neimark
; STREET: 419 Seventh Street, N.W.
; CITY: Suite 300
; STATE: DC
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WORDPERFECT 4.2
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/664, 989B
; FILING DATE: 19910301
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US89/03731
; FILING DATE: 01-SEP-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/487, 063
; FILING DATE: 02-MAR-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/240,160
; FILING DATE: 02-SEP-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Cooper, Iver P.
; REGISTRATION NUMBER: 28005
; REFERENCE/DOCKET NUMBER: LADNER 7
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; INFORMATION FOR SEQ ID NO: 51:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 58 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-07-664-989B-51
Alignment Scores:
Pred. No.: 8.89e-10 Length: 58
Score: 166.00 Matches: 26
Percent Similarity: 61.82% Conservative: 8
Best Local Similarity: 47.27% Mismatches: 21
Query Match: 21.73% Indels: 0
DB: 1 Gaps: 0
US-10-807-204-11 (1-396) x US-07-664-989B-51 (1-58)
Qy 217 AGAAGATATATGAGTATGCCAGAGGCTGCGCCCTCGCTCCATACACAC 276
Db 1 ArgProaspPheCysLeuGluProProTyrThrGlyProCysValAlaMetPheProArg 20

Qy 277 TGGTGGTACATAAATAAATAAAGATCTGCTCCGAATTCTATCTATGCGGTTGCCAGGG 336
Db 21 TyrPheTyrAsnAlaLysAlaGlyLeuCysGlnThrPheValTyrGlyGlyCysMetGly 40
Qy 337 AACAAATACAACTTCCAAACTGAAGCTATCTGCTGTCACCTGC 381
Db 41 AsnGlyAsnAsnPhelYsSerAlaGluAspCysMetArgThrCys 55

RESULT 23
US-08-358-160-1
; Sequence 1, Application US/08358160
; Patent No. 5663143
; GENERAL INFORMATION:
; APPLICANT: LEY, Arthur C.
; APPLICANT: LADNER, Robert C.
; APPLICANT: GUTERMAN, Sonia K.
; APPLICANT: ROBERTS, Bruce L.
; APPLICANT: MARKLAND, William
; APPLICANT: KENT, Rachel B.
; TITLE OF INVENTION: ENGINEERED HUMAN-DERIVED KUNITZ
; TITLE OF INVENTION: DOMAINS THAT INHIBIT HUMAN NEUTROPHIL ELASTASE
; NUMBER OF SEQUENCES: 234
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W. Suite 300
; CITY: Washington
; STATE: District of Columbia
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/358,160
; FILING DATE: 16-DEC-1994
; CLASSIFICATION: 514
; PRIOR APPLICATION NUMBER: US 08/133,031
; FILING DATE: 13-OCT-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/009,319
; FILING DATE: 26-JAN-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/664,989
; FILING DATE: 01-MAR-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/487,063
; FILING DATE: 02-MAR-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/240,160
; FILING DATE: 02-SEP-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Cooper, Iver P.
; REGISTRATION NUMBER: 28,005
; REFERENCE/DOCKET NUMBER: LEY=1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; TELEX: 248633
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 58 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-358-160-1

Alignment Scores: 8.89e-10 Length: 58
Pred. No.: 166.00 Matches: 26
Score:

Percent Similarity: 61.82% Conservative: 8
Best Local Similarity: 47.27% Mismatches: 21
Query Match: 21.73% Indels: 0
DB: 1 Gaps: 0

US-10-807-204-11 (1-396) x US-08-358-160-1 (1-58)
Qy 217 AGAAGGATATATGACAGTATGCGACAGAGGCTGGCCCTGCTGGCTCCATACACAC 276
Db 1 ArgProAspPheCysLeuGluProTyrThrGlyProCysValAlaMetPheProArg 20
Qy 277 TGGTGGTACATAAATAAATAAAGATCTGCTCCGAATTCTATCTATGCGGTTGCCAGGG 336
Db 21 TyrPheTyrAsnAlaLysAlaGlyLeuCysGlnThrPheValTyrGlyGlyCysMetGly 40
Qy 337 AACAAATACAACTTCCAAACTGAAGCTATCTGCTGTCACCTGC 381
Db 41 AsnGlyAsnAsnPhelYsSerAlaGluAspCysMetArgThrCys 55

RESULT 24
US-08-358-160-15
; Sequence 15, Application US/08358160
; Patent No. 5663143
; GENERAL INFORMATION:
; APPLICANT: LEY, Arthur C.
; APPLICANT: LADNER, Robert C.
; APPLICANT: GUTERMAN, Sonia K.
; APPLICANT: ROBERTS, Bruce L.
; APPLICANT: MARKLAND, William
; APPLICANT: KENT, Rachel B.
; TITLE OF INVENTION: ENGINEERED HUMAN-DERIVED KUNITZ
; TITLE OF INVENTION: DOMAINS THAT INHIBIT HUMAN NEUTROPHIL ELASTASE
; NUMBER OF SEQUENCES: 234
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W. Suite 300
; CITY: Washington
; STATE: District of Columbia
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/358,160
; FILING DATE: 16-DEC-1994
; CLASSIFICATION: 514
; PRIOR APPLICATION NUMBER: US 08/133,031
; FILING DATE: 13-OCT-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/009,319
; FILING DATE: 26-JAN-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/664,989
; FILING DATE: 01-MAR-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/487,063
; FILING DATE: 02-MAR-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/240,160
; FILING DATE: 02-SEP-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Cooper, Iver P.
; REGISTRATION NUMBER: 28,005
; REFERENCE/DOCKET NUMBER: LEY=1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; TELEX: 248633
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 58 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-358-160-15

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; SEQUENCE CHARACTERISTICS:
; LENGTH: 58 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-358-160-15

Alignment Scores:
Pred. No.: 8.89e-10 Length: 58
Score: 166.00 Matches: 27
Percent Similarity: 62.50% Conservative: 8
Best Local Similarity: 48.21% Mismatches: 21
Query Match: 21.73% Indels: 0
DB: 1 Gaps: 0

US-10-807-204-11 (1-396) x US-08-358-160-15 (1-58)

Qy 217 AGAAGGATATATGCGAGTATGCCACAGGAGGCTGGCCCTGCCTCCATACCACAC 276
Db 1 LysGluaspPheCysGlnLeuGlyTyrSerAlaGlyProCysValAlaMetPheProArg 20
Qy 277 TGGTGGTACATAAAAAAAGATCTGCTCCGAATTCATCTATGGCGGTGCCAGGGG 336
Db 21 TyrPheTyrAsnGlyThrSerMetAlaCysGlnThrPheGlnTyrGlyGlyCysMetGly 40
Qy 337 AACAAATACAACTCCAACTGAAGCTATCTGTCTGTCACTGCAAA 384
Db 41 AsnGlyAsnAsnPheValThrGluLysAspCysLeuGlnThrCysArg 56

RESULT 25
; Sequence 26, Application US/08358160
; Patent No. 5663143
; GENERAL INFORMATION:
; APPLICANT: LEY, Arthur C.
; APPLICANT: LADNER, Robert C.
; APPLICANT: GUTERMAN, Sonia K.
; APPLICANT: ROBERTS, Bruce L.
; APPLICANT: MARKLAND, William
; APPLICANT: KENT, Rachel B.
; TITLE OF INVENTION: ENGINEERED HUMAN-DERIVED KUNITZ
; TITLE OF INVENTION: DOMAINS THAT INHIBIT HUMAN NEUTROPHIL ELASTASE
; NUMBER OF SEQUENCES: 234
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W. Suite 300
; CITY: Washington
; STATE: District of Columbia
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/358,160
; FILING DATE: 16-DEC-1994
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/133,031
; FILING DATE: 13-OCT-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/009,319
; FILING DATE: 26-JAN-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/664,989
; FILING DATE: 01-MAR-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/487,063
; FILING DATE: 02-MAR-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/133,031

; APPLICATION NUMBER: US 07/240,160
; FILING DATE: 02-SEP-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Cooper, Iver P.
; REGISTRATION NUMBER: 28,005
; REFERENCE/DOCKET NUMBER: LEY=1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; TELEX: 248633
; INFORMATION FOR SEQ ID NO: 26:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 58 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-358-160-26

Alignment Scores:
Pred. No.: 8.89e-10 Length: 58
Score: 166.00 Matches: 26
Percent Similarity: 61.82% Conservative: 8
Best Local Similarity: 47.27% Mismatches: 21
Query Match: 21.73% Indels: 0
DB: 1 Gaps: 0

US-10-807-204-11 (1-396) x US-08-358-160-26 (1-58)

Qy 217 AGAAGGATATATGCGAGTATGCCACAGGAGGCTGGCCCTGCCTCCATACCACAC 276
Db 1 ArgProAspPheCysLeuGluProProTyrThrGlyProCysAlaLeaPheProArg 20
Qy 277 TGGTGGTACATAAAAAAAGATCTGCTCCGAATTCATCTATGGCGGTGCCAGGGG 336
Db 21 TyrPheTyrAsnAlaLysAlaGlyLeuCysGlnThrPheValTyrGlyGlyCysMetGly 40
Qy 337 AACAAATACAACTCCAACTGAAGCTATCTGTCTGTCACTGTC 381
Db 41 AsnGlyAsnAsnPheLysSerAlaGluAspCysMetArgThrCys 55

RESULT 26
; Sequence 27, Application US/08358160
; Patent No. 5663143
; GENERAL INFORMATION:
; APPLICANT: LEY, Arthur C.
; APPLICANT: LADNER, Robert C.
; APPLICANT: GUTERMAN, Sonia K.
; APPLICANT: ROBERTS, Bruce L.
; APPLICANT: MARKLAND, William
; APPLICANT: KENT, Rachel B.
; TITLE OF INVENTION: ENGINEERED HUMAN-DERIVED KUNITZ
; TITLE OF INVENTION: DOMAINS THAT INHIBIT HUMAN NEUTROPHIL ELASTASE
; NUMBER OF SEQUENCES: 234
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W. Suite 300
; CITY: Washington
; STATE: District of Columbia
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/358,160
; FILING DATE: 16-DEC-1994
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/133,031
; FILING DATE: 13-OCT-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/009,319
; FILING DATE: 26-JAN-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/664,989
; FILING DATE: 01-MAR-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/487,063
; FILING DATE: 02-MAR-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/133,031
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; FILING DATE: 13-OCT-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/009,319
; FILING DATE: 26-JAN-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/664,989
; FILING DATE: 01-MAR-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/487,063
; FILING DATE: 02-MAR-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/240,160
; FILING DATE: 02-SEP-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Cooper, Iver P.
; REGISTRATION NUMBER: 28,005
; REFERENCE/DOCKET NUMBER: LEY=1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; TELEX: 248633
; INFORMATION FOR SEQ ID NO: 27:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 62 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-358-160-27

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Alignment Scores:
Pred. No.: 9,048-10 Length: 62
Score: 166.00 Matches: 26
Percent Similarity: 61.82% Conservative: 8
Best Local Similarity: 47.27% Mismatches: 21
Query Match: 1 Indels: 0
Gaps: 0

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US-10-807-204-11 (1-396) x US-08-358-160-27 (1-62)

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QY 217 AGAAGGATATATGAGTATGCCAGGAGGCTGCGCTCCATACACAC 276
Db 5 ArgProAspPheCysLeuGluProProTyrThrGlyProCysIleAlaPheProArg 24
QY 277 TGGTGGTACATAAATAAAGTATCGTCCGAATTCATCTATGGCGGTGCCAGGG 336
Db 25 TyrPheTyrAsnAlaLysAlaGlyLeuCysGlnThrPheValTyrGlyCysMetGly 44
QY 337 AACATAACAACCTCCAACTGAAGCTATCTCTGTGGTCACCTGC 381
Db 45 AsnGlyAsnAsnPhelysSerAlaGluAspCysMetArgThrCys 59

```

```

RESULT 27
; Sequence 49, Application US/07664989B
; Patent No. 5223409
; GENERAL INFORMATION:
; APPLICANT: Ladner, Robert Charles
; APPLICANT: Guterman, Sonia Kosow
; APPLICANT: Roberts, Bruce Lindsay
; APPLICANT: Markland, William
; APPLICANT: Lev, Arthur Charles
; APPLICANT: Kent, Rachel Baribault
; TITLE OF INVENTION: Directed Evolution of No. 5223409el
; TITLE OF INVENTION: Binding Proteins
; NUMBER OF SEQUENCES: 121
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Browdy and Neimark
; STREET: 419 Seventh Street, N.W.
; CITY: Washington,
; STATE: DC
; COUNTRY: USA

```

```

; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WORDPERFECT 4.2
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/664,989B
; FILING DATE: 19910301
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US89/03731
; FILING DATE: 01-SEP-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/487,063
; FILING DATE: 02-MAR-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/240,160
; FILING DATE: 02-SEP-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Cooper, Iver P.
; REGISTRATION NUMBER: 28005
; REFERENCE/DOCKET NUMBER: LADNER 7
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; INFORMATION FOR SEQ ID NO: 49:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 58 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-07-664-989B-49

```

```

Alignment Scores:
Pred. No.: 1,148-09 Length: 58
Score: 165.00 Matches: 26
Percent Similarity: 61.82% Conservative: 8
Best Local Similarity: 47.27% Mismatches: 21
Query Match: 1 Indels: 0
Gaps: 0

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US-10-807-204-11 (1-396) x US-07-664-989B-49 (1-58)

```

QY 217 AGAAGGATATATGAGTATGCCAGGAGGCTGCGCTCCATACACAC 276
Db 1 ArgProAspPheCysLeuGluProProTyrThrGlyProCysValAlaIlePheProArg 20
QY 277 TGGTGGTACATAAATAAAGTATCGTCCGAATTCATCTATGGCGGTGCCAGGG 336
Db 21 TyrPheTyrAsnAlaLysAlaGlyLeuCysGlnThrPheValTyrGlyCysMetGly 40
QY 337 AACATAACAACCTCCAACTGAAGCTATCTCTGTGGTCACCTGC 381
Db 41 AsnGlyAsnAsnPhelysSerAlaGluAspCysMetArgThrCys 55

```

```

RESULT 28
; Sequence 24, Application US/08358160
; Patent No. 5663143
; GENERAL INFORMATION:
; APPLICANT: LEY, Arthur C.
; APPLICANT: LADNER, Robert C.
; APPLICANT: GUTERMAN, Sonia K.
; APPLICANT: ROBERTS, Bruce L.
; APPLICANT: MARKLAND, William
; APPLICANT: KENT, Rachel B.
; TITLE OF INVENTION: ENGINEERED HUMAN-DERIVED KUNITZ
; TITLE OF INVENTION: DOMAINS THAT INHIBIT HUMAN NEUTROPHIL ELASTASE
; NUMBER OF SEQUENCES: 234
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W. Suite 300

```

;
; CITY: Washington
; STATE: District of Columbia
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/358,160
; FILING DATE: 16-DEC-1994
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/133,031
; FILING DATE: 13-OCT-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/009,319
; FILING DATE: 26-JAN-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/664,989
; FILING DATE: 01-MAR-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/487,063
; FILING DATE: 02-MAR-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/240,160
; FILING DATE: 02-SEP-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Cooper, Iver P.
; REGISTRATION NUMBER: 28,005
; REFERENCE/DOCKET NUMBER: LEY=1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; TELEX: 248633
; INFORMATION FOR SEQ ID NO: 24:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 58 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-358-160-24

Alignment Scores:

Pred. No.:	1.14e-09	Length:	58
Score:	165.00	Matches:	26
Percent Similarity:	61.82%	Conservative:	8
Best Local Similarity:	47.27%	Mismatches:	21
Query Match:	21.60%	Indels:	0
DB:	1	Gaps:	0

US-10-807-204-11 (1-396) x US-08-358-160-24 (1-58)

Qy	217	AGAAAGGATATATGAGTATGCCACAGAGCTGGCCCTGCCTCCATACACAC	276
Db	1	ArgProaspPheCysLeuGluProProTyrThrGlyProCysValAlaIlePheProArg	20
Qy	277	TGGTGGTACATAAAAACTAAGATCTGCTCCGAATTCATCTATGGCGGTGCCAGGG	336
Db	21	TyrPheTyrAsnAlaLysAlaGlyLeuCysGlnThrPheValTyrGlyGlyCysMetGly	40
Qy	337	AACAATACAACTCCAAACTGAAGCTATCTGTCTGTGCACCTGC	381
Db	41	AsnGlyAsnAsnPheLysSerAlaGluAspCysMetArgThrCys	55

RESULT 29

US-08-358-160-9
; Sequence 9, Application US/08358160
; Patent No. 5663143
; GENERAL INFORMATION:
; APPLICANT: LEY, Arthur C.

;
; APPLICANT: LADNER, Robert C.
; APPLICANT: GUTERMAN, Sonia K.
; APPLICANT: ROBERTS, Bruce L.
; APPLICANT: MARKLAND, William
; APPLICANT: KENT, Rachel B.
; TITLE OF INVENTION: ENGINEERED HUMAN-DERIVED KUNITZ
; NUMBER OF SEQUENCES: 234
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W. Suite 300
; CITY: Washington
; STATE: District of Columbia
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/358,160
; FILING DATE: 16-DEC-1994
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/133,031
; FILING DATE: 13-OCT-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/009,319
; FILING DATE: 26-JAN-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/664,989
; FILING DATE: 01-MAR-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/487,063
; FILING DATE: 02-MAR-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/240,160
; FILING DATE: 02-SEP-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Cooper, Iver P.
; REGISTRATION NUMBER: 28,005
; REFERENCE/DOCKET NUMBER: LEY=1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; TELEX: 248633
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 58 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-358-160-9

Alignment Scores:

Pred. No.:	1.46e-09	Length:	58
Score:	164.00	Matches:	27
Percent Similarity:	62.50%	Conservative:	8
Best Local Similarity:	48.21%	Mismatches:	21
Query Match:	21.47%	Indels:	0
DB:	1	Gaps:	0

US-10-807-204-11 (1-396) x US-08-358-160-9 (1-58)

Qy	217	AGAAAGGATATATGAGTATGCCACAGAGCTGGCCCTGCCTCCATACACAC	276
Db	1	LysGluaspSerCysGlnLeuGlyTyrSerAlaGlyProCysValAlaMetPheProArg	20
Qy	277	TGGTGGTACATAAAAACTAAGATCTGCTCCGAATTCATCTATGGCGGTGCCAGGG	336
Db	21	TyrPheTyrAsnGlyThrSerMetAlaCysGluThrPheGlnTyrGlyGlyCysMetGly	40

QY 340 AATAACAACATTCCAAACTGAAGCTATCTGTCTGTCTCACCTGC 381

QY 340 AATAACAACTTCCAAACTGAAGCTATCTGTCTCTGGTACCTGC 38

pB 44 ArgAsnAsnPheAspThrGluGluTyrCysMetAlaValCys 57

RESULT 32

Lesikar, David D.
McFadden, Kathleen
Garrick, Brett L.
TITLE OF INVENTION: PROTEASE INHIBITOR PEPTIDES
NUMBER OF SEQUENCES: 228
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/234,873A
FILING DATE: 21-Jan-1999
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/829,876
FILING DATE: 02-APR-1997
APPLICATION NUMBER: 08/436,555
FILING DATE: 08-MAY-1995
ATTORNEY/AGENT INFORMATION:
NAME: Bent, Stephen
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 056324/0116
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 211:
SEQUENCE CHARACTERISTICS:
LENGTH: 61 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 211:
US-09-234-873A-211

Alignment Scores:
Pred. No.: 1.48e-09 Length: 61
Score: 164.00 Matches: 25
Percent Similarity: 62.96% Conservative: 9
Best Local Similarity: 46.30% Mismatches: 20
Query Match: 21.47% Indels: 0
DB: 4 Gaps: 0

US-10-807-204-11 (1-396) x US-09-234-873A-211 (1-61)

QY 220 AAGGATATATGCAGTATGCCACAGGAGCTGCCCTGCCTCCATACACACTGG 279
Db 4 ArgGluValCysSerGluGlnAlaGluThrGlyProCysArgAlaAlaIleGlnHisTrp 23
QY 280 TGGTACATAAAATACTAAGATCTGCTCCGAATTCATCTATGGCGGTTGCCAGGGGAC 339
Db 24 TyrPheAspValThrGluGlyLysCysAlaProPhePheThrGlyGlyCysGlyGlyAen 43
QY 340 AATAACAACCTCCAACTCAAGCTATCTGTGGTCACCTGC 381
Db 44 ArgAsnAsnPheAspThrGluGluTyrCysMetalAlaValCys 57

RESULT 35

US-09-234-873A-214
; Sequence 214, Application US/09234873A
; Patent No. 6613890
; GENERAL INFORMATION:
; APPLICANT: White, Tyler R.
; Damir, Deborah
; Lesikar, David D.

McFadden, Kathleen
Garrick, Brett L.
TITLE OF INVENTION: PROTEASE INHIBITOR PEPTIDES
NUMBER OF SEQUENCES: 228
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/234,873A
FILING DATE: 21-Jan-1999
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/829,876
FILING DATE: 02-APR-1997
APPLICATION NUMBER: 08/436,555
FILING DATE: 08-MAY-1995
ATTORNEY/AGENT INFORMATION:
NAME: Bent, Stephen
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 056324/0116
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 214:
SEQUENCE CHARACTERISTICS:
LENGTH: 61 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 214:
US-09-234-873A-214

Alignment Scores:
Pred. No.: 1.48e-09 Length: 61
Score: 164.00 Matches: 25
Percent Similarity: 62.96% Conservative: 9
Best Local Similarity: 46.30% Mismatches: 20
Query Match: 21.47% Indels: 0
DB: 4 Gaps: 0

US-10-807-204-11 (1-396) x US-09-234-873A-214 (1-61)

QY 220 AAGGATATATGCAGTATGCCACAGGAGCTGCCCTGCCTCCATACACACTGG 279
Db 4 ArgGluValCysSerGluGlnAlaGluThrGlyProCysArgAlaAlaIleGlnHisTrp 23
QY 280 TGGTACATAAAATACTAAGATCTGCTCCGAATTCATCTATGGCGGTTGCCAGGGGAC 339
Db 24 TyrPheAspValThrGluGlyLysCysAlaProPhePheThrGlyGlyCysArgGlyAen 43
QY 340 AATAACAACCTCCAACTCAAGCTATCTGTGGTCACCTGC 381
Db 44 ArgAsnAsnPheAspThrGluGluTyrCysMetalAlaValCys 57

RESULT 36

US-07-664-989B-84
; Sequence 84, Application US/07664989B
; Patent No. 5223409
; GENERAL INFORMATION:
; APPLICANT: Ladner, Robert Charles
; APPLICANT: Guterman, Sonia Kosow
; APPLICANT: Roberts, Bruce Lindsay
; APPLICANT: Markland, William

```

1  APPLICANT: LEY, Arthur C.
2  APPLICANT: LADNER, Robert C.
3  APPLICANT: GUTERMAN, Sonia K.
4  APPLICANT: ROBERTS, Bruce L.
5  APPLICANT: MARKLAND, William
6  APPLICANT: KENT, Rachel B.
7  TITLE OF INVENTION: ENGINEERED HUMAN-DERIVED KUNITZ
8  TITLE OF INVENTION: DOMAINS THAT INHIBIT HUMAN NEUTROPHIL ELASTASE
9  NUMBER OF SEQUENCES: 234
10 CORRESPONDENCE ADDRESS:
11 ADDRESSES: BROWDY AND NEIMARK
12 STREET: 419 Seventh Street, N.W. Suite 300
13 CITY: Washington
14 STATE: District of Columbia
15 COUNTRY: USA
16 ZIP: 20004
17 COMPUTER READABLE FORM:
18 MEDIUM TYPE: Floppy disk
19 COMPUTER: IBM PC compatible
20 OPERATING SYSTEM: PC-DOS/MS-DOS
21 SOFTWARE: PatentIn Release #1.0, Version #1.25
22 CURRENT APPLICATION DATA:
23 APPLICATION NUMBER: US/08/358,160
24 FILING DATE: 16-DEC-1994
25 CLASSIFICATION: 514
26 PRIOR APPLICATION DATA:
27 APPLICATION NUMBER: US 08/133,031
28 FILING DATE: 13-OCT-1993
29 PRIOR APPLICATION DATA:
30 APPLICATION NUMBER: US 08/009,319
31 FILING DATE: 26-JAN-1993
32 PRIOR APPLICATION DATA:
33 APPLICATION NUMBER: US 07/664,989
34 FILING DATE: 01-MAR-1991
35 PRIOR APPLICATION DATA:
36 APPLICATION NUMBER: US 07/487,063
37 FILING DATE: 02-MAR-1990
38 PRIOR APPLICATION DATA:
39 APPLICATION NUMBER: US 07/240,160
40 FILING DATE: 02-SEP-1988
41 ATTORNEY/AGENT INFORMATION:
42 NAME: Cooper, Iver P.
43 REGISTRATION NUMBER: 28,005
44 REFERENCE/DOCKET NUMBER: LEY=1
45 TELECOMMUNICATION INFORMATION:
46 TELEPHONE: 202-628-5197
47 TELEFAX: 202-737-3528
48 TELEX: 248633
49 INFORMATION FOR SEQ ID NO: 12:
50 SEQUENCE CHARACTERISTICS:
51 LENGTH: 58 amino acids
52 TYPE: amino acid
53 STRANDEDNESS: single
54 TOPOLOGY: linear
55 MOLECULE TYPE: protein
56 US-08-358-160-12
57
58 Alignment Scores:
59 Pred. No.: 1.88e-09 Length: 58
60 Score: 163.00 Matches: 27
61 Percent Similarity: 58.93% Conservative: 6
62 Best Local Similarity: 48.21% Mismatches: 23
63 Query Match: 21.34% Indels: 0
64 DB: Gaps: 0
65
66 US-10-807-204-11 (1-396) x US-08-358-160-12 (1-58)
67
68 Qy 217 AGAAGGATATATGAGTATGCCACAGAGCGTGGCCCTGCTGCCTCCATACCACAC 276
69 Db 1 ArgProAspPheCysGlnLeuGlyTyrSerThrGlyProCysValIleMetPheProArg 20
70 Qy 277 TGGTGGTACAAATAAAAAAACAATGAGATGTCCTCCGAATTCACTATATGCGCGTTGCCAGGGG 336

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Db 21 TyrPheTyraAaGlyThrSerMetAlaCysGluThrPheGlnTyrglyGlyCysMetGly 40
QY 337 AACAAACAACTCCAACTGAAGCTATCTGCTGGTCACTGCAAA 384
Db 41 AaGlyAaAaPheValThrGluLysAspCysLeuGlnThrCysArg 56
RESULT 38
US-08-358-160-61
; Sequence 61, Application US/08358160
; Patent No. 5663143
; GENERAL INFORMATION:
; APPLICANT: LEY, Arthur C.
; APPLICANT: LADNER, Robert C.
; APPLICANT: GUTERMAN, Sonia K.
; APPLICANT: ROBERTS, Bruce L.
; APPLICANT: MARKLAND, William
; APPLICANT: KENT, Rachel B.
; TITLE OF INVENTION: ENGINEERED HUMAN-DERIVED KUNITZ
; TITLE OF INVENTION: DOMAINS THAT INHIBIT HUMAN NEUTROPHIL ELASTASE
; NUMBER OF SEQUENCES: 234
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W. Suite 300
; CITY: Washington
; STATE: District of Columbia
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/358,160
; FILING DATE: 16-DEC-1994
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/133,031
; FILING DATE: 13-OCT-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/009,319
; FILING DATE: 26-JAN-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/664,989
; FILING DATE: 01-MAR-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/487,063
; FILING DATE: 02-MAR-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/240,160
; FILING DATE: 02-SEP-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Cooper, Iver P.
; REGISTRATION NUMBER: 28,005
; REFERENCE/DOCKET NUMBER: LEY=1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; TELEX: 248633
; INFORMATION FOR SEQ ID NO: 61:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 58 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-358-160-61
Alignment Scores:
Pred. No.: 1.88e-09 Length: 58
Score: 163.00 Matches: 26
Percent Similarity: 61.82% Conservative: 8
Best Local Similarity: 47.27% Mismatches: 21

Query Match: 21.34% Indels: 0
DB: 1 Gaps: 0
US-10-807-204-11 (1-396) x US-08-358-160-61 (1-58)
QY 217 AGAAAGGATATATGTCAGTATGCCACAGAGGCTGGCCCTGCTGCCTCCATACCACAC 276
Db 1 ArgProAspPheCysLeuGluProProTyThrGlyProCysValAlaMetPheProArg 20
QY 277 TGTGTGTACATAAATAAACTAAGATCTGTCCGAATTCATCTATATGCGGTGTCAGGGG 336
Db 21 TyrPheTyraAaLysAlaGlyLeuCysGlnThrPheMetTyrglyGlyCysGlnGly 40
QY 337 AACAAACAACTCCAACTGAAGCTATCTGTCTGCTCACTGC 381
Db 41 LysGlyAaAaPheLysSerAlaGluAspCysMetArgThrCys 55
RESULT 39
US-08-463-155A-56
; Sequence 56, Application US/08463155A
; Patent No. 5780265
; GENERAL INFORMATION:
; APPLICANT: Dennis, Mark S.
; APPLICANT: Lazarus, Robert A.
; TITLE OF INVENTION: KUNITZ TYPE PLASMA KALLIKREIN INHIBITORS
; NUMBER OF SEQUENCES: 72
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/463,155A
; FILING DATE: 05-Jun-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Kubinec, Jeffrey S.
; REGISTRATION NUMBER: 36,575
; REFERENCE/DOCKET NUMBER: P0944
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/225-8228
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 56:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 58 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
US-08-463-155A-56
Alignment Scores:
Pred. No.: 1.88e-09 Length: 58
Score: 163.00 Matches: 26
Percent Similarity: 62.98% Conservative: 8
Best Local Similarity: 48.15% Mismatches: 20
Query Match: 21.34% Indels: 0
DB: 1 Gaps: 0
US-10-807-204-11 (1-396) x US-08-463-155A-56 (1-58)
QY 220 AAGGATATATGCGTATGCCACAGAGGCTGGCCCTGCTGCCTCCATACCACACTGG 279
Db 2 ArgGluValCysSerGluGlnAlaGluAspGlyProCysArgAlaAlaIleProArgTrp 21
QY 280 TGGTACATAAATAAACTAAGATCTGTCCGAAATTCATCTATGCGGTGTCAGGGGAC 339

```
Db      22 TyrPheAspValThrGluGlyLysCysAlaProPheIleTyrGlyGlyCysGlyGlyAsn 41
Qy      340 AATAACAACCTTCCAAACTGAAGCTATCTGCTGTCACCTGC 381
Db      42 ArgAsnAenPheAspThrGluGluTyrCysAlaAlaValCys 55
RESULT 40
US-08-463-432B-56
; Sequence 56, Application US/08463432B
; Patent No. 5786328
; GENERAL INFORMATION:
; APPLICANT: Dennis, Mark S.
; APPLICANT: Lazarus, Robert A.
; TITLE OF INVENTION: KUNITZ TYPE PLASMA KALLIKREIN INHIBITORS
; NUMBER OF SEQUENCES: 72
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/463.432B
; FILING DATE: 05-Jun-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Kubinec, Jeffrey S.
; REGISTRATION NUMBER: 36,575
; REFERENCE/DOCKET NUMBER: P0944-2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/225-8228
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 56:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 58 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
US-08-463-432B-56
Alignment Scores:
Pred. No.: 1.88e-09 Length: 58
Score: 163.00 Matches: 26
Percent Similarity: 62.96% Conservative: 8
Best Local Similarity: 48.15% Mismatches: 20
Query Match: 21.34% Indels: 0
DB: 1 Gaps: 0
US-10-807-204-11 (1-396) x US-08-463-432B-56 (1-58)
Qy      220 AAGATATATGCAGTATGCCACAGAGGCTGGCCCTGCTGCCTCATACCACACTGG 279
Db      2 ArgGluValCysSerGluGlnAlaGluAspGlyProCysArgAlaAlaIleProArgTrp 21
Qy      280 TGGTACATAAAAAAACTAAGATCTGCTCCGAATTCATCTATGGCGGTGGCAGGGGAAC 339
Db      22 TyrPheAspValThrGluGlyLysCysAlaProPheIleTyrGlyGlyCysGlyGlyAsn 41
Qy      340 AATAACAACCTTCCAAACTGAAGCTATCTGCTGTCACCTGC 381
Db      42 ArgAsnAenPheAspThrGluGluTyrCysAlaAlaValCys 55
RESULT 41
US-08-676-124-69
; Sequence 69, Application US/08676124
; Patent No. 6010880
; GENERAL INFORMATION:
```

```
; APPLICANT: MARKLAND, William
; APPLICANT: LADNER, Robert Charles
; TITLE OF INVENTION: INHIBITORS OF HUMAN PLASMIN DERIVED
; NUMBER OF SEQUENCES: 137
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Browdy and Neimark
; STREET: 419 Seventh Street N.W., Ste. 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: United States of America
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/676,124
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/00298
; FILING DATE: 11-JAN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/179,658
; FILING DATE: 11-JAN-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/208,265
; FILING DATE: 10-MAR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: COOPER, IVER P.
; REGISTRATION NUMBER: 28,005
; REFERENCE/DOCKET NUMBER: MARKLAND=3B
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; INFORMATION FOR SEQ ID NO: 69:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 58 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-676-124-69
Alignment Scores:
Pred. No.: 1.88e-09 Length: 58
Score: 163.00 Matches: 25
Percent Similarity: 62.26% Conservative: 8
Best Local Similarity: 47.17% Mismatches: 20
Query Match: 21.34% Indels: 0
DB: 3 Gaps: 0
US-10-807-204-11 (1-396) x US-08-676-124-69 (1-58)
Qy      223 GATATATGCAGTATGCCACAGAGGCTGGCCCTGCTGCCTCATACCACACTGGTGG 282
Db      3 AspIleCysLysLeuProLysAspThrGlyProCysArgAlaArgPheAspLysTrpTyr 22
Qy      283 TACAATAAAAAAACTAAGATCTGCTCCGAATTCATCTATGGCGGTGGCAGGGGAACAAT 342
Db      23 TyrAspProAsnThrLysSerCysGluGluPheValTyrGlyGlyCysGlyGlyAsnGlu 42
Qy      343 AACAACTTCCAAACTGAAGCTATCTGCTGTCACCTGC 381
Db      43 AsnLysPheGlySerGlnLysGluCysGluLysValCys 55
RESULT 42
US-09-414-878-69
; Sequence 69, Application US/09414878
; Patent No. 6071723
; GENERAL INFORMATION:
```


APPLICANT: DYAX CORP
APPLICANT: MARKLAND, William
APPLICANT: LADNER, Robert C
TITLE OF INVENTION: Inhibitors of Human Plamin Derived
TITLE OF INVENTION: From The Kunitz Domains
NUMBER OF SEQUENCES: 139
CORRESPONDENCE ADDRESS:
ADDRESSEE: Yankwich & Associates
STREET: 130 Bishop Allen Drive
CITY: Cambridge
STATE: Massachusetts
COUNTRY: USA
ZIP: 02139
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5-inch diskette
COMPUTER: IBM PC compatible
OPERATING SYSTEM: Microsoft Windows 98
SOFTWARE: Microsoft Word 97 SR-1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/414,878
FILING DATE: (concurrently herewith)
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/240,136
FILING DATE: 29-JAN-1999
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/676,124
FILING DATE: 07-JAN-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/00298
FILING DATE: 11-JAN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/208,265
FILING DATE: 10-MAR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/179,685
FILING DATE: 11-JAN-1994
ATTORNEY/AGENT INFORMATION:
NAME: YANKWICH, Leon R
REGISTRATION NUMBER: 30,237
REFERENCE/DOCKET NUMBER: DYX-007.2P US-2
TELEPHONE: 617-491-4343
TELEFAX: 617-491-8801
INFORMATION FOR SEQ ID NO: 69:
SEQUENCE CHARACTERISTICS:
LENGTH: 58 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-414-878-69

Alignment Scores:
Pred. No.: 1,88e-09 Length: 58
Score: 163.00 Matches: 25
Percent Similarity: 62.26% Conservative: 8
Best Local Similarity: 47.17% Mismatches: 20
Query Match: 21.34% Indels: 0
DB: 3 Gaps: 0

US-10-807-204-11 (1-396) x US-09-414-878-69 (1-58)

QY 223 GATATATGAGTATGCCACAGAGGCTGGCCCTGCTCCATACACACTGGTGG 282
Db 3 AsplleCysleuProllysAspThrGlyProCysArgAlaArgPheAspLysTyrTyr 22
QY 283 TACAATAAAAACTAAGATCTCTCCGAATTCATCTATGGCGGTGGCCAGGGGAACAT 342
Db 23 TyrAspProAsnThrLysSerCysGluGluPheValTyrGlyGlyCysGlyAenGlu 42

QY 343 AACAACTTCCAAACTGAAGCTATCTGTCTGGTGCACCTGC 381
Db 43 AsnLysPheGlySerGlnLysGluCysGluLysValCys 55
RESULT 43
US-09-240-136-69
Sequence 69, Application US/09240136
Patent No. 6103499
GENERAL INFORMATION:
APPLICANT: DYAX CORP
APPLICANT: MARKLAND, William
APPLICANT: LADNER, Robert C
TITLE OF INVENTION: Inhibitors of Human Plamin Derived
TITLE OF INVENTION: From The Kunitz Domains
NUMBER OF SEQUENCES: 139
CORRESPONDENCE ADDRESS:
ADDRESSEE: Yankwich & Associates
STREET: 130 Bishop Allen Drive
CITY: Cambridge
STATE: Massachusetts
COUNTRY: USA
ZIP: 02139
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5-inch diskette
COMPUTER: IBM PC compatible
OPERATING SYSTEM: Microsoft Windows 98
SOFTWARE: Microsoft Word 97 SR-1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/240,136
FILING DATE: (concurrently herewith)
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/676,124
FILING DATE: 07-JAN-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/00298
FILING DATE: 11-JAN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/208,265
FILING DATE: 10-MAR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/179,685
FILING DATE: 11-JAN-1994
ATTORNEY/AGENT INFORMATION:
NAME: YANKWICH, Leon R
REGISTRATION NUMBER: 30,237
REFERENCE/DOCKET NUMBER: DYX-007.2P US-1
TELEPHONE: 617-491-4343
TELEFAX: 617-491-8801
INFORMATION FOR SEQ ID NO: 69:
SEQUENCE CHARACTERISTICS:
LENGTH: 58 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-240-136-69
Alignment Scores:
Pred. No.: 1,88e-09 Length: 58
Score: 163.00 Matches: 25
Percent Similarity: 62.26% Conservative: 8
Best Local Similarity: 47.17% Mismatches: 20
Query Match: 21.34% Indels: 0
DB: 3 Gaps: 0
US-10-807-204-11 (1-396) x US-09-240-136-69 (1-58)
QY 223 GATATATGAGTATGCCACAGAGGCTGGCCCTGCTCCATACACACTGGTGG 282

Db 3 AspileCysLysLeuProLysAspThrGlyProCysArgAlaAaPheAspLysTrpTyr 22
Qy 283 TACAATAAAAAAAGATCTGCTCCGAATTCATCTATGCGGTGCGAGGGGAACAAT 342
Db 23 TyrAspProAnthrLysSerCysGluGluPheValTyrGlyGlyCysGlyGlyAsnGlu 42
Qy 343 AACAACTTCCAAACTGAAGCTATCTGCTGCTGCACCTGC 381
Db 43 AsnLysPheGlySerGlnLysGluCysGluLysValCys 55

RESULT 44

US-09-638-770A-69
; Sequence 69, Application US/09638770A
; Patent No. 6423498
; GENERAL INFORMATION:
; APPLICANT: DYAX CORP
; MARKLAND, William
; LADNER, Robert C
; TITLE OF INVENTION: Inhibitors of Human Plasmin Derived
; From The Kunitz Domains
; NUMBER OF SEQUENCES: 140
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Yankwich & Associates
; STREET: 130 Bishop Allen Drive
; CITY: Cambridge
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02139

COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5-inch diskette
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: Microsoft Windows 98
; SOFTWARE: Microsoft Word 97 SR-1

CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/638,770A
; FILING DATE: 15-Aug-2000
; CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/676,124
; FILING DATE: 07-JAN-1997
; APPLICATION NUMBER: PCT/US95/00298
; FILING DATE: 11-JAN-1995
; APPLICATION NUMBER: 08/208,265
; FILING DATE: 10-MAR-1994
; APPLICATION NUMBER: 08/179,685
; FILING DATE: 11-JAN-1994

ATTORNEY/AGENT INFORMATION:
; NAME: ZWICKER, Kenneth P
; REGISTRATION NUMBER: 43,310
; REFERENCE/DOCKET NUMBER: DYX-007.2P US-1
; TELEPHONE: 617-491-4343
; TELEFAX: 617-491-8801

INFORMATION FOR SEQ ID NO: 69:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 58 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 69:
US-09-638-770A-69

Alignment Scores:
Pred. No.: 1.88e-09 Length: 58
Score: 163.00 Matches: 25
Percent Similarity: 62.26% Conservative: 8
Best Local Similarity: 47.17% Mismatches: 20
Query Match: 21.34% Indels: 0
DB: 4 Gaps: 0

US-10-807-204-11 (1-396) x US-09-638-770A-69 (1-58)

Qy 223 GATATATGCAAGTATGCCACAGGAGCTGCGCCTGCTCCATACACACTGGTGG 282
Db 3 AspileCysLysLeuProLysAspThrGlyProCysArgAlaAaPheAspLysTrpTyr 22
Qy 283 TACAATAAAAAAAGATCTGCTCCGAATTCATCTATGCGGTGCGAGGGGAACAAT 342
Db 23 TyrAspProAnthrLysSerCysGluGluPheValTyrGlyGlyCysGlyGlyAsnGlu 42
Qy 343 AACAACTTCCAAACTGAAGCTATCTGCTGCTGCACCTGC 381
Db 43 AsnLysPheGlySerGlnLysGluCysGluLysValCys 55

RESULT 45

US-08-829-876-180
; Sequence 180, Application US/08829876
; Patent No. 5962266
; GENERAL INFORMATION:
; APPLICANT: White, Tyler R.
; APPLICANT: Damm, Deborah
; APPLICANT: Lesikar, David D.
; APPLICANT: McFadden, Kathleen
; APPLICANT: Garrick, Brett L.
; TITLE OF INVENTION: PROTEASE INHIBITOR PEPTIDES
; NUMBER OF SEQUENCES: 228
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109

COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/829,876
; FILING DATE:

CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/436,555
; FILING DATE: 08-MAY-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Pelto, Don J.
; REGISTRATION NUMBER: 33,754
; REFERENCE/DOCKET NUMBER: 56324/106/SCNO
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136

INFORMATION FOR SEQ ID NO: 180:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 61 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-829-876-180

Alignment Scores:
Pred. No.: 1.9e-09 Length: 61
Score: 163.00 Matches: 25
Percent Similarity: 61.11% Conservative: 8
Best Local Similarity: 46.30% Mismatches: 21
Query Match: 21.34% Indels: 0
DB: 2 Gaps: 0

US-10-807-204-11 (1-396) x US-08-829-876-180 (1-61)

Qy 220 AAGATATATGCAAGTATGCCACAGGAGCTGCGCCTGCTCCATACACACTGG 279
Db 4 ArgGluValCysSerGluGlnAlaGluThrGlyProCysArgAlaGlyIleProArgTrp 23

Db 24 TyrPheaspValThrGluGlyLysCysAlaProPhePheTyrGlyGlyCysGlyGlyAsn 43
Qy 340 AATAACAACACTTCCAAACTGAAGTATCTGTCTGTGTCACCTGC 381
Db 44 ArgAsnAenPheaspThrGluGlyLysCysMetAlaValCys 57
RESULT 47
US-09-234-874A-180
; Sequence 180, Application US/09234874A
; Patent No. 6376648
; GENERAL INFORMATION:
; APPLICANT: White, Tyler R.
; Damm, Deborah
; Lesikar, David D.
; McFadden, Kathleen
; Garrick, Brett L.
; TITLE OF INVENTION: PROTEASE INHIBITOR PEPTIDES
; NUMBER OF SEQUENCES: 228
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/234.874A
; FILING DATE: 11-Jun-2001
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/436.555
; FILING DATE: 08-MAY-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Bent, Stephen
; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 056324/0106
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 180:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 61 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 180:
US-09-234-874A-180
Alignment Scores:
Pred. No.: 1.9e-09 Length: 61
Score: 163.00 Matches: 25
Percent Similarity: 61.11% Conservative: 8
Best Local Similarity: 46.30% Mismatches: 21
Query Match: 21.34% Indels: 0
DB: 3 Gaps: 0
US-10-807-204-11 (1-396) x US-09-234-874A-180 (1-61)
Qy 220 AAGGATATATGCAGTATGCCACAGGAGCTGCGCCCTGCCTCATACACACTGG 279
Db 4 ArgGluValCysSerGluGlnAlaGluThrGlyProCysArgAlaGlyLeuProArgTrp 23
Qy 280 TGGTACAATAAAAAAATAAGATCTGTCTCGGAATTCATCTATGGCGGTGGCCAGGGGAAC 339
Db 24 TyrPheaspValThrGluGlyLysCysAlaProPhePheTyrGlyGlyCysGlyGlyAsn 43
Qy 340 AATAACAACACTTCCAAACTGAAGTATCTGTCTGTGTCACCTGC 381

Qy 280 TGGTACAATAAAAAAATAAGATCTGTCTCGGAATTCATCTATGGCGGTGGCCAGGGGAAC 339
Db 24 TyrPheaspValThrGluGlyLysCysAlaProPhePheTyrGlyGlyCysGlyGlyAsn 43
Qy 340 AATAACAACACTTCCAAACTGAAGTATCTGTCTGTGTCACCTGC 381
Db 44 ArgAsnAenPheaspThrGluGlyLysCysMetAlaValCys 57
RESULT 46
US-08-829-876-218
; Sequence 218, Application US/08829876
; Patent No. 5962266
; GENERAL INFORMATION:
; APPLICANT: White, Tyler R.
; Damm, Deborah
; Lesikar, David D.
; McFadden, Kathleen
; Garrick, Brett L.
; TITLE OF INVENTION: PROTEASE INHIBITOR PEPTIDES
; NUMBER OF SEQUENCES: 228
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/829.876
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/436.555
; FILING DATE: 08-MAY-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Felto, Don J.
; REGISTRATION NUMBER: 33,754
; REFERENCE/DOCKET NUMBER: 56324/106/SCNO
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 218:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 61 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-829-876-218
Alignment Scores:
Pred. No.: 1.9e-09 Length: 61
Score: 163.00 Matches: 25
Percent Similarity: 64.81% Conservative: 10
Best Local Similarity: 46.30% Mismatches: 19
Query Match: 21.34% Indels: 0
DB: 2 Gaps: 0
US-10-807-204-11 (1-396) x US-08-829-876-218 (1-61)
Qy 220 AAGGATATATGCAGTATGCCACAGGAGCTGCGCCCTGCCTCATACACACTGG 279
Db 4 ArgGluValCysSerGluGlnAlaGluThrGlyProCysArgAlaGlyLeuTrp 23
Qy 280 TGGTACAATAAAAAAATAAGATCTGTCTCGGAATTCATCTATGGCGGTGGCCAGGGGAAC 339

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US-09-234-873A-218
; Sequence 218, Application US/09234873A
; Patent No. 6613890
; GENERAL INFORMATION:
; APPLICANT: White, Tyler R.
; Damm, Deborah
; Lesikar, David D.
; McFadden, Kathleen
; Garrick, Brett L.
; TITLE OF INVENTION: PROTEASE INHIBITOR PEPTIDES
; NUMBER OF SEQUENCES: 228
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/234,873A
; FILING DATE: 21-Jan-1999
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/829,876
; FILING DATE: 02-APR-1997
; APPLICATION NUMBER: 08/436,555
; FILING DATE: 08-MAY-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Bent, Stephen
; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 056324/0116
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 218:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 61 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 218:
US-09-234-873A-218

Alignment Scores:
Pred. No.: 1.9e-09 Length: 61
Score: 163.00 Matches: 25
Percent Similarity: 64.81% Conservative: 10
Best Local Similarity: 46.30% Mismatches: 19
Query Match: 21.34% Indels: 0
DB: 4 Gaps: 0

US-10-807-204-11 (1-396) x US-09-234-873A-218 (1-61)
QY 220 AAGGATATATGAGTATGCCACAGGAGGCTGGCCCTGCTGCCTCCATACCACTGG 279
Db 4 ArgGluValCysSerGluGlnAlaGluSerGlyProCysArgAlaAlaIleTyrHisTrp 23
QY 280 TGGTACAATAAATAAACTAAGATCGCTCGAATTCATCTATGGCGGTGCCAGGGGAAC 339
Db 24 TyrPheAspValThrGluGlyLysCysAlaProPhePheTyrGlyGlyCysGlyGlyAsn 43
QY 340 AATAACAACATCCAACTGAAGCTATCTGTCTGTCACCTGC 381
Db 44 ArgAsnAsnPheAspThrGluGluTyrCysMetAlaValCys 57

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Delop 6.0 , Delext 7.0

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Maximum Match 100%

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-FGAPOP=6 -FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

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13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep.*
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16: /cgn2_6/ptodata/2/pubpaa/US10D_PUBCOMB.pep.*
17: /cgn2_6/ptodata/2/pubpaa/US10E_PUBCOMB.pep.*
18: /cgn2_6/ptodata/2/pubpaa/US10F_NEW_PUB.pep.*
19: /cgn2_6/ptodata/2/pubpaa/US11A_PUBCOMB.pep.*
20: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep.*
21: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*
22: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	741	97.0	131	16	US-10-807-204-1	Sequence 1, Appl
2	741	97.0	131	16	US-10-807-204-12	Sequence 12, Appl
3	739	96.7	131	16	US-10-807-204-15	Sequence 15, Appl
4	613	80.2	106	16	US-10-807-204-2	Sequence 2, Appl
5	559	73.2	98	16	US-10-807-204-9	Sequence 9, Appl
6	480	62.8	136	16	US-10-807-204-16	Sequence 16, Appl
7	455	59.6	133	9	US-09-853-161-75	Sequence 75, Appl
8	455	59.6	133	9	US-09-852-659A-75	Sequence 75, Appl
9	455	59.6	133	9	US-09-852-797-75	Sequence 75, Appl
10	455	59.6	133	15	US-10-058-993-75	Sequence 75, Appl
11	455	59.6	133	16	US-10-807-204-13	Sequence 13, Appl
12	412	53.9	86	17	US-10-480-988-21	Sequence 21, Appl
13	412	53.9	101	15	US-10-276-774-2606	Sequence 2606, Ap
14	389.5	51.0	117	9	US-09-852-659A-119	Sequence 119, App
15	389.5	51.0	117	15	US-10-058-993-120	Sequence 120, App
16	388	50.8	102	9	US-09-852-659A-120	Sequence 120, App
17	388	50.8	102	15	US-10-058-993-121	Sequence 121, App
18	386	50.5	134	16	US-10-807-204-14	Sequence 14, Appl
19	246	32.2	43	16	US-10-807-204-5	Sequence 5, Appl
20	236	30.9	58	17	US-10-361-997-5	Sequence 21, Appl
21	236	30.9	58	17	US-10-331-153-21	Sequence 118, App
22	219	28.7	51	15	US-10-058-993-118	Sequence 48, Appl
23	189.5	24.8	759	17	US-10-825-692-48	Sequence 160, App
24	184	24.1	64	10	US-09-896-095-160	Sequence 103, App
25	184	24.1	64	14	US-10-038-722-103	Sequence 17, Appl
26	184	24.1	64	15	US-10-115-134-17	Sequence 3, Appl
27	180.5	23.6	571	14	US-10-369-736-3	Sequence 49, Appl
28	180.5	23.6	571	14	US-10-369-738-49	Sequence 3, Appl
29	180.5	23.6	571	14	US-10-369-738-3	Sequence 49, Appl
30	180.5	23.6	571	14	US-10-369-738-49	Sequence 3, Appl
31	180.5	23.6	571	19	US-11-028-058-3	Sequence 49, Appl
32	180.5	23.6	571	19	US-11-028-058-49	Sequence 7, Appl
33	180	23.6	33	16	US-10-807-204-7	Sequence 10, Appl
34	180	23.6	33	16	US-10-038-722-5	Sequence 5, Appl
35	177	23.2	58	14	US-10-038-722-5	Sequence 147, App
36	175	22.9	67	10	US-09-896-095-147	Sequence 90, Appl
37	175	22.9	67	14	US-10-038-722-90	Sequence 4, Appl
38	175	22.9	67	15	US-10-115-134-4	Sequence 17, Appl
39	173	22.6	58	14	US-10-038-722-17	Sequence 18, Appl
40	173	22.6	58	14	US-10-038-722-18	Sequence 19, Appl
41	173	22.6	58	15	US-10-115-134-88	Sequence 88, Appl
42	173	22.6	58	15	US-10-115-134-89	Sequence 89, Appl
43	173	22.6	58	15	US-10-115-134-90	Sequence 90, Appl
44	173	22.6	58	15	US-10-456-986A-42	Sequence 42, Appl
45	173	22.6	58	15	US-10-456-986A-43	Sequence 43, Appl
46	173	22.6	58	15	US-10-456-986A-44	Sequence 44, Appl
47	173	22.6	58	15	US-10-953-902A-42	Sequence 42, Appl
48	173	22.6	58	18	US-10-953-902A-43	Sequence 43, Appl
49	173	22.6	58	18	US-10-953-902A-43	Sequence 44, Appl
50	173	22.6	58	18	US-10-953-902A-44	Sequence 44, Appl

ALIGNMENTS

RESULT 1
US-10-807-204-1
; Sequence 1, Application US/10807204
; Publication No. US20040229312A1
; GENERAL INFORMATION:
; APPLICANT: Bougueleret, Lydie
; APPLICANT: Bairoch, Amos
; APPLICANT: Niknejad, Anne
; TITLE OF INVENTION: Engineered Human Kunitz-Type Protease
; TITLE OF INVENTION: Inhibitor
; FILE REFERENCE: 54720-8015.US00
; CURRENT APPLICATION NUMBER: US/10/807,204
; CURRENT FILING DATE: 2004-03-22
; PRIOR APPLICATION NUMBER: PCT/EP03/01629
; PRIOR FILING DATE: 2003-02-18

```

; PRIOR APPLICATION NUMBER: US 60/358,683
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 131
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (1)...(131)
; OTHER INFORMATION: eppin-like precursor
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: (1)...(25)
; OTHER INFORMATION: predicted by SignalP 2.0
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (26)...(131)
; OTHER INFORMATION: mature peptide
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (77)...(127)
; OTHER INFORMATION: Kunitz domain predicted by pfscan
; FEATURE:
; NAME/KEY: DISULFID
; LOCATION: (33)...(61)
; OTHER INFORMATION: predicted disulfide bond
; FEATURE:
; NAME/KEY: DISULFID
; LOCATION: (40)...(65)
; OTHER INFORMATION: predicted disulfide bond
; FEATURE:
; NAME/KEY: DISULFID
; LOCATION: (48)...(60)
; OTHER INFORMATION: predicted disulfide bond
; FEATURE:
; NAME/KEY: DISULFID
; LOCATION: (54)...(69)
; OTHER INFORMATION: predicted disulfide bond
; FEATURE:
; NAME/KEY: DISULFID
; LOCATION: (77)...(127)
; OTHER INFORMATION: predicted disulfide bond
; FEATURE:
; NAME/KEY: DISULFID
; LOCATION: (86)...(110)
; OTHER INFORMATION: predicted disulfide bond
; FEATURE:
; NAME/KEY: DISULFID
; LOCATION: (102)...(123)
; OTHER INFORMATION: predicted disulfide bond
; OTHER INFORMATION: predicted disulfide bond
; US-10-807-204-11

Alignment Scores:
Pred. No.: 2,1e-70 Length: 131
Score: 741.00 Matches: 130
Percent Similarity: 99.24% Conservative: 0
Best Local Similarity: 99.24% Mismatches: 1
Query Match: 96.99% Indels: 0
DB: 16 Gaps: 0

US-10-807-204-11 (1-396) x US-10-807-204-1 (1-131)
QY 1 ATGGGACTCTCAGGACTTCTGCCAATCTGGTACCATTCCTTTGGGGACATCCAG 60
DB 1 MetGlyLeuSerGlyLeuLeuProIleLeuValProPheIleLeuGlyAspIleGln 20
QY 61 GAACCTGGGCACGCTGAAGCATCTTGGCAGCCGTGTCACCAATCAAGTGAATGC 120
DB 21 GluProGlyHisAlaGluGlyIleLeuGlyLysProCysProLysIleLysValGluCys 40
QY 121 GAAGTGAAGAAATAGACCATGCTACCAACCCAGAGATGCCAGAAACATGAAGTGT 180
DB 41 GluValGluGluIleAspGlnCysThrLysProArgAspCysProGluAsnMetLysCys 60
QY 181 TGCCCGTTTCAGCCGTGGAAAGAAATGTTAGACTTCAGAAAGGATATATGACGTATGCCA 240
DB 61 CysProPheSerCysGlyLysCysLeuAspPheArgLysAspIleCysSerMetPro 80
QY 241 CAGGAGGCTGGCCCTGCCTGCGCTCCATACACACTGGTGGTACATAAATAAATAAG 300
DB 81 GlnGluAlaGlyProCysLeuAlaSerIleProHisTrpTrpTyrAsnLysLysThrLys 100
QY 301 ATCTGCTCCGAATTCATCTATGCGGTTGTCAGGGGAACAATAACAACTTCCAAACTGAA 360
DB 101 IleCysSerGluPheIleTyrGlyCysGlnGlyAsnAsnAsnAsnPheGlnThrGlu 120
QY 361 GCTATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 393
DB 121 AlaIleCysLeuValThrCysLysLysTyrHis 131

RESULT 2
US-10-807-204-12
; Sequence 12, Application US/10807204
; Publication No. US20040229312A1
; GENERAL INFORMATION:
; APPLICANT: Bougueleret, Lydie
; APPLICANT: Bairoch, Amos
; TITLE OF INVENTION: Engineered Human Kunitz-Type Protease
; TITLE OF INVENTION: Inhibitor
; FILE REFERENCE: 54720-8015.US00
; CURRENT APPLICATION NUMBER: US/10/807,204
; CURRENT FILING DATE: 2004-03-22
; PRIOR APPLICATION NUMBER: PCT/EP03/01629
; PRIOR FILING DATE: 2003-02-18
; PRIOR APPLICATION NUMBER: US 60/358,683
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12
; LENGTH: 131
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-807-204-12

Alignment Scores:
Pred. No.: 2,1e-70 Length: 131
Score: 741.00 Matches: 130
Percent Similarity: 99.24% Conservative: 0
Best Local Similarity: 99.24% Mismatches: 1
Query Match: 96.99% Indels: 0
DB: 16 Gaps: 0

US-10-807-204-11 (1-396) x US-10-807-204-1 (1-131)
QY 1 ATGGGACTCTCAGGACTTCTGCCAATCTGGTACCATTCCTTTGGGGACATCCAG 60
DB 1 MetGlyLeuSerGlyLeuLeuProIleLeuValProPheIleLeuGlyAspIleGln 20
QY 61 GAACCTGGGCACGCTGAAGCATCTTGGCAGCCGTGTCACCAATCAAGTGAATGC 120
DB 21 GluProGlyHisAlaGluGlyIleLeuGlyLysProCysProLysIleLysValGluCys 40
QY 121 GAAGTGAAGAAATAGACCATGCTACCAACCCAGAGATGCCAGAAACATGAAGTGT 180
DB 41 GluValGluGluIleAspGlnCysThrLysProArgAspCysProGluAsnMetLysCys 60
QY 181 TGCCCGTTTCAGCCGTGGAAAGAAATGTTAGACTTCAGAAAGGATATATGACGTATGCCA 240
DB 61 CysProPheSerCysGlyLysCysLeuAspPheArgLysAspIleCysSerMetPro 80
QY 241 CAGGAGGCTGGCCCTGCCTGCGCTCCATACACACTGGTGGTACATAAATAAATAAG 300
DB 81 GlnGluAlaGlyProCysLeuAlaSerIleProHisTrpTrpTyrAsnLysLysThrLys 100

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Qy 301 ATCTGCTCCGAATTCATCTATGGCGTTGCCAGGGGAACAATAACAACCTTCCAAACTGAA 360
Db 101 IleCysSerGluPheIleTyrGlyCysGlnGlyAsnAsnAsnAsnGlnThrGlu 120
Qy 361 GCTATCTCTGCTGCTACCTGCAAAAATAACCAT 393
Db 121 AlaIleCysLeuValThrCysLysLysTyrHis 131

RESULT 3

US-10-807-204-15
; Sequence 15, Application US/10807204
; Publication No. US20040229312A1
; GENERAL INFORMATION:
; APPLICANT: Bougueleret, Lydie
; APPLICANT: Bairoch, Amos
; APPLICANT: Niknejad, Anne
; TITLE OF INVENTION: Engineered Human Kunitz-Type Protease
; TITLE OF INVENTION: Inhibitor
; FILE REFERENCE: 54720-8015.US00
; CURRENT APPLICATION NUMBER: US/10/807,204
; CURRENT FILING DATE: 2004-03-22
; PRIOR APPLICATION NUMBER: PCT/EP03/01629
; PRIOR FILING DATE: 2003-02-18
; PRIOR APPLICATION NUMBER: US 60/358,683
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15
; LENGTH: 131
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-807-204-15

Alignment Scores:
Pred. No.: 3,44e-70 Length: 131
Score: 739.00 Matches: 130
Percent Similarity: 99.24% Conservative: 0
Best Local Similarity: 99.24% Mismatches: 1
Query Match: 96.73% Indels: 0
DB: 16 Gaps: 0

US-10-807-204-11 (1-396) x US-10-807-204-15 (1-131)

Qy 1 ATGGGACTCTCAGGACTTCGCAATCTCGTGTACCATTCCTTTTGGGGACATCCAG 60
Db 1 MetGlyLeuSerGlyLeuLeuProIleLeuValProPheIleLeuLeuGlyAspIleGln 20
Qy 61 GAACCTGGGCACGCTGAGGACATCTTGGCAAGCCGTGTCCAAATCAAACTGGAATGC 120
Db 21 GluProGlyHisAlaGluGlyLeuGlyLysProCysProLysIleLysValGluCys 40
Qy 121 GAAGTGGAAATAGACAGGTGTACCAACCCAGAGATTGCCAGAAACATGAAGTGT 180
Db 41 GluValGluGluIleAspGlnCysThrLysProArgAspCysProGluAsnMetLysCys 60
Qy 181 TCCCGCTTCAGCGCTGGAAGAAATCTTTAGACTTCAGAAAGATATATGCAAGTATGCCA 240
Db 61 CysProPheSerArgGlyLysLysCysLeuAspPheArgLysAspIleCysSerMetPro 80
Qy 241 CAGGAGGCTGGCCCTCGCTCCATACCACTGGTGTGTACATAAATAAATAAAGTAAAG 300
Db 81 GlnGluAlaGlyProCysLeuAlaSerIleProHisTyrTyrAsnLysLysThrLys 100
Qy 301 ATCTGCTCCGAATTCATCTATGGCGTTGCCAGGGGAACAATAACAACCTTCCAAACTGAA 360
Db 101 IleCysSerGluPheIleTyrGlyGlySerGlnGlyAsnAsnAsnAsnGlnThrGlu 120
Qy 361 GCTATCTCTGCTGCTACCTGCAAAAATAACCAT 393
Db 121 AlaIleCysLeuValThrCysLysLysTyrHis 131

RESULT 4

US-10-807-204-2
; Sequence 2, Application US/10807204
; Publication No. US20040229312A1
; GENERAL INFORMATION:
; APPLICANT: Bougueleret, Lydie
; APPLICANT: Bairoch, Amos
; APPLICANT: Niknejad, Anne
; TITLE OF INVENTION: Engineered Human Kunitz-Type Protease
; TITLE OF INVENTION: Inhibitor
; FILE REFERENCE: 54720-8015.US00
; CURRENT APPLICATION NUMBER: US/10/807,204
; CURRENT FILING DATE: 2004-03-22
; PRIOR APPLICATION NUMBER: PCT/EP03/01629
; PRIOR FILING DATE: 2003-02-18
; PRIOR APPLICATION NUMBER: US 60/358,683
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 106
; TYPE: PRT
; ORGANISM: Homo sapiens
; NAME/KEY: VARIANT
; LOCATION: (1)...(106)
; OTHER INFORMATION: mature form
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (52)...(102)
; OTHER INFORMATION: Kunitz domain predicted by pfscan
; FEATURE:
; NAME/KEY: DISULFID
; LOCATION: (8)...(36)
; OTHER INFORMATION: predicted disulfide bond
; FEATURE:
; NAME/KEY: DISULFID
; LOCATION: (15)...(40)
; OTHER INFORMATION: predicted disulfide bond
; FEATURE:
; NAME/KEY: DISULFID
; LOCATION: (23)...(35)
; OTHER INFORMATION: predicted disulfide bond
; FEATURE:
; NAME/KEY: DISULFID
; LOCATION: (29)...(44)
; OTHER INFORMATION: predicted disulfide bond
; FEATURE:
; NAME/KEY: DISULFID
; LOCATION: (52)...(102)
; OTHER INFORMATION: predicted disulfide bond
; FEATURE:
; NAME/KEY: DISULFID
; LOCATION: (61)...(85)
; OTHER INFORMATION: predicted disulfide bond
; FEATURE:
; NAME/KEY: DISULFID
; LOCATION: (77)...(98)
; OTHER INFORMATION: predicted disulfide bond
US-10-807-204-2

Alignment Scores:
Pred. No.: 1.07e-56 Length: 106
Score: 613.00 Matches: 105
Percent Similarity: 99.06% Conservative: 0
Best Local Similarity: 99.06% Mismatches: 1
Query Match: 80.24% Indels: 0
DB: 16 Gaps: 0

US-10-807-204-11 (1-396) x US-10-807-204-2 (1-106)

Qy 76 GAAGCATCTTGGCAAGCCGTGTCCAAATCAAAAGTGAATGCAAGTGAAGAAATA 135
Db 1 GluGlyIleLeuGlyLysProCysProLysIleLysValGluCysGluValGluGluIle 20

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Qy 136 GACCAGTGTACCAACCCAGAGATTGCCAGAAACATGAAGTGTGCGCGTTCAGCGT 195
Db 21 AspGlnCysThrLysProArgAspCysProGluAsnMetLysCysCysProPheSerCys 40
Qy 196 GAAAGAAATGTTAGACTTCAGAAAGGATATATGACAGTATGCCACAGAGCGTGGCCCC 255
Db 41 GlyLysLysCysLeuAspPheArgLysAspLysCysSerMetProGlnGluAlaGlyPro 60
Qy 256 TGCTGGCCTCCATACCACTGGTGTGTACAAATAAATAAATAAATAAATAAATAAATAA 315
Db 61 CysLeuAlaSerIleProHisTrpTrpTrpTrpTrpTrpTrpTrpTrpTrpTrpTrp 80
Qy 316 ATCTATGCGGTGTCAGGGGAAACAATAAACAACCTCCAAACTGGAAGCTATCTGCTGTC 375
Db 81 IleTrpGlyGlyCysGlnGlyAsnAsnAsnAsnAsnAsnAsnAsnAsnAsnAsnAsn 100
Qy 376 ACCTGCAAAAATACCAT 393
Db 101 ThrCysLysLysTyrHis 106

RESULT 5
US-10-807-204-9
; Sequence 9, Application US/10807204
; Publication No. US20040229312A1
; GENERAL INFORMATION:
; APPLICANT: Bougueleret, Lydie
; APPLICANT: Baïroch, Amos
; APPLICANT: Niknejad, Anne
; TITLE OF INVENTION: Engineered Human Kunitz-Type Protease
; FILE REFERENCE: 54720-8015 US00
; CURRENT APPLICATION NUMBER: US/10/807,204
; PRIOR FILING DATE: 2004-03-22
; PRIOR APPLICATION NUMBER: PCT/EP03/01629
; PRIOR FILING DATE: 2003-02-18
; PRIOR APPLICATION NUMBER: US 60/358,683
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 98
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-807-204-9

Alignment Scores:
Pred. No.: 6.47e-51 Length: 98
Score: 559.00 Matches: 98
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 73.17% Indels: 0
DB: 16 Gaps: 0

US-10-807-204-11 (1-396) x US-10-807-204-9 (1-98)
Qy 1 ATGGGACTCTCAGGACTTCTGCCAATCTGTGTACATTCATCTTTGGGGGACATCCAG 60
Db 1 MetGlyLeuSerGlyLeuLeuProIleLeuValProPheIleLeuLeuGlyAspIleGln 20
Qy 61 GAACCTGGGACGCTGAAGGATCTTGGCAAGCGGTGTCACCAAAATCAAAGTGAATGC 120
Db 21 GluProGlyHisAlaGluGlyIleLeuGlyLysProCysProLysLysValGluCys 40
Qy 121 GAAGTGAAGAAATAGACAGTGTACCAACCCAGAGATTGCCAGAAACATCAAGTGT 180
Db 41 GluValGluIleAspGlnCysThrLysProArgAspCysProGluAsnMetLysCys 60
Qy 181 TGCCCGTTCAGCGTGGAAAGAAATGTTAGACTTCAGAAAGGATATATGCAATGCA 240
Db 61 CysProPheSerArgGlyLysLysCysLeuAspPheArgLysAspIleCysSerMetPro 80
Qy 241 CAGGAGGCTGGCCCTGCCTGCCTCCATACCACTGGTGTACATTCATCTTTGGGGGACATCCAG 294

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Db 81 GlnGluAlaGlyProCysLeuAlaSerIleProHisTrpTrpTrpTrpTrpTrpTrp 98

RESULT 6
US-10-807-204-16
; Sequence 16, Application US/10807204
; Publication No. US20040229312A1
; GENERAL INFORMATION:
; APPLICANT: Bougueleret, Lydie
; APPLICANT: Baïroch, Amos
; APPLICANT: Niknejad, Anne
; TITLE OF INVENTION: Engineered Human Kunitz-Type Protease
; FILE REFERENCE: 54720-8015 US00
; CURRENT APPLICATION NUMBER: US/10/807,204
; PRIOR FILING DATE: 2004-03-22
; PRIOR APPLICATION NUMBER: PCT/EP03/01629
; PRIOR FILING DATE: 2003-02-18
; PRIOR APPLICATION NUMBER: US 60/358,683
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 16
; LENGTH: 136
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-807-204-16

Alignment Scores:
Pred. No.: 2.02e-42 Length: 136
Score: 480.00 Matches: 80
Percent Similarity: 77.52% Conservative: 20
Best Local Similarity: 62.02% Mismatches: 29
Query Match: 62.83% Indels: 0
DB: 16 Gaps: 0

US-10-807-204-11 (1-396) x US-10-807-204-16 (1-136)
Qy 1 ATGGGACTCTCAGGACTTCTGCCAATCTGTGTACATTCATCTTTGGGGGACATCCAG 60
Db 1 MetArgLeuTrpGlyLeuLeuProPheLeuValProPheIleLeuLeuTrpSerIleGln 20
Qy 61 GAACCTGGGACGCTGAAGGATCTTGGCAAGCGGTGTCACCAAAATCAAAGTGAATGC 120
Db 21 GluProGluLeuAlaGluGlyPheIleArgThrCysProArgValArgValLysCys 40
Qy 121 GAAGTGAAGAAATAGACAGTGTACCAACCCAGAGATTGCCAGAAACATCAAGTGT 180
Db 41 GluValGluGluArgAsnGluCysThrArgHisArgGlnCysProAsnLysLysArgCys 60
Qy 181 TGCCCGTTCAGCGTGGAAAGAAATGTTAGACTTCAGAAAGGATATATGCAATGCA 240
Db 61 CysLeuPheSerCysGlyLysLysCysMetAspLeuArgGlnAspValCysSerLeuPro 80
Qy 241 CAGGAGGCTGGCCCTGCCTGCCTCCATACCACTGGTGTGTACATTCATCTTTGGGGGACATTAAG 300
Db 81 GluAspProGlyProCysLeuAlaTyrLeuProArgTrpTrpTrpTrpTrpTrpTrp 100
Qy 301 ATCTGCTCCGAATTCATCTATGCGGTGTCAGGGGAAACAATAACAATCTTCCAACTGAA 360
Db 101 LeuCysThrGluPheIleTyrGlyCysGlnGlyAsnProAsnAsnAsnAsnAsnAsn 120
Qy 361 GCTATCTGTCTGTCTACCTGCAAAAAA 387
Db 121 GlyIleCysThrValValCysLysLys 129

RESULT 7
US-09-853-161-75
; Sequence 75, Application US/09853161
; Patent No. US20020076756A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 28 Human Secreted Proteins

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FILE REFERENCE: P2003P3
CURRENT APPLICATION NUMBER: US/09/853,161
SEQUENCE FILING DATE: 2001-05-11
PRIOR APPLICATION NUMBER: 60/265,583
PRIOR FILING DATE: 2001-02-02
PRIOR APPLICATION NUMBER: 09/152,060
PRIOR FILING DATE: 1998-09-11
PRIOR APPLICATION NUMBER: PCT/US98/04858
PRIOR FILING DATE: 1998-03-12
PRIOR APPLICATION NUMBER: 60/040,762
PRIOR FILING DATE: 1997-03-14
PRIOR APPLICATION NUMBER: 60/040,710
PRIOR FILING DATE: 1997-03-14
PRIOR APPLICATION NUMBER: 60/050,934
PRIOR FILING DATE: 1997-05-30
PRIOR APPLICATION NUMBER: 60/048,100
PRIOR FILING DATE: 1997-05-30
PRIOR APPLICATION NUMBER: 60/048,357
PRIOR FILING DATE: 1997-05-30
PRIOR APPLICATION NUMBER: 60/048,189
PRIOR FILING DATE: 1997-05-30
PRIOR APPLICATION NUMBER: 60/057,765
PRIOR FILING DATE: 1997-09-05
PRIOR APPLICATION NUMBER: 60/048,970
PRIOR FILING DATE: 1997-06-06
PRIOR APPLICATION NUMBER: 60/068,368
PRIOR FILING DATE: 1997-12-19
NUMBER OF SEQ ID NOS: 118
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 75
LENGTH: 133
TYPE: PRT
ORGANISM: Homo sapiens
US-09-853-161-75

Alignment Scores:
Pred. No.: 133
Score: 455.00
Percent Similarity: 74.22%
Best Local Similarity: 60.16%
Query Match: 59.55%
DB: 9
Gaps: 0

US-10-807-204-11 (1-396) x US-09-853-161-75 (1-133)

QY 1 ATGGGACTCTCAGGACTTCTGCAATCTCTGGTACCATTATCTCTTTGGGGACATCCAG 60
DB 1 MetGlySerSerGlyLeuLeuSerLeuValLeuPheValLeuLeuAlaAsnValGln 20
QY 61 GAACCTGGCGACGCTGAAGGCATCTCTGGCAAGCCGTGTCCCAAAATCAAAGTGAATGC 120
DB 21 GlyProGlyLeuThrAspTrpLeuPheProArgArgCysProLysIleArgGluCys 40
QY 121 GAAGTGGAAAGAAATAGACAGGTGTACCAACCCAGAGATTGCCAGAAACATGAAGTGT 180
DB 41 GluPheGlnGluArgAspValCysThrLysAspArgGlnCysGlnAspAsnLysLysCys 60
QY 181 TGCCCGTTGCGCGTGAAGAAATGTTTAGACTTTCAGAAAGATATATGAGTATGCCA 240
DB 61 CysValPheSerCysGlyLysLysCysLeuAspLeuLysGlnAspValCysGluMetPro 80
QY 241 CAGGAGGCTGGCCCTGCGCTCCATACCCACACTGGTGTGTAACATAAAAACTAAG 300
DB 81 LysGluThrGlyProCysLeuAlaTyrPheLeuHisTyrTrpTyrAspLysLysAspAsn 100
QY 301 ATCTGCTCCGAATTCATCTATGCGGTTGCCAGGGGAAACAATAACAACTTCCAAACTGAA 360
DB 101 ThrCysSerMetPheValTyrGlyGlyCysGlnGlyAsnAsnAsnAsnPheGlnSerLys 120
QY 361 GCTATCTGCTGCTACCTGCATAA 384
DB 121 AlaAsnCysLeuAsnThrCysLys 128

RESULT 8
US-09-852-659A-75
SEQUENCE 75, Application US/09852659A
PATENT NO. US20020077287A1
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: 28 Human Secreted Proteins
FILE REFERENCE: P2003P4
CURRENT APPLICATION NUMBER: US/09/852,659A
SEQUENCE FILING DATE: 2001-05-11
PRIOR APPLICATION NUMBER: 60/265,583
PRIOR FILING DATE: 2001-02-02
PRIOR APPLICATION NUMBER: 09/152,060
PRIOR FILING DATE: 1998-09-11
PRIOR APPLICATION NUMBER: PCT/US98/04858
PRIOR FILING DATE: 1998-03-12
PRIOR APPLICATION NUMBER: 60/040,762
PRIOR FILING DATE: 1997-03-14
PRIOR APPLICATION NUMBER: 60/040,710
PRIOR FILING DATE: 1997-03-14
PRIOR APPLICATION NUMBER: 60/050,934
PRIOR FILING DATE: 1997-05-30
PRIOR APPLICATION NUMBER: 60/048,100
PRIOR FILING DATE: 1997-05-30
PRIOR APPLICATION NUMBER: 60/048,357
PRIOR FILING DATE: 1997-05-30
PRIOR APPLICATION NUMBER: 60/048,189
PRIOR FILING DATE: 1997-05-30
PRIOR APPLICATION NUMBER: 60/057,765
PRIOR FILING DATE: 1997-09-05
PRIOR APPLICATION NUMBER: 60/048,970
PRIOR FILING DATE: 1997-06-06
PRIOR APPLICATION NUMBER: 60/068,368
PRIOR FILING DATE: 1997-12-19
NUMBER OF SEQ ID NOS: 121
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 75
LENGTH: 133
TYPE: PRT
ORGANISM: Homo sapiens
US-09-852-659A-75

Alignment Scores:
Pred. No.: 133
Score: 455.00
Percent Similarity: 74.22%
Best Local Similarity: 60.16%
Query Match: 59.55%
DB: 9
Gaps: 0

US-10-807-204-11 (1-396) x US-09-852-659A-75 (1-133)

QY 1 ATGGGACTCTCAGGACTTCTGCAATCTCTGGTACCATTATCTCTTTGGGGACATCCAG 60
DB 1 MetGlySerSerGlyLeuLeuSerLeuValLeuPheValLeuLeuAlaAsnValGln 20
QY 61 GAACCTGGCGACGCTGAAGGCATCTCTGGCAAGCCGTGTCCCAAAATCAAAGTGAATGC 120
DB 21 GlyProGlyLeuThrAspTrpLeuPheProArgArgCysProLysIleArgGluCys 40
QY 121 GAAGTGGAAAGAAATAGACAGGTGTACCAACCCAGAGATTGCCAGAAACATGAAGTGT 180
DB 41 GluPheGlnGluArgAspValCysThrLysAspArgGlnCysGlnAspAsnLysLysCys 60
QY 181 TGCCCGTTGCGCGTGAAGAAATGTTTAGACTTTCAGAAAGATATATGAGTATGCCA 240
DB 61 CysValPheSerCysGlyLysLysCysLeuAspLeuLysGlnAspValCysGluMetPro 80
QY 241 CAGGAGGCTGGCCCTGCGCTCCATACCCACACTGGTGTGTAACATAAAAACTAAG 300
DB 81 LysGluThrGlyProCysLeuAlaTyrPheLeuHisTyrTrpTyrAspLysLysAspAsn 100
QY 301 ATCTGCTCCGAATTCATCTATGCGGTTGCCAGGGGAAACAATAACAACTTCCAAACTGAA 360

Db	1	MetGlySerSerGlyLeuLeuSerLeuValLeuPheValLeuLeuAlaAsnValGln	20
Qy	61	GAACCTGGCGCAGCTGAAGGCATCTTGGCAAGCCGTGCCCAAAATCAAAGTGGAAATGC	120
Db	21	GlyProGlyLeuThrAspTrpLeuPheProArgCysProLysIleArgGluGluCys	40
Qy	121	GAAGTGGGAAGAAATAGACCACTGTACCAAAACCCAGAGATTGCCAGAAACATGAAGTGT	180
Db	41	GlupheGlnGluArgAspValCysThrLysAspArgGlnCysGlnAspAsnLysLysCys	60
Qy	181	TGCCCGTTCCGCCGTGGAAAGAAATGTTAGACTTCAGAAAGGATATATGCCAGTATGCCA	240
Db	61	CysValPheSerCysGlyLysCysLeuAspLeuLysGlnAspValCysGluMetPro	80
Qy	241	CAGGAGGCTGGCCCTGCTCGCTCCATACCACTGGTGGTACAAATAAAAAAACAATAAG	300
Db	81	LysGluThrGlyProCysLeuAlaTyrPheLeuHisTrpTrpAspLysLysAspAsn	100
Qy	301	ATCTGCTCCGAATTCATCTATGGCGGTGGCCAGGGGAACAATAACAACATTCCAACATGA	360
Db	101	ThrCysSerMetPheValTyrGlyCysGlnGlyAsnAsnAsnAsnPheGlnSerLys	120
Qy	361	GCTATCTGTCTGGTCACCTGCAAA	384
Db	121	AlaAsnCysLeuAsnThrCysLys	128
RESULT 11			
US-10-807-204-13			
; Sequence 13, Application US/10807204			
; Publication No. US20040229312A1			
; GENERAL INFORMATION:			
; APPLICANT: Bougueleret, Lydie			
; APPLICANT: Bairoch, Amos			
; APPLICANT: Miknejad, Anne			
; TITLE OF INVENTION: Engineered Human Kunitz-Type Protease			
; TITLE OF INVENTION: Inhibitor			
; FILE REFERENCE: 54720-8015.US00			
; CURRENT APPLICATION NUMBER: US/10/807,204			
; CURRENT FILING DATE: 2004-03-22			
; PRIOR APPLICATION NUMBER: PCT/EP03/01629			
; PRIOR FILING DATE: 2003-02-18			
; PRIOR APPLICATION NUMBER: US 60/358,683			
; PRIOR FILING DATE: 2002-02-21			
; NUMBER OF SEQ ID NOS: 16			
; SOFTWARE: FastSeq for Windows Version 4.0			
; SEQ ID NO 13			
; LENGTH: 133			
; TYPE: PRT			
; ORGANISM: Homo sapiens			
US-10-807-204-13			
Alignment Scores:			
Pred. No.: 9,65e-40 Length: 133			
Score: 455.00 Matches: 77			
Percent Similarity: 74.22% Conservative: 18			
Best Local Similarity: 60.16% Mismatches: 33			
Query Match: 59.55% Indels: 0			
DB: 16 Gaps: 0			
US-10-807-204-11 (1-396) x US-10-807-204-13 (1-133)			
Qy	1	ATGGGACTCTCAGGACTCTCGCAATCTGTGTACCATTCCTTTTGGGGACATCCAG	60
Db	1	MeGlySerSerGlyLeuLeuSerLeuValLeuPheValLeuLeuAlaAsnValGln	20
Qy	61	GAACCTGGGCAGCTGAAGGCATCTTGGCAAGCCGTGCCCAAAATCAAAGTGGAAATGC	120
Db	21	GlyProGlyLeuThrAspTrpLeuPheProArgCysProLysIleArgGluGluCys	40
Qy	121	GAAGTGGGAAGAAATAGACCACTGTACCAAAACCCAGAGATTGCCAGAAACATGAAGTGT	180
Db	41	GlupheGlnGluArgAspValCysThrLysAspArgGlnCysGlnAspAsnLysLysCys	60

Pred. No.: 3.63e-35 Length: 86
Score: 412.00 Matches: 74
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 53.93% Indels: 0
DB: 17 Gaps: 0

US-10-807-204-11 (1-396) x US-10-480-988-21 (1-86)

Qy 1 ATGGGACTCTCAGACTTCTGCCAATCTGTGATACCAATTCATCCCTTTGGGGGACATCCAG 60
Dy |||||
Dy 1 MetGlyLeuSerGlyLeuLeuProIleLeuValProPheIleLeuLeuGlyAspIleGln 20
Qy 61 GAACCTGGGACGCTGAAGGATCCTTGGCAAGCGGTGCCAAATCAAAATCAAAAGTGAATGC 120
Dy |||||
Dy 21 GluProGlyHisAlaGluGlyLeuGlyProCysProIleLeuValGluCys 40
Qy 121 GAAGTGGAGAAATAGACCACTGTACCAAAACCCAGAGATTGCCAGAAACATGAAGTGT 180
Dy |||||
Dy 41 GluValGluGluIleAspGlnCysThrLysProArgAspCysProGluAsnMetLysCys 60
Qy 181 TGCCCGTTACCGCTGGAAAGAAATGTTTACACTTCAGAAAG 222
Dy |||||
Dy 61 CysProPheSerArgGlyLysCysLeuAspPheArgLys 74

RESULT 13

US-10-276-774-2606
; Sequence 2606, Application US/10276774
; Publication No. US20040053245A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; TITLE OF INVENTION: No. US20040053245A1el Nucleic Acids and Polypeptides
; FILE REFERENCE: 21272-030
; CURRENT APPLICATION NUMBER: US/10/276,774
; CURRENT FILING DATE: 2002-11-18
; PRIOR APPLICATION NUMBER: 09/560,875
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: 09/496,914
; PRIOR FILING DATE: 2000-02-03
; NUMBER OF SEQ ID NOS: 2700
; SOFTWARE: Custom
; SEQ ID NO 2606
; LENGTH: 101
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-276-774-2606

Alignment Scores:
Pred. No.: 3.74e-35 Length: 101
Score: 412.00 Matches: 74
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 53.93% Indels: 0
DB: 15 Gaps: 0

US-10-807-204-11 (1-396) x US-10-276-774-2606 (1-101)

Qy 1 ATGGGACTCTCAGACTTCTGCCAATCTGTGATACCAATTCATCCCTTTGGGGGACATCCAG 60
Dy |||||
Dy 16 MetGlyLeuSerGlyLeuLeuProIleLeuValProPheIleLeuLeuGlyAspIleGln 35
Qy 61 GAACCTGGGACGCTGAAGGATCCTTGGCAAGCGGTGCCAAATCAAAATCAAAAGTGAATGC 120
Dy |||||
Dy 36 GluProGlyHisAlaGluGlyLeuGlyProCysProIleLeuValGluCys 55
Qy 121 GAAGTGGAGAAATAGACCACTGTACCAAAACCCAGAGATTGCCAGAAACATGAAGTGT 180
Dy |||||
Dy 56 GluValGluGluIleAspGlnCysThrLysProArgAspCysProGluAsnMetLysCys 75
Qy 181 TGCCCGTTACCGCTGGAAAGAAATGTTTACACTTCAGAAAG 222
Dy |||||
Dy 76 CysProPheSerArgGlyLysCysLeuAspPheArgLys 89

RESULT 14
US-09-852-659A-119
; Sequence 119, Application US/09852659A
; Patent No. US20020077287A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 28 Human Secreted Proteins
; FILE REFERENCE: P2003P4
; CURRENT APPLICATION NUMBER: US/09/852,659A
; CURRENT FILING DATE: 2001-05-11
; PRIOR APPLICATION NUMBER: 60/265,583
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: 09/152,060
; PRIOR FILING DATE: 1998-09-11
; PRIOR APPLICATION NUMBER: PCT/US98/04858
; PRIOR FILING DATE: 1998-03-12
; PRIOR APPLICATION NUMBER: 60/040,762
; PRIOR FILING DATE: 1997-03-14
; PRIOR APPLICATION NUMBER: 60/040,710
; PRIOR FILING DATE: 1997-03-14
; PRIOR APPLICATION NUMBER: 60/050,934
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/048,100
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/048,357
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/048,189
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/057,765
; PRIOR FILING DATE: 1997-09-05
; PRIOR APPLICATION NUMBER: 60/048,970
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/068,368
; PRIOR FILING DATE: 1997-12-19
; NUMBER OF SEQ ID NOS: 121
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 119
; LENGTH: 117
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-852-659A-119

Alignment Scores:
Pred. No.: 9.92e-33 Length: 117
Score: 389.50 Matches: 65
Percent Similarity: 77.00% Conservative: 12
Best Local Similarity: 65.00% Mismatches: 22
Query Match: 50.98% Indels: 1
DB: 9 Gaps: 1

US-10-807-204-11 (1-396) x US-09-852-659A-119 (1-117)

Qy 85 CTTGGCAAGCCGTGTCCCAAAATCAAAAGTGGAAATGCGAAGTGGAAAGAAATAGACCACTGT 144
Dy |||||
Dy 14 LeuGlyArg---CysProLysIleArgGluCysGluPheGlnGluArgAspValCys 32
Qy 145 ACCAAACCCAGAGATTGCCCAAGAAACATGAAGTGTGCCCGTTGACCGCTGGAAAGAAA 204
Dy |||||
Dy 33 ThrLysAspArgGlnCysGlnAspAsnLysCysValPheSerCysGlyLysLys 52
Qy 205 TGTTTACACTTCAGAAAGGATATATGCAGTATGCCAGGAGGCTGCCCTGCCTGCC 264
Dy |||||
Dy 53 CysLeuAspLeuLysGlnAspValCysGluMetProLysGluThrGlyProCysLeuAla 72
Qy 265 TCCATACCACTGGTGGTACAATAAAAAAATAAGATCTGCTCCGAATTCATCTATGGC 324
Dy |||||
Dy 73 TyrPheLeuHisTrpTrpTyrAspLysLysAspAsnThrCysSerMetPheValTyrGly 92
Qy 325 GGTTCGCGAGGGGACAACTTCCAACTGAAGCTATCTCTGGTCACTGCTGCACTGCAAA 384
Dy |||||
Dy 93 GlyCysGlnGlyAsnAsnAsnPheGlnSerLysAlaAsnCysLeuAsnThrCysLys 112

Thu Sep 22 07:16:44 2005

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RESULT 15
US-10-058-993-120
; Sequence 120, Application US/10058993
; Publication No. US20030225009A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 28 Human Secreted Proteins
; FILE REFERENCE: PZ003P5
; CURRENT APPLICATION NUMBER: US/10/058,993
; CURRENT FILING DATE: 2002-01-30
; PRIOR APPLICATION NUMBER: 09/852,659
; PRIOR FILING DATE: 2001-05-11
; PRIOR APPLICATION NUMBER: 09/852,797
; PRIOR FILING DATE: 2001-05-11
; PRIOR APPLICATION NUMBER: 09/853,161
; PRIOR FILING DATE: 2001-05-11
; PRIOR APPLICATION NUMBER: 60/265,583
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: 09/152,060
; PRIOR FILING DATE: 1998-09-11
; PRIOR APPLICATION NUMBER: PCT/US98/04858
; PRIOR FILING DATE: 1998-03-12
; PRIOR APPLICATION NUMBER: 60/068,368
; PRIOR FILING DATE: 1997-12-19
; PRIOR APPLICATION NUMBER: 60/057,765
; PRIOR FILING DATE: 1997-09-05
; PRIOR APPLICATION NUMBER: 60/048,970
; PRIOR FILING DATE: 1997-06-05
; PRIOR APPLICATION NUMBER: 60/050,934
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/048,100
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/048,189
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/048,357
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/040,710
; PRIOR FILING DATE: 1997-03-14
; PRIOR APPLICATION NUMBER: 60/040,762
; PRIOR FILING DATE: 1997-03-14
; NUMBER OF SEQ ID NOS: 122
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 120
; LENGTH: 117
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-058-993-120

Alignment Scores:
Pred. No.: 9,92e-33 Length: 117
Score: 389.50 Matches: 65
Percent Similarity: 77.00% Conservative: 12
Best Local Similarity: 65.00% Mismatches: 22
Query Match: 50.98% Indels: 1
DB: 15 Gaps: 1

US-10-807-204-11 (1-396) x US-10-058-993-120 (1-117)
Qy 85 CTTGGCAAGCCGTGTCCCAAAATCAAAGTGAATGCCAGTGGAGAAATAGACCACTGT 144
Db 14 LeuGlyArg--CysProLysIleArgGluGluCysGluPheGlnGluArgAspValCys 32
Qy 145 ACCAAACCCAGAGATTGCCGAGAAACATGAAGTGTGCCCGTTTCAGCCGTGGAAAAGAAA 204
Db 33 ThrLysAspArgGlnCysGlnAspAsnLysCysCysValPheSerCysGlyLysLys 52
Qy 205 TGTTTTAGCTTCGAAAGGATATATGCAGTATGCCAGAGAGGCTGCCCTCGCTGGCC 264
Db 53 CysLeuAspLeuLysGlnAspValCysGluMetProLysGluThrGlyProCysLeuAla 72
Qy 265 TCCATACCACTGGTGGTACAAATAAAAACTAAGATCTGCTCCGAATTCATCTATGCC 324
Db 73 TyrPheLeuHisTrpTrpAspLysLysAspAsnThrCysSerMetPheValTyrGly 92

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QY	325	GTTTGGCAGGGGAACAATAACAACTTCACCAACTGGAAGCTATCTGTCTGGTGCCACCTGCACAA	384
Db	93	GlycylGlnGlyAsnAsnAsnAsnPheGlnSerIysAlaAsnCysLeuAenThrCysLys	112
RESULT 16			
US-09-852-659A-120			
; Sequence 120, Application US/09852659A			
; Patent No. US2002007287A1			
; GENERAL INFORMATION:			
; APPLICANT: Rosen et al.			
; TITLE OF INVENTION: 28 Human Secreted Proteins			
; FILE REFERENCE: PZ003P4			
; CURRENT APPLICATION NUMBER: US/09/852,659A			
; CURRENT FILING DATE: 2001-05-11			
; PRIOR APPLICATION NUMBER: 60/265,583			
; PRIOR FILING DATE: 2001-02-02			
; PRIOR APPLICATION NUMBER: 09/152,060			
; PRIOR FILING DATE: 1998-09-11			
; PRIOR APPLICATION NUMBER: PCT/US98/04858			
; PRIOR FILING DATE: 1998-03-12			
; PRIOR APPLICATION NUMBER: 60/040,762			
; PRIOR FILING DATE: 1997-03-14			
; PRIOR APPLICATION NUMBER: 60/040,710			
; PRIOR FILING DATE: 1997-03-14			
; PRIOR APPLICATION NUMBER: 60/050,934			
; PRIOR FILING DATE: 1997-05-30			
; PRIOR APPLICATION NUMBER: 60/048,100			
; PRIOR FILING DATE: 1997-05-30			
; PRIOR APPLICATION NUMBER: 60/057,765			
; PRIOR FILING DATE: 1997-09-05			
; PRIOR APPLICATION NUMBER: 60/048,970			
; PRIOR FILING DATE: 1997-06-06			
; PRIOR APPLICATION NUMBER: 60/068,368			
; PRIOR FILING DATE: 1997-12-19			
; NUMBER OF SEQ ID NOS: 121			
; SOFTWARE: PatentIn Ver. 2.0			
; SEQ ID NO 120			
; LENGTH: 102			
; TYPE: PR1			
; ORGANISM: Homo sapiens			
; US-09-852-659A-120			
Alignment Scores:			
Pred. No.:	1.4e-32	Length:	102
Score:	388.00	Matches:	63
Percent Similarity:	77.08%	Conservative:	11
Best Local Similarity:	65.62%	Mismatches:	22
Query Match:	50.79%	Indels:	0
DB:	9	Gaps:	0
US-10-807-204-11 (1-396) x US-09-852-659A-120 (1-102)			
Qy	97	TGTCGCCAAAATCAAAGTGGAAATCGCAAGTGGAGAANAATAGACCAGTGTACCAAAACCAGA	156
Db	2	CysProIysIleAArgGluGluCysGluPheGlnGluArGAspValCysThrLysAspArg	21
Qy	157	GATTGCCCGCCAGAAACATGAAGTGTGCCCGTTCAGCCGTGGAAAGAAATGTTTTAGACTTC	216
Db	22	GlnCysGlnAspAsnLysLysCysValPheSerCysGlyLysLysCysLeuAspLeu	41
Qy	217	AGAAAGGATATATGTCAGTATGCCACAGGAGGCTGCCCTCTGCCTGCCCTCCCATACCCACAC	276
Db	42	LysGlnAspValCysGluMetProIysGluThrGlyProCysLeuAlaTyrPheLeuHis	61
Qy	277	TGGTGGTCAATAAAAAAACATAAGATCTGCTCCGGAATTCATCTATGGCGGTGCCAGGGG	336
Db	62	TroIroTyAspLysLysAspAsnThrCysSerMetPheValTyrGlyCysGlnGly	81

; APPLICANT: Williamson, Angela

APPLICANT: MARKLAND, WILLIAM

127	QY	GAAGAAATAGACCAAGTGTACAA--	-----CCAGAGATTGCCCAGAA	168
496	Db	GluSerMetGluGluCysThrArgThrCysLysLysAlaValProGluProGluProGlu	515	
169	QY	ACATGAAGTCTTC---CCGTTCAAGCGGTGA--	-----198	
516	Db	LysGluThrCysSerGlnProIleGluAlaGlyProCysLysAlaMetValArgArgPhe	535	
199	QY	-----AGAAATGTTAGATTC--	-----216	
536	Db	AlaTyrAspAsnAlaLysGluLysCysValGluPhePheTyrGlyCysLysGlyAsn	555	
216	QY	-----	-----216	
556	Db	LysAsnAsnPheGluThrMetGluAspCysThrPheThrCysGluGlnArgLeuAlaLys	575	
217	QY	-----AGAAAGGATATATCGAGTATCCACAGAGGCTGGCCCTCGCTGGCCTCC	267	
576	Db	ProGluLeuGluLysAspValCysSerGlnProIleThrAlaGlyProCysArgAlaSer	595	
268	QY	ATACCACTGGTGGTACATAAAAAAACTAAGATCTGTCCGAAATTCATCTATGGCGGT	327	
596	Db	IleProArgTyrGlyTyrAspSerLysLysArgLysCysValLysPheThrTyrGlyGly	615	
328	QY	TGCCAGGGGAACAATACACTTCCAACTGAAGCTATCTGTCTGGTCACTGCAAAAAA	387	
616	Db	CysLysGlyValAsnGlnValAsnArgPheProThrLysAsnGluCysGluLysThrCysLysArg	635	

APPLICANT: KENT, Rachel B.
; TITLE OF INVENTION: DIRECTED EVOLUTION OF NOVEL BINDING PROTEINS
; FILE REFERENCE: LADNER=7L
; CURRENT APPLICATION NUMBER: US/09/896,095
; CURRENT FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: 08/415,922
; PRIOR FILING DATE: 1995-03-04
; PRIOR APPLICATION NUMBER: 08/009,319
; PRIOR FILING DATE: 1993-01-26
; PRIOR APPLICATION NUMBER: 07/664,989
; PRIOR FILING DATE: 1991-03-01
; PRIOR APPLICATION NUMBER: 08/993,776
; PRIOR FILING DATE: 1997-12-18
; NUMBER OF SEQ ID NOS: 274
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 160
; LENGTH: 64
; TYPE: PRT
; ORGANISM: Caretta sp.
US-09-896-095-160

Alignment Scores:
Pred. No.: 9.55e-11 Length: 64
Score: 184.00 Matches: 27
Percent Similarity: 73.21% Conservative: 14
Best Local Similarity: 48.21% Mismatches: 15
Query Match: 24.08% Indels: 0
DB: 10 Gaps: 0

US-10-807-204-11 (1-396) x US-09-896-095-160 (1-64)

QY 217 AGAAGGATATATGCAGTATGCCACAGGAGGCTGGCCCTGCCTCCATACACAC 276
Db 4 LysArgAspIleCysArgLeuProGluGlnGlyProCysGlyArgLeuProArg 23
QY 277 TGGTGTACAAATAAAAAAATTAAGATCTGCTCCGAATTCATCTATGGCGGTTGCCAGGG 336
Db 24 TyrPheTyrAsnProAlaSerArgMetCysGluSerPheIleTyrGlyGlyCysGly 43
QY 337 AACATAACAATTCCTCAAACTGAAGCTATCTGCTGGTCACCTGCAAA 384
Db 44 AsnLysAsnAsnPheLysThrLysAlaGluCysValArgAlaCysArg 59

RESULT 25
US-10-038-722-103
; Sequence 103, Application US/10038722
; Publication No. US20030175919A1
; GENERAL INFORMATION:
; APPLICANT: LEY, Arthur C.
; APPLICANT: GUTERMAN, Sonia K.
; APPLICANT: MARKLAND, William
; APPLICANT: KENT, Rachel B.
; APPLICANT: ROBERTS, Bruce L.
; APPLICANT: LADNER, Robert C.
; TITLE OF INVENTION: ITI-D1 KUNITZ DOMAIN MUTANTS AS mHE INHIBITORS
; FILE REFERENCE: LEY-1B
; CURRENT APPLICATION NUMBER: US/10/038,722
; CURRENT FILING DATE: 2002-01-08
; PRIOR APPLICATION NUMBER: US 08/849,406
; PRIOR FILING DATE: 1999-07-21
; PRIOR APPLICATION NUMBER: PCT/US95/16349
; PRIOR FILING DATE: 1995-12-15
; PRIOR APPLICATION NUMBER: US 08/358,160
; PRIOR FILING DATE: 1994-12-16
; NUMBER OF SEQ ID NOS: 129
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 103
; LENGTH: 64
; TYPE: PRT
; ORGANISM: Caretta sp.
US-10-038-722-103

Alignment Scores:

Pred. No.: 9.55e-11 Length: 64
Score: 184.00 Matches: 27
Percent Similarity: 73.21% Conservative: 14
Best Local Similarity: 48.21% Mismatches: 15
Query Match: 24.08% Indels: 0
DB: 10 Gaps: 0

US-10-807-204-11 (1-396) x US-10-038-722-103 (1-64)

QY 217 AGAAGGATATATGCAGTATGCCACAGGAGGCTGGCCCTGCCTCCATACACAC 276
Db 4 LysArgAspIleCysArgLeuProGluGlnGlyProCysGlyArgLeuProArg 23
QY 277 TGGTGTACAAATAAAAAAATTAAGATCTGCTCCGAATTCATCTATGGCGGTTGCCAGGG 336
Db 24 TyrPheTyrAsnProAlaSerArgMetCysGluSerPheIleTyrGlyGlyCysGly 43
QY 337 AACATAACAATTCCTCAAACTGAAGCTATCTGCTGGTCACCTGCAAA 384
Db 44 AsnLysAsnAsnPheLysThrLysAlaGluCysValArgAlaCysArg 59

RESULT 26

US-10-115-134-17
; Sequence 17, Application US/10115134
; Publication No. US20030223977A1

; GENERAL INFORMATION:
; APPLICANT: LEY, Arthur Charles
; APPLICANT: GUTERMAN, Sonia Kosow
; APPLICANT: MARKLAND, William
; APPLICANT: KENT, Rachel Baribault
; APPLICANT: ROBERTS, Bruce Lindsey
; APPLICANT: LADNER, Robert Charles
; TITLE OF INVENTION: DOMAIN MUTANTS AS CATHEPSIN G INHIBITORS
; FILE REFERENCE: LEY-1C
; CURRENT APPLICATION NUMBER: US/10/115,134
; CURRENT FILING DATE: 2002-04-04
; PRIOR APPLICATION NUMBER: 08/849,406
; PRIOR FILING DATE: 2001-07-21
; NUMBER OF SEQ ID NOS: 92
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 17
; LENGTH: 64
; TYPE: PRT
; ORGANISM: Caretta sp.
US-10-115-134-17

Alignment Scores:
Pred. No.: 9.55e-11 Length: 64
Score: 184.00 Matches: 27
Percent Similarity: 73.21% Conservative: 14
Best Local Similarity: 48.21% Mismatches: 15
Query Match: 24.08% Indels: 0
DB: 15 Gaps: 0

US-10-807-204-11 (1-396) x US-10-115-134-17 (1-64)

QY 217 AGAAGGATATATGCAGTATGCCACAGGAGGCTGGCCCTGCCTCCATACACAC 276
Db 4 LysArgAspIleCysArgLeuProGluGlnGlyProCysGlyArgLeuProArg 23
QY 277 TGGTGTACAAATAAAAAAATTAAGATCTGCTCCGAATTCATCTATGGCGGTTGCCAGGG 336
Db 24 TyrPheTyrAsnProAlaSerArgMetCysGluSerPheIleTyrGlyGlyCysGly 43
QY 337 AACATAACAATTCCTCAAACTGAAGCTATCTGCTGGTCACCTGCAAA 384
Db 44 AsnLysAsnAsnPheLysThrLysAlaGluCysValArgAlaCysArg 59

RESULT 27
US-10-369-736-3
; Sequence 3, Application US/10369736
; Publication No. US20030162714A1
; GENERAL INFORMATION:

```
; APPLICANT: HILL, JENNIFER J.
; APPLICANT: WOLFMAN, NEIL M.
; TITLE OF INVENTION: FOLLISTATIN DOMAIN CONTAINING PROTEINS
; FILE REFERENCE: 08702.0015-00
; CURRENT APPLICATION NUMBER: US/10/369,736
; CURRENT FILING DATE: 2003-02-21
; PRIOR APPLICATION NUMBER: 60/357,846
; PRIOR FILING DATE: 2002-02-21
; PRIOR APPLICATION NUMBER: 60/434,645
; PRIOR FILING DATE: 2002-12-20
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 571
; TYPE: PRF
; ORGANISM: Mus sp.
US-10-369-736-3

Alignment Scores:
Pred. No.: 3.36e-10 Length: 571
Score: 180.50 Matches: 35
Percent Similarity: 42.73% Conservative: 12
Best Local Similarity: 31.82% Mismatches: 34
Query Match: 23.63% Indels: 29
DB: 14 Gaps: 3

US-10-807-204-11 (1-396) x US-10-369-736-49 (1-571)
QY 139 CAGTGTACCAAAACCC-----AGAGATTGCCAGAAACATG----- 174
Db 322 GluCysLeuLysProProAspSerGluAspCysGlyGluGlnThrArgTrpHisPhe 341
QY 175 -----AAGTGTGCCGTTCCAGCGGTGGAAG----- 201
Db 342 AspAlaGlnAlaAsnAsnCysLeuThrPheThrPheGlyHisCysHisAsnLeuAsn 361
QY 202 -----AAATGTTTACACTTCAGAAAGGATATATGC 231
Db 362 HisPheGluThrTyrGluAlaCysMetLeuAlaCysMetSerGlyProLeuAlaThrCys 381
QY 232 AGTATGCCACAGGAGGCTGCCCTGCCTCCATACACACTGGTGGTACAATAAA 291
Db 382 SerLeuProAlaLeuGlnGlyProCysLysAlaTyrValProArgTrpAlaTyrAsnSer 401
QY 292 AAAACTAAGATCTCTCGGAATTCATCTATGGCGGTTGCCAGGGGAAACAATAA 351
Db 402 GlnThrGlyLeuCysGlnSerPheValTyrGlyCysGluGlyAsnGlyAsnAsnPhe 421
QY 352 CAAACTGAAGCTATCTGTCTGTGCACCTGC 381
Db 422 GluSerArgGluAlaCysGluGluSerCys 431

RESULT 29
US-10-369-738-3
; Sequence 3, Application US/10369738
; Publication No. US20030180306A1
; GENERAL INFORMATION:
; APPLICANT: HILL, JENNIFER J.
; APPLICANT: WOLFMAN, NEIL M.
; TITLE OF INVENTION: FOLLISTATIN DOMAIN CONTAINING PROTEINS
; FILE REFERENCE: 08702.0014-00
; CURRENT APPLICATION NUMBER: US/10/369,738
; CURRENT FILING DATE: 2003-02-21
; PRIOR APPLICATION NUMBER: 60/357,846
; PRIOR FILING DATE: 2002-02-21
; PRIOR APPLICATION NUMBER: 60/434,645
; PRIOR FILING DATE: 2002-12-20
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 571
; TYPE: PRF
; ORGANISM: Mus sp.
US-10-369-738-3

Alignment Scores:
Pred. No.: 3.36e-10 Length: 571
Score: 180.50 Matches: 35
Percent Similarity: 42.73% Conservative: 12
Best Local Similarity: 31.82% Mismatches: 34
Query Match: 23.63% Indels: 29
DB: 14 Gaps: 3

US-10-807-204-11 (1-396) x US-10-369-738-3 (1-571)
QY 139 CAGTGTACCAAAACCC-----AGAGATTGCCAGAAACATG----- 174
Db 322 GluCysLeuLysProProAspSerGluAspCysGlyGluGlnThrArgTrpHisPhe 341
QY 175 -----AAGTGTGCCGTTCCAGCGGTGGAAG----- 201
Db 342 AspAlaGlnAlaAsnAsnCysLeuThrPheThrPheGlyHisCysHisAsnLeuAsn 361
QY 202 -----AAATGTTTACACTTCAGAAAGGATATATGC 231
Db 362 HisPheGluThrTyrGluAlaCysMetLeuAlaCysMetSerGlyProLeuAlaThrCys 381
QY 232 AGTATGCCACAGGAGGCTGCCCTGCCTCCATACACACTGGTGGTACAATAAA 291
Db 382 SerLeuProAlaLeuGlnGlyProCysLysAlaTyrValProArgTrpAlaTyrAsnSer 401
QY 292 AAAACTAAGATCTCTCGGAATTCATCTATGGCGGTTGCCAGGGGAAACAATAA 351
Db 402 GlnThrGlyLeuCysGlnSerPheValTyrGlyCysGluGlyAsnGlyAsnAsnPhe 421
QY 352 CAAACTGAAGCTATCTGTCTGTGCACCTGC 381
Db 422 GluSerArgGluAlaCysGluGluSerCys 431

RESULT 28
US-10-369-736-49
; Sequence 49, Application US/10369736
; Publication No. US20030162714A1
; GENERAL INFORMATION:
; APPLICANT: HILL, JENNIFER J.
; APPLICANT: WOLFMAN, NEIL M.
; TITLE OF INVENTION: FOLLISTATIN DOMAIN CONTAINING PROTEINS
; FILE REFERENCE: 08702.0015-00
; CURRENT APPLICATION NUMBER: US/10/369,736
; CURRENT FILING DATE: 2003-02-21
; PRIOR APPLICATION NUMBER: 60/357,846
; PRIOR FILING DATE: 2002-02-21
; PRIOR APPLICATION NUMBER: 60/434,645
; PRIOR FILING DATE: 2002-12-20
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 49
; LENGTH: 571
; TYPE: PRF
; ORGANISM: Mus sp.
```

QY 175 -----AAGTGTGCGCCGTTACGCGGTGGAAG----- 201
 Db 342 AspAlaGlnAlaAsnAsnCysLeuThrPheThrPheGlyHisCysHisAsnLeuAen 361
 QY 202 -----AAATGTTTAGACTTCAGAAAGGATATATGC 231
 Db 362 HisPheGluThrTyrrGluAlaCysMetLeuAlaCysMetSerGlyProLeuAlaThrCys 381
 QY 232 AGTATGCCACAGAGGCGTCCCTGCGCTCCATACACACACTGCGTGGTACAAATAA 291
 Db 382 SerLeuProAlaLeuGlnGlyProCysLysAlaTyrrValProArgTrrPalaTyrrAsnSer 401
 QY 292 AAAAATAAGATCTGCTCCGAATTCATATGCGCGTTCGCCAGGGGAAACAATAACAACCTTC 351
 Db 402 GlnThrGlyLeuCysGlnSerPheValTyrrGlyGlyCysGluGlyAsnGlyAsnAenPhe 421
 QY 352 CAAACTGAAGCTATCTGCTGTCACCTGC 381
 Db 422 GluSerArgGluAlaCysGluGluSerCys 431
 RESULT 30
 US-10-369-738-49
 ; Sequence 49, Application US/10369738
 ; Publication No. US20030180306A1
 ; GENERAL INFORMATION:
 ; APPLICANT: WOLFMAN, NEIL M.
 ; TITLE OF INVENTION: FOLLISTATIN DOMAIN CONTAINING PROTEINS
 ; FILE REFERENCE: 08702.0014-00
 ; CURRENT APPLICATION NUMBER: 2003-02-21
 ; PRIOR FILING DATE: 2003-02-21
 ; PRIOR FILING DATE: 2002-02-21
 ; PRIOR FILING DATE: 2002-12-20
 ; NUMBER OF SEQ ID NOS: 53
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 49
 ; LENGTH: 571
 ; TYPE: PRT
 ; ORGANISM: Mus sp.
 US-10-369-738-49
 Alignment Scores:
 Pred. No.: 3 36e-10 Length: 571
 Score: 180.50 Matches: 35
 Percent Similarity: 42.73% Conservative: 12
 Best Local Similarity: 31.82% Mismatches: 34
 Query Match: 23.63% Indels: 29
 DB: 14 Gaps: 3
 US-10-807-204-11 (1-396) x US-10-369-738-49 (1-571)
 QY 139 CAGTGTACCAACCC-----AGAGATTGCCAGAAACATG----- 174
 Db 322 GluCysLeuLysProAspSerGluAspCysGlyGluGlnThrArgTrpHisPhe 341
 QY 175 -----AAGTGTGCGCCGTTACGCGGTGGAAG----- 201
 Db 342 AspAlaGlnAlaAsnAsnCysLeuThrPheThrPheGlyHisCysHisAsnLeuAen 361
 QY 202 -----AAATGTTTAGACTTCAGAAAGGATATATGC 231
 Db 362 HisPheGluThrTyrrGluAlaCysMetLeuAlaCysMetSerGlyProLeuAlaThrCys 381
 QY 232 AGTATGCCACAGAGGCGTCCCTGCGCTCCATACACACACTGCGTGGTACAAATAA 291
 Db 382 SerLeuProAlaLeuGlnGlyProCysLysAlaTyrrValProArgTrrPalaTyrrAsnSer 401
 QY 292 AAAAATAAGATCTGCTCCGAATTCATATGCGCGTTCGCCAGGGGAAACAATAACAACCTTC 351
 Db 402 GlnThrGlyLeuCysGlnSerPheValTyrrGlyGlyCysGluGlyAsnGlyAsnAenPhe 421
 QY 352 CAAACTGAAGCTATCTGCTGTCACCTGC 381
 Db 422 GluSerArgGluAlaCysGluGluSerCys 431
 RESULT 32
 US-11-028-058-49
 ; Sequence 49, Application US/11028058
 ; Publication No. US20050106154A1
 ; GENERAL INFORMATION:
 ; APPLICANT: WOLFMAN, NEIL M.
 ; TITLE OF INVENTION: FOLLISTATIN DOMAIN CONTAINING PROTEINS
 ; FILE REFERENCE: 08702.0015-00
 ; CURRENT APPLICATION NUMBER: US/11/028,058

QY 352 CAAACTGAAGCTATCTGCTGTCACCTGC 381
 Db 422 GluSerArgGluAlaCysGluGluSerCys 431
 RESULT 31
 US-11-028-058-3
 ; Sequence 3, Application US/11028058
 ; Publication No. US20050106154A1
 ; GENERAL INFORMATION:
 ; APPLICANT: HILL, JENNIFER J.
 ; APPLICANT: WOLFMAN, NEIL M.
 ; TITLE OF INVENTION: FOLLISTATIN DOMAIN CONTAINING PROTEINS
 ; FILE REFERENCE: 08702.0015-00
 ; CURRENT APPLICATION NUMBER: US/11/028,058
 ; CURRENT FILING DATE: 2005-01-04
 ; PRIOR APPLICATION NUMBER: US/10/369,736
 ; PRIOR FILING DATE: 2003-02-21
 ; PRIOR FILING DATE: 2002-02-21
 ; PRIOR FILING DATE: 2002-02-21
 ; PRIOR FILING DATE: 2002-12-20
 ; NUMBER OF SEQ ID NOS: 53
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 3
 ; LENGTH: 571
 ; TYPE: PRT
 ; ORGANISM: Mus sp.
 US-11-028-058-3
 Alignment Scores:
 Pred. No.: 3 36e-10 Length: 571
 Score: 180.50 Matches: 35
 Percent Similarity: 42.73% Conservative: 12
 Best Local Similarity: 31.82% Mismatches: 34
 Query Match: 23.63% Indels: 29
 DB: 19 Gaps: 3
 US-10-807-204-11 (1-396) x US-11-028-058-3 (1-571)
 QY 139 CAGTGTACCAACCC-----AGAGATTGCCAGAAACATG----- 174
 Db 322 GluCysLeuLysProAspSerGluAspCysGlyGluGlnThrArgTrpHisPhe 341
 QY 175 -----AAGTGTGCGCCGTTACGCGGTGGAAG----- 201
 Db 342 AspAlaGlnAlaAsnAsnCysLeuThrPheThrPheGlyHisCysHisAsnLeuAen 361
 QY 202 -----AAATGTTTAGACTTCAGAAAGGATATATGC 231
 Db 362 HisPheGluThrTyrrGluAlaCysMetLeuAlaCysMetSerGlyProLeuAlaThrCys 381
 QY 232 AGTATGCCACAGAGGCGTCCCTGCGCTCCATACACACACTGCGTGGTACAAATAA 291
 Db 382 SerLeuProAlaLeuGlnGlyProCysLysAlaTyrrValProArgTrrPalaTyrrAsnSer 401
 QY 292 AAAAATAAGATCTGCTCCGAATTCATATGCGCGTTCGCCAGGGGAAACAATAACAACCTTC 351
 Db 402 GlnThrGlyLeuCysGlnSerPheValTyrrGlyGlyCysGluGlyAsnGlyAsnAenPhe 421
 QY 352 CAAACTGAAGCTATCTGCTGTCACCTGC 381
 Db 422 GluSerArgGluAlaCysGluGluSerCys 431
 RESULT 32
 US-11-028-058-49
 ; Sequence 49, Application US/11028058
 ; Publication No. US20050106154A1
 ; GENERAL INFORMATION:
 ; APPLICANT: WOLFMAN, NEIL M.
 ; TITLE OF INVENTION: FOLLISTATIN DOMAIN CONTAINING PROTEINS
 ; FILE REFERENCE: 08702.0015-00
 ; CURRENT APPLICATION NUMBER: US/11/028,058

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; CURRENT FILING DATE: 2005-01-04
; PRIOR APPLICATION NUMBER: US/10/369,736
; PRIOR FILING DATE: 2003-02-21
; PRIOR APPLICATION NUMBER: 60/357,846
; PRIOR FILING DATE: 2002-02-21
; PRIOR APPLICATION NUMBER: 60/434,645
; PRIOR FILING DATE: 2002-12-20
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 49
; LENGTH: 571
; TYPE: PRT
; ORGANISM: Mus sp.
US-11-028-058-49

Alignment Scores:
Pred. No.: 3.36e-10 Length: 571
Score: 180.50 Matches: 35
Percent Similarity: 42.73% Conservative: 12
Best Local Similarity: 31.82% Mismatches: 34
Query Match: 23.63% Indels: 29
DB: 19 Gaps: 3

US-10-807-204-11 (1-396) x US-11-028-058-49 (1-571)

Qy 139 CAGGTACCACCC-----AGAGATTGCCAGAAACATG----- 174
Db 322 GluCysLeuYsPProAspSerGluAspCysGlyGluGluGlnThrArgTrpHisPhe 341
Qy 175 -----AAGTGTGCGCGTTACGCGTGGAAAG----- 201
Db 342 AspAlaGlnAlaAsnAsnCysLeuThrPheThrPheGlyHisCysHisAsnLeuAsn 361
Qy 202 -----AAATGTTTAGACTTCAGAAAGATATATGC 231
Db 362 HisPheGluThrTyTGluAlaCysMetLeuAlaCysMetSerGlyProLeuAlaThrCys 381
Qy 232 AGTATGCCACAGGAGGCGCTGCTGCCTCCATACCACACTGGTGGTACAATAAA 291
Db 382 SerLeuProAlaLeuGlnGlyProCysLysAlaTyValProArgTrpAlaTyAsnSer 401
Qy 292 AAAACTAAGATCTGCTCCGAATTCATCTATGCGGTTGCCAGGGGAACAATAACAACCTTC 351
Db 402 GlnThrGlyLeuCysGlnSerPheValTyGlyGlyCysGluGlyAsnGlyAsnAsnPhe 421
Qy 352 CAAACTAAGCTATCTGCTGGTCACCTGC 381
Db 422 GluSerArgGluAlaCysGluGluSerCys 431

RESULT 33
US-10-807-204-7
; Sequence 7, Application US/10807204
; Publication No. US20040229312A1
; GENERAL INFORMATION:
; APPLICANT: Bougueleret, Lydie
; APPLICANT: Bairoch, Amos
; APPLICANT: Niknejad, Anne
; TITLE OF INVENTION: Engineered Human Kunitz-Type Protease
; FILE REFERENCE: 54720-8015.US00
; CURRENT APPLICATION NUMBER: US/10/807,204
; CURRENT FILING DATE: 2004-03-22
; PRIOR APPLICATION NUMBER: PCT/EP03/01629
; PRIOR FILING DATE: 2003-02-18
; PRIOR APPLICATION NUMBER: US 60/358,683
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 33
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-807-204-10

Alignment Scores:
Pred. No.: 2.27e-10 Length: 33
Score: 180.00 Matches: 33
Percent Similarity: 96.97% Conservative: 0
Best Local Similarity: 96.97% Mismatches: 1
Query Match: 23.56% Indels: 0
DB: 16 Gaps: 0

US-10-807-204-11 (1-396) x US-10-807-204-10 (1-33)

Qy 295 ACTAAGATCTGCTCCGAATTCATCTATGCGGTTGCCAGGGGAACAATAACAACCTTCAA 354
Db 1 ThrLysIleCysSerGluPheIleTyTGlySerGlnGlyAsnAsnAsnPheGln 20
Qy 355 ACTGAAGCTATCTGCTGGTCACCTGCACCAAAAAATACCAT 393
Db 21 ThrGluAlaIleCysLeuValThrCysLysLysTyHis 33

RESULT 34
US-10-807-204-10
; Sequence 10, Application US/10807204
; Publication No. US20040229312A1
; GENERAL INFORMATION:
; APPLICANT: Bougueleret, Lydie
; APPLICANT: Bairoch, Amos
; APPLICANT: Niknejad, Anne
; TITLE OF INVENTION: Engineered Human Kunitz-Type Protease
; FILE REFERENCE: 54720-8015.US00
; CURRENT APPLICATION NUMBER: US/10/807,204
; CURRENT FILING DATE: 2004-03-22
; PRIOR APPLICATION NUMBER: PCT/EP03/01629
; PRIOR FILING DATE: 2003-02-18
; PRIOR APPLICATION NUMBER: US 60/358,683
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 33
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-807-204-10

Alignment Scores:
Pred. No.: 2.27e-10 Length: 33
Score: 180.00 Matches: 33
Percent Similarity: 96.97% Conservative: 0
Best Local Similarity: 96.97% Mismatches: 1
Query Match: 23.56% Indels: 0
DB: 16 Gaps: 0

US-10-807-204-11 (1-396) x US-10-807-204-10 (1-33)

Qy 295 ACTAAGATCTGCTCCGAATTCATCTATGCGGTTGCCAGGGGAACAATAACAACCTTCAA 354
Db 1 ThrLysIleCysSerGluPheIleTyTGlySerGlnGlyAsnAsnAsnPheGln 20
Qy 355 ACTGAAGCTATCTGCTGGTCACCTGCACCAAAAAATACCAT 393
Db 21 ThrGluAlaIleCysLeuValThrCysLysLysTyHis 33

RESULT 35
US-10-038-722-5
; Sequence 5, Application US/10038722
; Publication No. US20030175919A1
; GENERAL INFORMATION:
; APPLICANT: LEY, Arthur C.
; APPLICANT: GUTERMAN, Sonia K.
; APPLICANT: MARKLAND, William
; APPLICANT: KENT, Rachel B.
; APPLICANT: ROBERTS, Bruce L.
; APPLICANT: LADNER, Robert C.
```

;; TITLE OF INVENTION: ITI-D1 KUNITZ DOMAIN MUTANTS AS nHE INHIBITORS

;; FILE REFERENCE: LEY=1B
;; CURRENT APPLICATION NUMBER: US/10/038,722
;; CURRENT FILING DATE: 2002-01-08
;; PRIOR APPLICATION NUMBER: US 08/849,406
;; PRIOR FILING DATE: 1999-07-21
;; PRIOR APPLICATION NUMBER: PCT/US95/16349
;; PRIOR FILING DATE: 1995-12-15
;; PRIOR APPLICATION NUMBER: US 08/358,160
;; PRIOR FILING DATE: 1994-12-16
;; NUMBER OF SEQ ID NOS: 129
;; SOFTWARE: PatentIn version 3.1
;; SEQ ID NO 5
;; LENGTH: 58
;; TYPE: PRT
;; ORGANISM: Artificial Sequence
;; FEATURE:

;; OTHER INFORMATION: Consensus Kunitz domain

US-10-038-722-5

Alignment Scores:
Pred. No.: 5 28e-10 Length: 58
Score: 177.00 Matches: 31
Percent Similarity: 65.43% Conservative: 5
Best Local Similarity: 56.36% Mismatches: 19
Query Match: 23.17% Indels: 0
DB: 14 Gaps: 0

US-10-807-204-11 (1-396) x US-10-038-722-5 (1-58)

QY 217 AGAAGGATATATGCAAGTATGCCACAGGAGGCTGGCCCTGCTCCATACACAC 276
Db 1 ArgProAspPheCysLeuLeuProAlaGluThrGlyProCysArgAlaMetileProArg 20
QY 277 TGGTGGTACAAATAAAACTAAGATCTGCTCCGATTCATCTATGCGGTTGCCAGGG 336
Db 21 PheTyrTyrAsnAlaSerGlyLysCysGluProPheIleTyrGlyGlyCysGlyGly 40
QY 337 AACATAACAACTTCCAACTCAAGCTATCTGTGTCACCTGC 381
Db 41 AsnAlaAsnAsnPheLysThrGluGluGluCysArgArgThrCys 55

RESULT 36
US-09-896-095-147
; Sequence 147, Application US/09896095
; Publication No. US20030219886A1
; GENERAL INFORMATION:
; APPLICANT: LADNER, Charles C.
; APPLICANT: GUTERMAN, Sonia K.
; APPLICANT: ROBERTS, Bruce L.
; APPLICANT: MARKLAND, William
; APPLICANT: LEY, Arthur C.
; APPLICANT: KENT, Rachel B.
; TITLE OF INVENTION: DIRECTED EVOLUTION OF NOVEL BINDING PROTEINS
; FILE REFERENCE: LADNER=7L
; CURRENT APPLICATION NUMBER: US/09/896,095
; CURRENT FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: 08/415,922
; PRIOR FILING DATE: 1995-03-04
; PRIOR APPLICATION NUMBER: 08/009,319
; PRIOR FILING DATE: 1993-01-26
; PRIOR APPLICATION NUMBER: 07/664,989
; PRIOR FILING DATE: 1991-03-01
; PRIOR APPLICATION NUMBER: 08/993,776
; PRIOR FILING DATE: 1997-12-18
; NUMBER OF SEQ ID NOS: 274
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 147
; LENGTH: 67
; TYPE: PRT
; ORGANISM: Bos taurus
US-09-896-095-147

Alignment Scores:
Pred. No.: 8 88e-10 Length: 67
Score: 175.00 Matches: 27
Percent Similarity: 68.52% Conservative: 10
Best Local Similarity: 50.00% Mismatches: 17
Query Match: 22.91% Indels: 0
DB: 10 Gaps: 0

US-10-807-204-11 (1-396) x US-09-896-095-147 (1-67)

QY 223 GATATATGCAAGTATGCCACAGGAGGCTGGCCCTGCTCCATACACACTGGTGG 282
Db 6 AspLeuCysGlnLeuProGlnAlaArgGlyProCysLysAlaAlaLeuLeuArgTyrPhe 25
QY 283 TACAATAAAAAAATAAGATCTGCTCCGAATTCATCTATGCGGTTGCCAGGGAAACAAT 342
Db 26 TyrAsnSerThrSerAsnAlaCysGluProPheThrTyrGlyGlyCysGlnGlyAsnAsn 45
QY 343 AACAACTTCCAACTGAAGCTATCTGTGTCACCTGCAAA 384
Db 46 AsnAsnPheGluThrThrGluMetCysLeuArgIleCysGlu 59

RESULT 37

US-10-038-722-90
; Sequence 90, Application US/10038722
; Publication No. US20030175919A1
; GENERAL INFORMATION:
; APPLICANT: LEY, Arthur C.
; APPLICANT: GUTERMAN, Sonia K.
; APPLICANT: MARKLAND, William
; APPLICANT: KENT, Rachel B.
; APPLICANT: ROBERTS, Bruce L.
; APPLICANT: LADNER, Robert C.
; TITLE OF INVENTION: ITI-D1 KUNITZ DOMAIN MUTANTS AS nHE INHIBITORS
; FILE REFERENCE: LEY=1B
; CURRENT APPLICATION NUMBER: US/10/038,722
; CURRENT FILING DATE: 2002-01-08
; PRIOR APPLICATION NUMBER: US 08/849,406
; PRIOR FILING DATE: 1999-07-21
; PRIOR APPLICATION NUMBER: PCT/US95/16349
; PRIOR FILING DATE: 1995-12-15
; PRIOR APPLICATION NUMBER: US 08/358,160
; PRIOR FILING DATE: 1994-12-16
; NUMBER OF SEQ ID NOS: 129
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 90
; LENGTH: 67
; TYPE: PRT
; ORGANISM: Bos taurus
US-10-038-722-90

Alignment Scores:
Pred. No.: 8 88e-10 Length: 67
Score: 175.00 Matches: 27
Percent Similarity: 68.52% Conservative: 10
Best Local Similarity: 50.00% Mismatches: 17
Query Match: 22.91% Indels: 0
DB: 14 Gaps: 0

US-10-807-204-11 (1-396) x US-10-038-722-90 (1-67)

QY 223 GATATATGCAAGTATGCCACAGGAGGCTGGCCCTGCTCCATACACACTGGTGG 282
Db 6 AspLeuCysGlnLeuProGlnAlaArgGlyProCysLysAlaAlaLeuLeuArgTyrPhe 25
QY 283 TACAATAAAAAAATAAGATCTGCTCCGAATTCATCTATGCGGTTGCCAGGGAAACAAT 342
Db 26 TyrAsnSerThrSerAsnAlaCysGluProPheThrTyrGlyGlyCysGlnGlyAsnAsn 45
QY 343 AACAACTTCCAACTGAAGCTATCTGTGTCACCTGCAAA 384
Db 46 AsnAsnPheGluThrThrGluMetCysLeuArgIleCysGlu 59


```

Qy 217 AGAAGGATATATGAGTATGATCCACAGGAGGCTGGCCCTGCTCCATACACAC 276
Db 1 ArgProAspPheCysGlnLeuGlyTyrSerAlaGlyProCysValAlaMetPheProArg 20
Qy 277 TGGTGGTACATAAAAAAAGTATGCTCCGAAATTCATCTATGGCGGTGGCAGGG 336
Db 21 TyrPheTyrAsnGlyAlaSerMetAlaCysGlnThrPheValTyrGlyGlyCysMetGly 40
Qy 337 AACCAATACAACTCCAACTGAAGCTATCTGCTGGTCACCTGCATAA 384
Db 41 AsnGlyAsnAsnPheValThrGluLysAspCysLeuGlnThrCysArg 56

RESULT 44
US-10-115-134-90
; Sequence 90, Application US/10115134
; Publication No. US20030223977A1
; GENERAL INFORMATION:
; APPLICANT: LEY, Arthur Charles
; APPLICANT: GUTERMAN, Sonia Kosow
; APPLICANT: MARKLAND, William
; APPLICANT: KENT, Rachel Baribault
; APPLICANT: ROBERTS, Bruce Lindsay
; APPLICANT: LADNER, Robert Charles
; TITLE OF INVENTION: DOMAIN MUTANTS AS CATHEPSIN G INHIBITORS
; FILE REFERENCE: LEY=1C
; CURRENT APPLICATION NUMBER: US/10/115,134
; CURRENT FILING DATE: 2002-04-04
; PRIOR APPLICATION NUMBER: 08/849,406
; PRIOR FILING DATE: 2001-07-21
; NUMBER OF SEQ ID NOS: 92
; SOFTWARE: Patent In version 3.2
; SEQ ID NO 90
; LENGTH: 58
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: MUTQE
US-10-115-134-90

Alignment Scores:
Pred. No.: 1.42e-09 Length: 58
Score: 173.00 Matches: 28
Percent Similarity: 62.50% Conservative: 7
Best Local Similarity: 50.00% Mismatches: 21
Query Match: 22.64% Indels: 0
DB: 15 Gaps: 0

US-10-807-204-11 (1-396) x US-10-115-134-90 (1-58)
Qy 217 AGAAGGATATATGAGTATGATCCACAGGAGGCTGGCCCTGCTCCATACACAC 276
Db 1 ArgProAspPheCysGlnLeuGlyTyrSerAlaGlyProCysValAlaMetPheProArg 20
Qy 277 TGGTGGTACATAAAAAAAGTATGCTCCGAAATTCATCTATGGCGGTGGCAGGG 336
Db 21 TyrPheTyrAsnGlyAlaSerMetAlaCysGlnThrPheValTyrGlyGlyCysMetGly 40
Qy 337 AACCAATACAACTCCAACTGAAGCTATCTGCTGGTCACCTGCATAA 384
Db 41 AsnGlyAsnAsnPheValThrGluLysAspCysLeuGlnThrCysArg 56

RESULT 45
US-10-456-986A-42
; Sequence 42, Application US/10456986A
; Publication No. US20040038893A1
; GENERAL INFORMATION:
; APPLICANT: Ladner, Robert C.
; APPLICANT: Ley, Arthur C.
; APPLICANT: Hirani, Shirish
; APPLICANT: Williams, Anthony
; TITLE OF INVENTION: Prevention and Reduction of Blood Loss
; FILE REFERENCE: 3421.1001-002
; CURRENT APPLICATION NUMBER: US/10/456,986A
; CURRENT FILING DATE: 2003-06-06
; PRIOR APPLICATION NUMBER: 60/387,239
; PRIOR FILING DATE: 2002-06-07
; PRIOR APPLICATION NUMBER: 60/407,003
; PRIOR FILING DATE: 2002-08-28
; NUMBER OF SEQ ID NOS: 54
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 43
; LENGTH: 58
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: MUTT26A Sequence
US-10-456-986A-43

Alignment Scores:
Pred. No.: 1.42e-09 Length: 58
Score: 173.00 Matches: 28
Percent Similarity: 62.50% Conservative: 7
Best Local Similarity: 50.00% Mismatches: 21
Query Match: 22.64% Indels: 0
DB: 15 Gaps: 0

US-10-807-204-11 (1-396) x US-10-456-986A-43 (1-58)

```

```

; CURRENT FILING DATE: 2003-06-06
; PRIOR APPLICATION NUMBER: 60/387,239
; PRIOR FILING DATE: 2002-06-07
; PRIOR APPLICATION NUMBER: 60/407,003
; PRIOR FILING DATE: 2002-08-28
; NUMBER OF SEQ ID NOS: 54
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 42
; LENGTH: 58
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: BITT-E7-141 Sequence
US-10-456-986A-42

Alignment Scores:
Pred. No.: 1.42e-09 Length: 58
Score: 173.00 Matches: 28
Percent Similarity: 62.50% Conservative: 7
Best Local Similarity: 50.00% Mismatches: 21
Query Match: 22.64% Indels: 0
DB: 15 Gaps: 0

US-10-807-204-11 (1-396) x US-10-456-986A-42 (1-58)
Qy 217 AGAAGGATATATGAGTATGATCCACAGGAGGCTGGCCCTGCTCCATACACAC 276
Db 1 ArgProAspPheCysGlnLeuGlyTyrSerAlaGlyProCysValAlaMetPheProArg 20
Qy 277 TGGTGGTACATAAAAAAAGTATGCTCCGAAATTCATCTATGGCGGTGGCAGGG 336
Db 21 TyrPheTyrAsnGlyThrSerMetAlaCysGlnThrPheValTyrGlyGlyCysMetGly 40
Qy 337 AACCAATACAACTCCAACTGAAGCTATCTGCTGGTCACCTGCATAA 384
Db 41 AsnGlyAsnAsnPheValThrGluLysAspCysLeuGlnThrCysArg 56

RESULT 46
US-10-456-986A-43
; Sequence 43, Application US/10456986A
; Publication No. US20040038893A1
; GENERAL INFORMATION:
; APPLICANT: Ladner, Robert C.
; APPLICANT: Ley, Arthur C.
; APPLICANT: Hirani, Shirish
; APPLICANT: Williams, Anthony
; TITLE OF INVENTION: Prevention and Reduction of Blood Loss
; FILE REFERENCE: 3421.1001-002
; CURRENT APPLICATION NUMBER: US/10/456,986A
; CURRENT FILING DATE: 2003-06-06
; PRIOR APPLICATION NUMBER: 60/387,239
; PRIOR FILING DATE: 2002-06-07
; PRIOR APPLICATION NUMBER: 60/407,003
; PRIOR FILING DATE: 2002-08-28
; NUMBER OF SEQ ID NOS: 54
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 43
; LENGTH: 58
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: MUTT26A Sequence
US-10-456-986A-43

Alignment Scores:
Pred. No.: 1.42e-09 Length: 58
Score: 173.00 Matches: 28
Percent Similarity: 62.50% Conservative: 7
Best Local Similarity: 50.00% Mismatches: 21
Query Match: 22.64% Indels: 0
DB: 15 Gaps: 0

US-10-807-204-11 (1-396) x US-10-456-986A-43 (1-58)

```

;; TITLE OF INVENTION: KALLIKREIN-INHIBITOR THERAPIES
;; FILE REFERENCE: 10280-120001
;; CURRENT APPLICATION NUMBER: US/10/953,902A
;; CURRENT FILING DATE: 2004-09-27
;; PRIOR APPLICATION NUMBER: US 60/387,239
;; PRIOR FILING DATE: 2002-06-07
;; PRIOR APPLICATION NUMBER: US 60/407,003
;; PRIOR FILING DATE: 2002-08-28
;; PRIOR APPLICATION NUMBER: US 10/456,986
;; PRIOR FILING DATE: 2003-06-06
;; NUMBER OF SEQ ID NOS: 57
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO 42
;; LENGTH: 58
;; TYPE: PRT
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; OTHER INFORMATION: Synthetically generated peptide
US-10-953-902A-42

Alignment Scores:
Pred. No.: 1.42e-09 Length: 58
Score: 173.00 Matches: 28
Percent Similarity: 62.50% Conservative: 7
Best Local Similarity: 50.00% Mismatches: 21
Query Match: 22.64% Indels: 0
DB: Gaps: 0

US-10-807-204-11 (1-396) x US-10-953-902A-42 (1-58)
QY 217 AGAAGGATATATGCAGTATGCCAGGAGCTGCCTCCCTCCATACACAC 276
Db 1 ArgProAspPheCysGlnLeuGlyTyrSerAlaGlyProCysValAlaMetPheProArg 20
QY 277 TGGTGGTACATAAAAAAAGTCTGCTCCGAATTCATCTATGGCGGTTGCCAGGGG 336
Db 21 TyrPheTyrAsnGlyThrSerMetAlaCysGlnThrPheValTyrGlyCysMetGly 40
QY 337 AACATAACAACCTTCCAAACTGAAGCTATCTGTCTGGTCACCTGCAAA 384
Db 41 AsnGlyAsnAsnPheValThrGluLysAspCysLeuGlnThrCysArg 56

RESULT 49
US-10-953-902A-43
; Sequence 43, Application US/10953902A
; Publication No. US20050164928A1
; GENERAL INFORMATION:
; APPLICANT: Ladner, Robert C.
; APPLICANT: Ley, Arthur C.
; APPLICANT: Hirani, Shirish
; APPLICANT: Williams, Anthony
; APPLICANT: De Simoni, Maria Garzia
; APPLICANT: Bergamaschini, Luigi
; TITLE OF INVENTION: KALLIKREIN-INHIBITOR THERAPIES
; FILE REFERENCE: 10280-120001
; CURRENT APPLICATION NUMBER: US/10/953,902A
; CURRENT FILING DATE: 2004-09-27
; PRIOR APPLICATION NUMBER: US 60/387,239
; PRIOR FILING DATE: 2002-06-07
; PRIOR APPLICATION NUMBER: US 60/407,003
; PRIOR FILING DATE: 2002-08-28
; PRIOR APPLICATION NUMBER: US 10/456,986
; PRIOR FILING DATE: 2003-06-06
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 43
; LENGTH: 58
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetically generated peptide
US-10-953-902A-43

QY 217 AGAAGGATATATGCAGTATGCCAGGAGCTGCCTCCCTCCATACACAC 276
Db 1 ArgProAspPheCysGlnLeuGlyTyrSerAlaGlyProCysValAlaMetPheProArg 20
QY 277 TGGTGGTACATAAAAAAAGTCTGCTCCGAATTCATCTATGGCGGTTGCCAGGGG 336
Db 21 TyrPheTyrAsnGlyThrSerMetAlaCysGlnThrPheValTyrGlyCysMetGly 40
QY 337 AACATAACAACCTTCCAAACTGAAGCTATCTGTCTGGTCACCTGCAAA 384
Db 41 AsnGlyAsnAsnPheValThrGluLysAspCysLeuGlnThrCysArg 56

RESULT 47
US-10-456-986A-44
; Sequence 44, Application US/10456986A
; Publication No. US2004003893A1
; GENERAL INFORMATION:
; APPLICANT: Ladner, Robert C.
; APPLICANT: Hirani, Shirish
; APPLICANT: Williams, Anthony
; TITLE OF INVENTION: Prevention and Reduction of Blood Loss
; FILE REFERENCE: 3421.1001-002
; CURRENT APPLICATION NUMBER: US/10/456,986A
; CURRENT FILING DATE: 2003-06-06
; PRIOR APPLICATION NUMBER: 60/387,239
; PRIOR FILING DATE: 2002-06-07
; PRIOR APPLICATION NUMBER: 60/407,003
; PRIOR FILING DATE: 2002-08-28
; NUMBER OF SEQ ID NOS: 54
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 44
; LENGTH: 58
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: MUTQE Sequence
US-10-456-986A-44

Alignment Scores:
Pred. No.: 1.42e-09 Length: 58
Score: 173.00 Matches: 28
Percent Similarity: 62.50% Conservative: 7
Best Local Similarity: 50.00% Mismatches: 21
Query Match: 22.64% Indels: 0
DB: Gaps: 0

US-10-807-204-11 (1-396) x US-10-456-986A-44 (1-58)
QY 217 AGAAGGATATATGCAGTATGCCAGGAGCTGCCTCCCTCCATACACAC 276
Db 1 ArgProAspPheCysGlnLeuGlyTyrSerAlaGlyProCysValAlaMetPheProArg 20
QY 277 TGGTGGTACATAAAAAAAGTCTGCTCCGAATTCATCTATGGCGGTTGCCAGGGG 336
Db 21 TyrPheTyrAsnGlyThrSerMetAlaCysGlnThrPheValTyrGlyCysMetGly 40
QY 337 AACATAACAACCTTCCAAACTGAAGCTATCTGTCTGGTCACCTGCAAA 384
Db 41 AsnGlyAsnAsnPheValThrGluLysAspCysLeuGlnThrCysArg 56

RESULT 48
US-10-953-902A-42
; Sequence 42, Application US/10953902A
; Publication No. US20050164928A1
; GENERAL INFORMATION:
; APPLICANT: Ladner, Robert C.
; APPLICANT: Ley, Arthur C.
; APPLICANT: Hirani, Shirish
; APPLICANT: Williams, Anthony
; APPLICANT: De Simoni, Maria Garzia
; APPLICANT: Bergamaschini, Luigi

Alignment Scores:	
Pred. No.:	1.42e-09
Score:	173.00
Percent Similarity:	62.50%
Best Local Similarity:	50.00%
Query Match:	22.64%
DB:	18
Length:	58
Matches:	28
Conservative:	21
Mismatches:	7
Indels:	0
Gaps:	0

US-10-807-204-11 (1-396) x US-10-953-902A-43 (1-58)

Qy	217	AGAAAGGATATATGCAGTATATGCCACAGGAGGCTGGCCCTCTGGCTCATACACAC	276
Db	1	AtgProAspPheCysGlnLeuGlyTyrSerAlaGlyProCysValAlaMetPheProAtg	20
Qy	277	TGGTGGTACAATAAAAAAACTAAGATCTGCTCCGAATTCATCTATGGCGGTGGCAGGGG	336
Db	21	TyrPheTyrAsnGlyAlaSerMetAlaCysGlnThrPheValTyrGlyGlyCysMetGly	40
Qy	337	AACAATAACAACCTCCAAACTGAAGCTATCTGTCTGGTCACTCGCAA	384
Db	41	AsnGLYAspAsnPheValThrGluLysAspCysLeuGlnThrCysAsq	56

RESULT 50

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US-10-953-902A-44
; Sequence 44, Application US/10953902A
; Publication No. US20050164928A1
; GENERAL INFORMATION:
; APPLICANT: Ladner, Robert C.
; APPLICANT: Ley, Arthur C.
; APPLICANT: Hirani, Shirish
; APPLICANT: Williams, Anthony
; APPLICANT: De Simoni, Maria Garzia
; APPLICANT: Bergamaschini, Luigi
; TITLE OF INVENTION: KALLIKREIN-INHIBITOR THERAPIES
; FILE REFERENCE: 10280-120001
; CURRENT APPLICATION NUMBER: US/10/953,902A
; CURRENT FILING DATE: 2004-09-27
; PRIOR APPLICATION NUMBER: US 60/387,239
; PRIOR FILING DATE: 2002-06-07
; PRIOR APPLICATION NUMBER: US 60/407,003
; PRIOR FILING DATE: 2002-08-28
; PRIOR APPLICATION NUMBER: US 10/456,986
; PRIOR FILING DATE: 2003-06-06
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 44
; LENGTH: 58
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; US-10-953-902A-44
; OTHER INFORMATION: Synthetically generated peptide

```

Alignment Scores:	
Pred. No.:	1.42e-09
Score:	173.00
Percent Similarity:	62.50%
Best Local Similarity:	50.00%
Query Match:	22.64%
DB:	18
Length:	58
Matches:	28
Conservative:	7
Mismatches:	21
Indels:	0
Gaps:	0

US-10-807-204-11 (1-396) x US-10-953-902A-44 (1-58)

Qy	217	AGAAAGGATATATGCAGTATATGCCACAGAGAGCTGGCCCTCTGCTGCCTCATACACAC	276
Db	1	AtgProAspPheCysgluLeuGlyTyrSerAlaGlyProCysValAlaMetPheProArg	20
Qy	277	TGCTGGTACAAATAAAAAATCAAGATCTGCTCCGAATTCATCTATGCGGTGCCAGGG	336
Db	21	TyrPheTyArgNGlyThrSerMetAlaCysGluThrPheValTyrGlyGlyCysMetGly	40
Qy	337	AACAAATACAACTTCCAACTGAAGCTATCTCTGTGCTACCTGCAAA	384

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - protein search, using frame_plus_n2p model

Run on: September 21, 2005, 16:50:52 ; Search time 22 Seconds
(without alignments)
3463.803 Million cell updates/sec

Title: US-10-807-204-11
Perfect score: 764
Sequence: 1 atgggactctcaggactctt.....cctgcaaaaaataaccattaa 396

Scoring table: BLOSUM62

Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 566832

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 50 summaries

Command line parameters:

-MODE=frame-n2p.model -DEV=xlh
-Q=/cgn2_1/USPTO_spool/US10807204/runat_20092005_162900_29238/app_query.fasta_1.583
-DB=PIR_79 -QFMT=fastan -SUFFIX=std.rpr -MINMATCH=0.1 -LOOPEL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=1 -MATRIX=biosum62 -TRANS=human40.cdi -LIST=50
-DOALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=50 -MODE=LOCAL
-OUTFMT=ptc -NORM=ext -HEAPSIZ=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US10807204 @C@N 1 1 25 @runat_20092005_162900_29238 -NCPU=6 -ICPU=3
-NO MMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THRSADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

PIR_79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Prod. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	186	24.3	110	1 TITTOR	basic proteinase i
2	185.5	24.3	1522	2 H88380	protein T22F7.3 (i
3	173.5	22.7	1599	2 T16210	hypothetical prote
4	172	22.5	67	1 TIBOC	trypsin inhibitor,
5	171	22.4	1416	2 E88550	protein ZC84.1 (im
6	171	22.4	2844	2 S28291	hypothetical prote
7	168	22.0	1743	2 T26859	hypothetical prote
8	167.5	21.9	922	2 T23573	hypothetical prote
9	167.5	21.9	1474	2 D88550	protein ZC84.6 (im
10	165.5	21.7	337	1 TIGBI	alpha-1-microglobu
11	161.5	21.1	747	2 JH0773	Alzheimer's diseas
12	161	21.1	62	2 A44180	taicatoxin serine
13	161	21.1	751	2 A49574	beta-amyloid precu
14	160	20.9	57	2 A59204	basic proteinase i

15	160	20.9	252	2	JG0185	hepatocyte growth
16	157	20.5	58	1	TIHABK	isoinhibitor K (BP
17	157	20.5	111	2	S41082	amyloid precursor
18	157	20.5	763	2	A49321	amyloid beta (A4)
19	157	20.5	765	2	S42880	amyloid precursor-
20	154.5	20.2	300	2	S12143	lipoprotein-associ
21	154	20.2	484	4	A32761	hypothetical Alzhe
22	154	20.2	770	1	QRHUA4	Alzheimer's diseas
23	153	20.0	62	2	S19327	venom basic protei
24	153	20.0	299	2	I46937	tissue factor path
25	153	20.0	352	1	TI081	alpha-1-microglobu
26	152	19.9	62	2	S07451	proteinase inhibit
27	152	19.9	76	2	S06678	Alzheimer's diseas
28	152	19.9	76	2	S03607	Alzheimer's diseas
29	152	19.9	352	1	HCHU	alpha-1-microglobu
30	151.5	19.8	372	2	JC2556	venom basic protei
31	151	19.8	65	1	TIIVIC	Alzheimer's diseas
32	151	19.8	100	2	A32282	hypothetical prote
33	151	19.8	2150	2	T32437	hypothetical prote
34	150.5	19.7	1043	2	TI9734	chymotrypsin inhib
35	149.5	19.6	62	2	S01802	proteinase inhibit
36	149	19.5	57	1	TIHBP	Alzheimer's diseas
37	149	19.5	76	2	S04855	inter-alpha-trypsi
38	149	19.5	123	2	A29652	chymotrypsin inhib
39	148.5	19.4	62	2	S01803	hypothetical prote
40	148.5	19.4	249	2	T32060	alpha-1-microglobu
41	147.5	19.3	349	2	S21089	alpha-1-microglobu
42	147	19.2	125	1	TIHOB1	basic proteinase i
43	146	19.1	100	1	TI0	protein C37C3.6a (
44	146	19.1	1558	2	C89114	hypothetical prote
45	146	19.1	2167	2	T34395	uterine plasmin/tr
46	145	19.0	122	1	A55115	hypothetical prote
47	145	19.0	805	2	T34212	short epsilon-dend
48	144	18.8	57	2	B59399	venom basic protei
49	144	18.8	59	1	TI0EPD	isoaptrotinin G1 -
50	144	18.8	59	2	S00371	

ALIGNMENTS

RESULT 1

TITTOR

Basic proteinase inhibitor - loggerhead
C:Species: Carretta caretta (loggerhead)

C>Date: 31-May-1979 #sequence_revision 23-Oct-1991 #text_change 09-Jul-2004

C:Accession: A01224

R:Kato, I.; Tominaga, N.

Fed. Proc. 38, 832, 1979

A:Title: Trypsin--subtilisin inhibitor from red sea turtle eggwhite consists of two tand

A:Reference number: A01224

A:Accession: A01224

A:Molecule type: protein

A:Residues: 1-110 <KAT>

A:Cross-references: UNIPROT:P00993

C:Comment: This inhibitor, isolated from egg white, consists of two nonhomologous domain

C:Superfamily: loggerhead basic proteinase inhibitor; animal Kunitz-type proteinase inhi

C:Keywords: pyroglutamic acid; serine proteinase inhibitor

F:8-58/Domain: animal Kunitz-type proteinase inhibitor homology <BPI>

F:63-105/Domain: antileukoproteinase repeat homology <ALP>

F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

F:8-58,17-41,33-54,67-97,80-92,86-101/Disulfide bonds: #status predicted

F:18/Inhibitory site: Lys (trypsin) #status predicted

Alignment Scores:

Pred. No.:	3,748-10	Length:	110
Score:	186.00	Matches:	28
Percent Similarity:	73.21%	Conservative:	13
Best Local Similarity:	50.00%	Mismatches:	15
Query Match:	24.35%	Indels:	0
DB:	1	Gaps:	0

US-10-807-204-11 (1-396) x TITTOR (1-110)


```

||||| ||||| ||||| ||||| |||||
369 PropheThrTyrLeuGly-----AlaGlyGlyAsnTyrAsnAsnPhLeuSer--- 384
QY 94 CCGTGTCCCAAAATCAAGTGAATGCGAAGT----- 126
Db 385 -----ArgileAspCysGluLeuTyrCysAlaAargLeuGlnCysAspArg 399
QY 127 -----GAAGAAATACACAGTGTACCAAAACCCAGAGATTGCCCA 165
Db 400 GlyAsnProLeuArgIleGlyAspValThrGlnSerCysAlaSerAsnAsnAspCysPro 419
QY 166 GAAACATGAAG-----TGTTGCCCGTTCAGCCGTGGGAAGAAA 204
Db 420 SerSerHisGluCysLeuMetAspGlnAlaValCysCysPro----- 433
QY 205 TGTTAGACTTCAGAAAGATATGCGAGTATGCCACAGGAGGTGGCCCTGCTGGCC 264
Db 434 -----ArgMetGlnThrIleCysThrGlnProLeuArgValGlyAsnCysAspArg 450
QY 265 TCCATACCACACTGGTGTACATAAAAAAACTAAGATCTGCTCGAATTTCATCTATGCG 324
Db 451 SerValArgArgTyrTrpTyrSerAlaAlaThrArgGluCysGlnSerPheGluTyrThr 470
QY 325 GGTTCGCCAGGGAAACAATAACAACTTCCAACTGAAGCTATCTGCTGGTCACTGCAAA 384
Db 471 GlyCysGlnGlyAsnAspAsnAsnPhedGluThrLeuValAspCysGlnThrPheCysArg 490

RESULT 10
TIPGBI
alpha-1-microglobulin/inter-alpha-trypsin inhibitor precursor - pig (fragment)
N:Alternate names: bikunin; ITI; PI-14 (inhibitory fragment of ITI)
C:Species: Sus scrofa domestica (domestic pig)
C:Date: 30-Jun-1987 #sequence revision 04-Feb-2000 #text_change 09-Jul-2004
C:Accession: S11066; S13493; A01208
R:Gebhard, W.; Schreimuelier, T.; Vetr, H.; Wachter, E.; Hochstrasser, K.
FEBS Lett. 269, 32-36, 1990
A:Title: Complementary DNA and deduced amino acid sequences of porcine alpha1-microglobulin
A:Reference number: S11066; MUID: 90353595; PMID: 1696914
A:Accession: S11066
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-337 <GES>
A:Cross-references: UNIPROT:P04366; EMBL:X53685; NID:g1877; PIDN:CAA37725.1; PID:g1878
R:Tavakkol, A.
Biochim. Biophys. Acta 1088, 47-56, 1991
A:Title: Molecular cloning of porcine alpha (1)-microglobulin/HI-30 reveals developmental
A:Reference number: S13493; MUID:91113729; PMID:1703444
A:Accession: S13493
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 'M',3-48,'M',50-337 <TAV>
A:Cross-references: GB:X52087; NID:g1891; PIDN:CAA36306.1; PID:g1892
R:Hochstrasser, K.; Wachter, E.; Albrecht, G.J.; Reisinger, P.
Biol. Chem. Hoppe-Seyler 366, 473-478, 1985
A:Title: Kunitz-type proteinase inhibitors derived by limited proteolysis of the inter-a
A:Reference number: A90685; MUID:85225367; PMID:2408637
A:Accession: A01208
A:Molecule type: protein
A:Residues: 212-258,'Q',260-269,'S',271-277,'Q',279-282,'A',284,'IR',287-292,'A',294-310
C:Comment: This inhibitory fragment, released from native ITI after limited proteolysis
first domain interacts weakly with PMN-granulocytic elastase and not at all with pancrea
C:Comment: The amino acid at position P2 (228-Met) appears to determine the specificity
nd elastase; those with leucine interact strongly.
C:Superfamily: alpha-1-microglobulin and inter-alpha-trypsin inhibitor light chain precu
C:Keywords: duplication; glycoprotein; plasma; serine proteinase inhibitor
F:20-173/Domain: lipocalin homology <LIP>
F:216-266/Domain: animal Kunitz-type proteinase inhibitor homology <BP1>
F:272-322/Domain: animal Kunitz-type proteinase inhibitor homology <BP2>
F:216-266,225-249,241-262,272-322,281-305,297-318/Disulfide bonds: #status predicted
F:226/Inhibitory site: Leu (chymotrypsin, elastase) #status predicted
F:235/Binding site: carbohydrate (Asn) (covalent) #status experimental
F:282/Inhibitory site: Arg (trypsin) #status predicted
```

Alignment Scores:

Pred. No.: 3.64e-08 Length: 337
Score: 165.50 Matches: 51
Percent Similarity: 37.50% Conservative: 15
Best Local Similarity: 28.98% Mismatches: 51
Query Match: 21.66% Indels: 59
DB: 7
Gaps: 1

US-10-807-204-11 (1-396) x TIPGBI (1-337)

```

QY 32 TACCATTCATCTTTTGGGGACA----- 55
Db 94 TyrHisLysSerYstTyrAsnIleThrMetGluSerTyrValValHisThrAsnTyrAsp 113
QY 56 -----TCCAGGAACCTGGGC-----ACCTCGAAGGCA 82
Db 114 GluTyrAlaIlePheLeuThrLysLysPheSerArgArgHisGlyProThrLeuThrAla 133
QY 83 TCCTTGGCAAGCCGTGTCCCAAAATCAAAAGTGGAAATGCGAAGTGGAAATAAGACCAAGT 142
Db 134 LysLeuTyrGlyArgGluProGlnLeuArg--GluSerLeuLeuGluGluPheArgGluV 153
QY 143 GTACAAA-----CCCAGAGAT-----TGCCCAAAAACATGAAGT 178
Db 153 alAlaLeuGlyValGlyIleProGluAspSerIlePheThrMetProAspArgGlyGluC 173
QY 179 GTTCCCG-----TTCCAGCCGTGGAAAGAAATGTTTA- 210
Db 173 ysValProGlyGluGlnGluProGluProThrLeuLeuSerArgAlaArgAlaValL 193
QY 211 -----GACTTCAGAAAG----- 222
Db 193 euProGlnGluGluGlySerGlyAlaGlyGlnProValAlaAspPheSerLysLysG 213
QY 223 --GATATATGAGTATGCCACAGAGGTGGCCCTGCTGCTCCATACCACTGGT 280
Db 213 luAspSerCysGlnLeuGlyTyrSerGlnGlyProCysLeuGlyMetIleLysArgTyrP 233
QY 281 GGTACAATAAAAACTAAGATCTGCTCGAATTCATCTATGGCGGTGGCCAGGAACA 340
Db 233 heTyrAsnGlySerSerMetAlaCysGluThrPheHisTyrGlyGlyCysMetGlyAsnG 253
QY 341 ATAACAACATTCACAACTGAAGCTATCTGCTGGTCACCTGCAAA 384
Db 253 lyAsnAsnPheValSerGluLysGluCysLeuGlnThrCysArg 267

RESULT 11
JH0773
Alzheimer's disease amyloid beta protein precursor - African clawed frog
C:Species: Xenopus laevis (African clawed frog)
C:Date: 10-Jun-1993 #sequence_revision 10-Jun-1993 #text_change 13-Aug-1999
C:Accession: JH0773
R:Okado, H.; Okamoto, H.
Biochem. Biophys. Res. Commun. 189, 1561-1568, 1992
A:Title: A Xenopus homologue of the human beta-amyloid precursor protein: developmental
A:Reference number: JH0773; MUID:93129227; PMID:1282805
A:Accession: JH0773
A:Molecule type: mRNA
A:Residues: 1-747 <OKA>
A:Cross-references: GB:S52417; NID:g263150; PIDN:AAE24853.1; PID:g263151
A:Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase i
C:Keywords: alternative splicing; amyloid
F:287-337/Domain: animal Kunitz-type proteinase inhibitor homology <BPI>

Alignment Scores:
Pred. No.: 8.58e-08 Length: 747
Score: 161.50 Matches: 33
Percent Similarity: 44.76% Conservative: 14
Best Local Similarity: 31.43% Mismatches: 43
Query Match: 21.14% Indels: 15
DB: 2 Gaps: 1
```


Alignment Scores:

Pred. No.:	1.41e-07	Length:	57
Score:	160.00	Matches:	26
Percent Similarity:	58.18%	Conservative:	23
Best Local Similarity:	47.27%	Mismatches:	0
Query Match:	20.94%	Indels:	0
DB:	2	Gaps:	0

US-10-807-204-11 (1-396) x A59204 (1-57)

QY	217	AGAAAGCATATATGTCAGTATGCCACAGAGGCTGGCCCTGCTGCCCTCCATACCACAC	276
DB	1	LyAspAspIleCysSerLeuProSerGluThrGlyProCysLysGlyAsnPheLeuArg	20
QY	277	TGTTGGGTACAAATAAAAACTAAGATCTGCTCGAATTCATCTATGCGGTGCCAGGGG	336
DB	21	ThiHieTyAsnSerThrAsnAlaCysAspSerPheValTyGlyGlyCysLysGly	40
QY	337	AACAATAACAACTTCCAACTGAAGCTATCTGCTGGTCACCTGC	381
DB	41	AsnAlaAsnAsnPheGlnAspIleAspAspCysLysAlaAlaCys	55

RESULT 15

JG0185

hepatocyte growth factor activator inhibitor type 2 - mouse

C:Species: Mus musculus (house mouse)

C:Date: 23-Jul-1999 #sequence_revision 23-Jul-1999 #text_change 15-Mar-2004

C:Accession: JG0185

R:Ittoh, H.; Kataoka, H.; Hamaeuna, R.; Kitamura, N.; Koono, M.

Biochem. Biophys. Res. Commun. 255, 740-748, 1999

A:Title: Hepatocyte growth factor activator inhibitor type 2 lacking the first kunitz-

A:Reference number: JG0185; MUID:99160423; PMID:10049781

A:Accession: JG0185

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-252 <ITO>

A:Cross-references: GB:AF099016

F:133-183/Domain: animal Kunitz-type proteinase inhibitor homology <BPI>

Alignment Scores:

Pred. No.:	1.29e-07	Length:	252
Score:	160.00	Matches:	25
Percent Similarity:	62.75%	Conservative:	7
Best Local Similarity:	49.02%	Mismatches:	19
Query Match:	20.94%	Indels:	0
DB:	2	Gaps:	0

US-10-807-204-11 (1-396) x JG0185 (1-252)

QY	229	TGCAGTATGCCACAGAGGCTGGCCCTGCTGCCCTCCATACCACACTGGTGGTACAAT	288
DB	38	CysGlyValSerLysValValGlyLysCysArgAlaSerIleProArgTyrTyrAsn	57
QY	289	AAAAAACTAAGATCTGCTCGAATTCATCTATGCGGTGCCAGGGAACAATACAC	348
DB	58	IleThrAspGlySerCysGlnProPheValTyGlyGlyCysGluGlyAsnGlyAsnAsn	77
QY	349	TTCCAACTCAAGCTATCTGCTGGTCACCTGC	381
DB	78	TyrGlnSerLysGluGluCysLeuAspLysCys	88

RESULT 16

TIHABK

isoInhibitor K (BPI type) - Roman snail

C:Species: Helix pomatia (Roman snail)

C:Date: 23-Oct-1981 #sequence_revision 23-Oct-1981 #text_change 09-Jul-2004

C:Accession: A91232; A01225

R:Tschesche, H.; Dietl, T.

Eur. J. Biochem. 58, 439-451, 1975

A:Title: The amino-acid sequence of isoInhibitor K from snails (Helix pomatia). A sequen

A:Reference number: A91232; MUID:76043680; PMID:1183446

A:Accession: A91232

A:Molecule type: protein

A;Residues: 1-58 <TSC>
A;Cross-references: UNIPROT:P00994
R;Dietl, T.; Techesche, H.
Hoppe-Seyler's Z. Physiol. Chem. 357, 139-145, 1976
A;Title: Die Disulfidbruecken des Trypsin-Kallikrein-Inhibitors K aus Weinbergsschnecken
A;Reference number: A91666; MUID:76141310; PMID:3462
A;Contents: annotation; disulfide bonds
C;Comment: this is one of several isoinhibitors of broad specificity that are secreted i
C;Superfamily: basic proteinase inhibitor; animal Kunitz-type proteinase inhibitor homol
C;Keywords: pyroglutamic acid; serine proteinase inhibitor
F;7-57/Domain: animal Kunitz-type proteinase inhibitor homology <BPI>
F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F;7-57,16-40,32-53/Disulfide bonds: #status predicted

Alignment Scores:
Pred. No.: 2.79e-07 Length: 58
Score: 157.00 Matches: 26
Percent Similarity: 60.00% Conservative: 7
Best Local Similarity: 47.27% Mismatches: 22
Query Match: 20.55% Indels: 0
DB: 1 Gaps: 0

US-10-807-204-11 (1-396) x TIHABK (1-58)

QY 217 AGAAGGATATATGCAGTATGCCACAGAGGCTGCCCTGCCTGCCTCCATACCACAC 276
Db 3 AArgProSerPheCysAsnLeuProAlaGluThrGlyProCysLysAlaSerPheArgGln 22
QY 277 TGGTGGTACATAAAAAAAGTAAAGATCTGCTCCGAATTCATCTATGGCGGTTGCCAGGG 336
Db 23 TyrTyrTyrAsnSerLysSerGlyCysGlnGlnPheIleTyrGlyGlyCysArgGly 42
QY 337 AACAATAACAATCTCCAAACTGAAGCTATCTGTCTGGTCACCTGC 381
Db 43 AsnGlnAsnArgPheAspThrThrGlnGlnCysGlnGlyValCys 57

RESULT 17
S41082
amyloid precursor protein homolog - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 25-Dec-1994 #sequence_revision 03-Aug-1995 #text_change 09-Jul-2004
C;Accession: S41082
R;Pettersen, L.C.; Bjorn, S.E.; Norris, F.; Norris, K.; Sprecher, C.; Foster, D.C.
FEBS Lett. 338, 53-57, 1994
A;Title: Expression, purification and characterization of a Kunitz-type protease inhibit
A;Reference number: S41082; MUID:94139895; PMID:8307156
A;Accession: S41082
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-111 <PET>
A;Cross-references: UNIPROT:Q7M4L3
F;59-109/Domain: animal Kunitz-type proteinase inhibitor homology <BPI>

Alignment Scores:
Pred. No.: 2.68e-07 Length: 111
Score: 157.00 Matches: 25
Percent Similarity: 60.00% Conservative: 8
Best Local Similarity: 45.45% Mismatches: 22
Query Match: 20.55% Indels: 0
DB: 2 Gaps: 0

US-10-807-204-11 (1-396) x S41082 (1-111)

QY 220 AGGATATATGCAGTATGCCACAGAGGCTGCCCTGCCTGCCTCCATACCACACTGG 279
Db 56 LysAlaValCysSerGlnGluAlaMetThrGlyProCysArgAlaValMetProArgTrp 75
QY 280 TGGTACATAAAAAAAGTAAAGATCTGCTCCGAATTCATCTATGGCGGTTGCCAGGGGAAC 339
Db 76 TyrPheAspLeuSerLysGlyLysCysValArgPheIleTyrGlyGlyCysGlyGlyAen 95
QY 340 AATAACAACATCTCCAAACTGAAGCTATCTGTCTGGTCACCTGCAA 384

Db 96 ArgAsnAsnPheGluSerGluAspTyrCysMetAlaValCysLys 110

RESULT 18

A49321

amyloid beta (A4) homolog 2 precursor - human

N;Alternate names: CDEI-binding protein

C;Species: Homo sapiens (man)

C;Date: 24-Feb-1994 #sequence revision 18-Nov-1994 #text_change 09-Jul-2004

C;Accession: A49321; S34644; S40519

R;Sprecher, C.A.; Grant, F.J.; Grimm, G.; O'Hara, P.J.; Norris, F.; Norris, K.; Foster, R. Biochemistry 32, 4481-4486, 1993

A;Title: Molecular cloning of the cDNA for a human amyloid precursor protein homolog: evidence for a novel protein family

A;Reference number: A49321; MUID:93250009; PMID:8485127

A;Accession: A49321

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-763 <SPR>

A;Cross-references: UNIPROT:Q06481; GB:S60099; NID:G300168; PIDN:AAC60589.1; PID:G300169

A;Experimental source: placenta

A;Note: sequence extracted from NCBI backbone (NCBIN:131198, NCBI:P:131199)

A;Note: expression was shown in placenta, brain, heart, lung, liver, and kidney

R;von der Kammer, H.; Klaudiny, J.; Hanes, J.; Scheit, K.H. submitted to the EMBL Data Library, April 1993

A;Description: The human homologue of the murine CDEI binding protein is an amyloid precursor protein

A;Reference number: S34644

A;Accession: S34644

A;Molecule type: mRNA

A;Residues: 1-763 <VON>

A;Cross-references: EMBL:222572; NID:G394763; PIDN:CAA80295.1; PID:G394764

R;Waeo, W.; Gurbhagavatlula, S.; Paradis, M.; Romano, D.M.; Sisodia, S.S.; Hyman, B.T.; Nature Genet. 5, 95-99, 1993

A;Title: Isolation and characterization of APLP2 encoding a homologue of the Alzheimer's A2 protein

A;Reference number: S40519; MUID:94035131; PMID:8220435

A;Accession: S40519

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-763 <WAS>

A;Cross-references: GB:L27631; NID:G450391; PIDN:AAC41701.1; PID:G450392

C;Genetics:

A;Gene: GDB:APLP2; APLP2

A;Cross-references: GDB:139159; OMIM:104776

A;Map position: 11q23-11q25

C;Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase inhibitor

C;Keywords: alternative splicing; transmembrane protein

F;310-360/Domain: animal Kunitz-type proteinase inhibitor homology <BPI>

Alignment Scores:

Pred. No.:	2.38e-07	Length:	763
Score:	157.00	Matches:	25
Percent Similarity:	60.00%	Conservative:	8
Best Local Similarity:	45.45%	Mismatches:	22
Query Match:	20.55%	Indels:	0
DB:	2	Gaps:	0

US-10-807-204-11 (1-396) x A49321 (1-763)

Qy 220 AAGGATATGTCAGTATGCCACAGGAGCTGGCCCTGCTCCATACCACTGG 279

Db 307 LysAlaValCysSerGlnGluAlaMetThrGlyProCysArgAlaValMetProArgTrp 326

Qy 280 TGGTACAAATAAAAACTAAGATCTGCTCCGAATTCATCTATGCGGGTTGCCAGGGGAAC 339

Db 327 TyrPheAspLeuSerLysGlyCysValArgPheIleTyrGlyGlyCysGlyGlyAsn 346

Qy 340 AATTAACAACCTCCAACTGAAGCTATCTGCTGTCACCTGCATAA 384

Db 347 ArgAsnAsnPheGluSerGluAspTyrCysMetAlaValCysLys 361

RESULT 19

amyloid precursor-like protein - rat

C;Species: Rattus norvegicus (Norway rat)

C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 09-Jul-2004

C;Accession: S42880; S47528

R;Sandbrink, R.; Masters, C.L.; Beyreuther, K. submitted to the EMBL Data Library, March 1994

A;Description: Complete nucleotide ad deduced amino acid sequence of rat amyloid precursor protein

A;Reference number: S42880

A;Accession: S42880

A;Molecule type: mRNA

A;Residues: 1-765 <SAN>

A;Cross-references: UNIPROT:P15943; EMBL:X77934

R;Sandbrink, R.; Masters, C.L.; Beyreuther, K. Biochim. Biophys. Acta 1219, 167-170, 1994

A;Title: Complete nucleotide and deduced amino acid sequence of rat amyloid protein precursor

A;Reference number: S47528; MUID:94368849; PMID:8086458

A;Accession: S47528

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-765 <SA2>

A;Cross-references: EMBL:X77934

C;Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase inhibitor

C;Keywords: alternative splicing

F;312-362/Domain: animal Kunitz-type proteinase inhibitor homology <BPI>

Alignment Scores:

Pred. No.:	2.38e-07	Length:	765
Score:	157.00	Matches:	25
Percent Similarity:	60.00%	Conservative:	8
Best Local Similarity:	45.45%	Mismatches:	22
Query Match:	20.55%	Indels:	0
DB:	2	Gaps:	0

US-10-807-204-11 (1-396) x S42880 (1-765)

Qy 220 AAGGATATGTCAGTATGCCACAGGAGCTGGCCCTGCTCCATACCACTGG 279

Db 309 LysAlaValCysSerGlnGluAlaMetThrGlyProCysArgAlaValMetProArgTrp 328

Qy 280 TGGTACAAATAAAAACTAAGATCTGCTCCGAATTCATCTATGCGGGTTGCCAGGGGAAC 339

Db 329 TyrPheAspLeuSerLysGlyCysValArgPheIleTyrGlyGlyCysGlyGlyAsn 348

Qy 340 AATTAACAACCTCCAACTGAAGCTATCTGCTGTCACCTGCATAA 384

Db 349 ArgAsnAsnPheGluSerGluAspTyrCysMetAlaValCysLys 363

RESULT 20

S12143

lipoprotein-associated coagulation inhibitor precursor - rabbit

N;Alternate names: endothelial cell coagulation inhibitor; endothelial cell tissue factor inhibitor

C;Species: Oryctolagus cuniculus (domestic rabbit)

C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 16-Jul-1999

C;Accession: S12143; A61373

R;Wesselschmidt, R.L.; Girard, T.J.; Broze Jr., G.J. Nucleic Acids Res. 18, 6440, 1990

A;Title: cDNA sequence of rabbit lipoprotein-associated coagulation inhibitor.

A;Reference number: S12143; MUID:91057146; PMID:2136251

A;Accession: S12143

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-300 <WES>

A;Cross-references: EMBL:X54708; NID:G1612; PIDN:CAA38515.1; PID:G1613

R;Colburn, P.; Crabb, J.W.; Buonassisi, V. J. Cell. Physiol. 148, 320-326, 1991

A;Title: Enhanced inhibition of tissue factor by the extended form of an endothelial cell

A;Reference number: A61373; MUID:91349227; PMID:1880157

A;Accession: A61373

A;Molecule type: protein

A;Residues: 25-33, 'X', 35-46 <COL>

C;Superfamily: tissue factor pathway inhibitor; animal Kunitz-type proteinase inhibitor

C;Keywords: anticoagulant; glycoprotein

F;50-100/Domain: animal Kunitz-type proteinase inhibitor homology <BPI>

F;121-171/Domain: animal Kunitz-type proteinase inhibitor homology <BP2>

F;213-263/Domain: animal Kunitz-type proteinase inhibitor homology <BP3>

Alignment Scores:

Pred. No.: 4,44e-07 Length: 300
Score: 154.50 Matches: 48
Percent Similarity: 42.42% Conservative: 22
Best Local Similarity: 29.09% Mismatches: 50
Query Match: 20.22% Indels: 45
DB: 2 Gaps: 8

US-10-807-204-11 (1-396) x S12143 (1-300)

QY 7 CTCTCAGGACTTCTGCCATCTCTGTA-----CCATTTCATC 42
DB 14 LeuLeuGlyLeuValProAlaProValSerSerAlaAlaGluGluAspGluGluPheThr 33
QY 43 CTTTGTGGGGACATC-----CAGGAACCTGGCCACGCT----- 75
DB 34 AsnIleThrAspIleLysProLeuGlnLysProThrHisSerPheCysAlaMetLys 53
QY 76 -----GAAGGC-----ATCCTTGGCAG 93
DB 54 ValAspAspGlyProCysArgAlaTyrIleLysArgPhePhePheAsnIleLeuAlaHis 73
QY 94 CCGTGTCCCAA---ATCAAAGTGGATCGAA-----GTGGAAGAATA 135
DB 74 GlnCysGluGluPheIleTyrGlyGlyCysGluGlyAsnGluAsnArgPheGluSerLeu 93
QY 136 GACCAGTGTACCAA-----CCAGAGATTCGCCAGAAACATGAAGTGTGCCCGTTC 189
DB 94 GluGluCysLysGluLysCysAlaArgAspTyrProLysMetThrThrLysLeuThrPhe 113
QY 190 AGCCGTGGAAGAAATGTTTAGACTTCACAAAGGATATATGTCAGTATGCCACAGAGGCT 249
DB 114 GlnLysGlyLys-----ProAspPheCysPheLeuGluGluAspPro 127
QY 250 GGCCTCTGCTGCTCCATACACACTGGTGTACATAAATAAACTAAGTCTGCTCC 309
DB 128 GlyIleCysArgGlyTyrIleThrArgTyrPheTyrAsnAsnGlnSerLysGlnCysGlu 147
QY 310 GAATTCATCTATGGCGGTTCACAGGGGAAACAATAACAATTCACAACTCAAGCTATCTCT 369
DB 148 ArgPheLysTyrGlyGlyCysLeuGlyAsnLeuAsnAsnPheGluSerLeuGluCys 167
QY 370 CTGGTCACCTGCAAA 384
DB 168 LysAsnThrCysGlu 172

RESULT 21

A32761
hypothetical Alzheimer's disease amyloid beta protein, Alu-containing clone - human (fra
C:Species: Homo sapiens (man)
C:Date: 29-Jan-1990 #sequence_revision 10-Apr-1996 #text_change 10-Apr-1996
C:Accession: A32761
R:de Sauvage, F.; Octave, J.N.
Science 245, 651-653, 1989
A:Title: A novel mRNA of the A4 amyloid precursor gene coding for a possibly secreted pr
A:Reference number: A32761; MUID:89346754; PMID:2569763
A:Accession: A32761
A:Molecule type: mRNA
A:Residues: 1-484 <DES>
A:Cross-references: GB:M28373
A:Note: the authors translated the codon ATG for residue 433 as Leu
C:Comment: This is the hypothetical translation of a sequence believed to contain clonin
C:Keywords: cloning artifact

Alignment Scores:

Pred. No.: 4.83e-07 Length: 484
Score: 154.00 Matches: 24
Percent Similarity: 59.26% Conservative: 8
Best Local Similarity: 44.44% Mismatches: 22
Query Match: 20.16% Indels: 0
DB: 4 Gaps: 0

US-10-807-204-11 (1-396) x A32761 (1-484)

QY 220 AAGGATATATGCAGTATGCCACAGAGCTGGCCCTGCTGCTCCATACCACACTGG 279
DB 209 ArgGluValCysSerGluGlnAlaGluThrGlyProCysArgAlaMetIleSerArgTrp 228
QY 280 TGGTACATAAAAACTAAGATCTGCTCCCAATTCATCTATGGCGGTTCAGGGGAAC 339
DB 229 TyrPheAspValThrGluGlyLysCysAlaProPhePheTyrGlyGlyCysGlyGlyAsn 248
QY 340 AATAACAACCTCCAAACTGAAGCTATCTGTCTGCTCACCTGC 381
DB 249 ArgAsnAsnPheAspThrGluGluTyrCysMetAlaValCys 262

RESULT 22

QRHUA4

Alzheimer's disease amyloid beta protein precursor (validated) - human
N:Alternate names: Alzheimer's disease amyloid A4 protein; coagulation factor X1a inhibi
N:Contains: amyloid beta protein long, plaque form; amyloid beta protein short, vascular
protein precursor splice form APP(770)
C:Species: Homo sapiens (man)
C:Date: 30-Jun-1987 #sequence_revision 28-Jul-1995 #text_change 15-Sep-2000
C:Accession: S02260; S05194; A32277; A33260; A35486; I39452; I39451; I39453; A44
4668; A28583; A29302; A60805; J10038; S06121; A60355; A59011; A38384; S29076; S38252; S3
R:Leinair, H.G.; Salbaum, J.M.; Multhaup, G.; Kang, J.; Bayney, R.M.; Unterbeck, A.; Bey
Nucleic Acids Res. 17, 517-522, 1989
A:Title: The PreA4 (695) precursor protein of Alzheimer's disease A4 amyloid is encoded b
A:Reference number: S02260; MUID:89128427; PMID:2783775
A:Accession: S02260
A:Molecule type: DNA
A:Residues: 1-288, 'V', 365-770 <LEMI>
A:Cross-references: EMBL:X13466
A:Note: alternative splice form APP(695)
R:Leinair, H.G.
submitted to the EMBL Data Library, November 1988
A:Reference number: S05194
A:Accession: S05194
A:Molecule type: DNA
A:Residues: 1-14, 'VM', 17-288, 'V', 365-770 <LEW2>
A:Cross-references: EMBL:X13466; NID:G35598; PIDN:CAA31830.1; PID:G871360
A:Note: alternative splice form APP(695)
R:La Fauci, G.; Lahiri, D.K.; Salton, S.R.J.; Robakis, N.K.
Biochem. Biophys. Res. Commun. 159, 297-304, 1989
A:Title: Characterization of the 5'-end region and the first two exons of the beta-prote
A:Reference number: A32277; MUID:89165870; PMID:2538123
A:Accession: A32277
A:Molecule type: DNA
A:Residues: 1-75 <LAF>
A:Cross-references: GB:M24546; GB:M24547; NID:G341202; PIDN:AAC13654.1; PID:G516074
R:Johnstone, E.M.; Chaney, M.O.; Moore, R.E.; Ward, K.E.; Norris, F.H.; Little, S.P.
Biochem. Biophys. Res. Commun. 163, 1248-1255, 1989
A:Title: Alzheimer's disease amyloid peptide is encoded by two exons and shows similarit
A:Reference number: A33260; MUID:89392030; PMID:2675837
A:Accession: A33260
A:Molecule type: DNA
A:Residues: 656-737 <JOH>
A:Cross-references: GB:M29270; NID:G178863; PIDN:AAA51768.1; PID:G178865
R:Pirelli, F.; Levy, E.; van Duinen, S.G.; Bots, G.T.A.M.; Luyendijk, W.; Frangione, B.
Biochem. Biophys. Res. Commun. 170, 301-307, 1990
A:Title: Expression of a normal and variant Alzheimer's beta-protein gene in amyloid of
A:Reference number: A35486; MUID:90321244; PMID:2196878
A:Accession: A35486
A:Molecule type: DNA
A:Residues: 672-710 <PRE1>
A:Note: 693-Gln was found in DNA isolated from HCHWA-D patients
R:Yoshikaki, S.I.; Sasaki, H.; Doh-ura, K.; Furuya, H.; Sakaki, Y.
Gene 87, 257-263, 1990
A:Title: Genomic organization of the human amyloid beta-protein precursor gene.
A:Reference number: I39451; MUID:90236318; PMID:2110105
A:Accession: I39452
A>Status: nucleic acid sequence not shown; translation not shown; translated from GB/EM:
A:Molecule type: DNA
A:Residues: 1-770 <YOS1>
A:Cross-references: GB:M33112; NID:G178613; PIDN:AAB59502.1; PID:G178616

A:Accession: I39451
A:Status: nucleic acid sequence not shown; translation not shown; translated from GB/EMBL
A:Molecule type: DNA
A:Residues: 1-530, 'QMLMPVIPAFWEAKVGR' <YOS2>
A:Cross-references: GB:M34875; NID:g178608; PIDN:AA859501.1; PID:g178615
R:Yoshikaki, S.I.; Sasaki, H.; Doh-ura, K.; Furuya, H.; Sakaki, Y.
Gene 102, 291-292, 1991
A:Reference number: A59020; MUID:91340168; PMID:1908403
A:Contents: annotation; erratum
A:Note: revised physical map for reference I39451
R:Levy, E.; Carman, M.D.; Fernandez-Madrid, I.J.; Power, M.D.; Lieberburg, I.; van Duine
Science 248, 1124-1126, 1990
A:Title: Mutation of the Alzheimer's disease amyloid gene in hereditary cerebral hemorrh
A:Reference number: I39453; MUID:90260663; PMID:2111584
A:Accession: I39453
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 656-737 <LEV>
A:Cross-references: GB:M37896; NID:g178618; PIDN:AA51727.1; PID:g178620
A:Note: a mutation with 693-Gln is presented
R:Murrell, J.; Farlow, M.; Ghetti, B.; Benson, M.D.
Science 254, 97-99, 1991
A:Title: A mutation in the amyloid precursor protein associated with hereditary Alzheim
A:Reference number: I59562; MUID:90202553; PMID:1925564
A:Accession: I59562
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 689-716, 'F' 718-737 <MUR>
A:Cross-references: GB:S57665; NID:9236720; PIDN:AA819991.1; PID:g236721
R:Kamino, K.; Orr, H.T.; Payami, H.; Wijsman, E.M.; Alonso, M.E.; Pulst, S.M.; Anderson,
arakis, S.E.; Korenberg, J.R.; Sharma, V.; Kukull, W.; Larson, E.; Heston, L.L.; Martin,
Am. J. Hum. Genet. 51, 998-1014, 1992
A:Title: Linkage and mutational analysis of familial Alzheimer disease kindreds for the
A:Reference number: A44017; MUID:93035397; PMID:1415269
A:Accession: A44017
A:Molecule type: DNA
A:Residues: 687-692, 'G' 694-718 <KAM1>
A:Cross-references: GB:S45135; NID:g257377; PIDN:AA823645.1; PID:g257378
A:Experimental source: GB:M15315; NID:Alzheimer disease family SB
A:Note: sequence extracted from NCBI backbone (NCBIP:115374)
A:Accession: B44017
A:Molecule type: DNA
A:Residues: 687-718 <KAM2>
A:Cross-references: GB:S45136; NID:g257379; PIDN:AA823646.1; PID:g257380
A:Experimental source: familial Alzheimer disease family LIT
A:Note: sequence extracted from NCBI backbone (NCBIP:115376)
A:Note: this sequence has a silent mutation
R:Kang, J.; Lemaire, H.G.; Unterbeck, A.; Salbaum, J.M.; Masters, C.L.; Grzeschik, K.H.;
Nature 325, 733-736, 1987
A:Title: The precursor of Alzheimer's disease amyloid A4 protein resembles a cell-surfac
A:Reference number: A03134; MUID:87144572; PMID:2881207
A:Accession: A03134
A:Molecule type: mRNA
A:Residues: 1-288, 'V', 365-770 <KAN>
A:Cross-references: GB:Y00264; NID:g28525; PIDN:CAA68374.1; PID:g28526
A:Note: alternative splice form APP(695)
R:Robakis, N.K.; Ramakrishna, N.; Wolfe, G.; Wisniewski, H.M.
Proc. Natl. Acad. Sci. U.S.A. 84, 4190-4194, 1987
A:Title: Molecular cloning and characterization of a cDNA encoding the cerebrovascular a
A:Reference number: A29030; MUID:87231971; PMID:3035574
A:Accession: A29030
A:Molecule type: mRNA
A:Residues: 284-288, 'V', 365-646, 'E', 648-770 <ROB>
A:Cross-references: GB:M16785; NID:g178539; PIDN:AA851722.1; PID:g178540
A:Note: the authors translated the codon GAG for residue 647 as Asp
R:Goldberger, D.; Lerman, M.I.; McBride, O.W.; Saffiotti, U.; Gajdusek, D.C.
Science 235, 877-880, 1987
A:Title: Characterization and chromosomal localization of a cDNA encoding brain amyloid
A:Reference number: A47584; MUID:87120328; PMID:3810169
A:Accession: A47584
A:Molecule type: mRNA
A:Residues: 674-756, 'S', 758-770 <GOL>
A:Cross-references: GB:M15533; NID:g178706; PIDN:AAA35540.1; PID:g178707

A:Experimental source: brain
R:Tanzi, R.E.; Gusella, J.F.; Watkins, P.C.; Bruns, G.A.P.; St George-Hyslop, P.; Van Ken
Science 235, 880-884, 1987
A:Title: Amyloid beta protein gene: cDNA, mRNA distribution, and genetic linkage near the
A:Reference number: A47585; MUID:87120329; PMID:2949367
A:Accession: A47585
A:Molecule type: mRNA
A:Residues: 674-703 <TAN1>
A:Cross-references: GB:M15532; NID:g177957; PIDN:AAA51564.1; PID:g177958
R:Dykes, T.; Weidemann, A.; Multhaup, G.; Salbaum, J.M.; Lemaire, H.G.; Kang, J.; Mueller
EMBO J. 7, 949-957, 1988
A:Title: Identification, transmembrane orientation and biogenesis of the amyloid A4 precu
A:Reference number: S02638; MUID:88296437; PMID:2900137
A:Accession: S02638
A:Molecule type: mRNA
A:Residues: 672-678 <DYR>
R:Tanzi, R.E.; McClatchey, A.I.; Lamperti, E.D.; Villa-Komaroff, L.; Gusella, J.F.; Neve,
Nature 331, 528-530, 1988
A:Title: Protease inhibitor domain encoded by an amyloid protein precursor mRNA associat
A:Reference number: S00707; MUID:88122640; PMID:2893230
A:Accession: S00707
A:Molecule type: mRNA
A:Residues: 286-344, 'I', 365-366 <TAN2>
A:Cross-references: EMBL:X06982; NID:g28817; PIDN:CAA30042.1; PID:g292612
A:Experimental source: promyelocytic leukemia cell line HL60
A:Note: alternative splice form APP(751)
R:Ponte, P.; Gonzalez-DeWhitt, P.; Schilling, J.; Miller, J.; Hau, D.; Greenberg, B.; Dav
Nature 331, 525-527, 1988
A:Title: A new A4 amyloid mRNA contains a domain homologous to serine proteinase inhibito
A:Reference number: S00925; MUID:88122639; PMID:2893289
A:Accession: S00925
A:Molecule type: mRNA
A:Residues: 1-344, 'I', 365-770 <PO2>
A:Cross-references: GB:X06989; EMBL:X00297; NID:g28720; PIDN:CAA30050.1; PID:g28721
A:Note: alternative splice form APP(751)
R:Kitaguchi, N.; Takahashi, Y.; Tokushima, Y.; Shiojiri, S.; Ito, H.
Nature 331, 530-532, 1988
A:Title: Novel precursor of Alzheimer's disease amyloid protein shows protease inhibitory
A:Reference number: A38949; MUID:88122641; PMID:2893291
A:Accession: A38949
A:Molecule type: mRNA
A:Residues: 287-367 <KIT>
A:Cross-references: GB:X06981; NID:g28816; PIDN:CAA30041.1; PID:g9929611
A:Experimental source: glioblastoma cell line
A:Note: alternative splice form APP(770)
R:Vitek, M.P.; Rasool, C.G.; de Sauvage, F.; Vitek, S.M.; Bartus, R.T.; Beer, B.; Ashton,
Brain Res. Mol. Brain Res. 4, 121-133, 1988
A:Title: Absence of mutation in the beta-amyloid cDNAs cloned from the brains of three pa
A:Reference number: A30320
A:Accession: A30320
A:Status: not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 284-288, 'V', 365-770 <VIT1>
A:Accession: B30320
A:Status: not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 132-288, 'V', 365-770 <VIT2>
A:Accession: C30320
A:Status: not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 606-770 <VIT3>
R:Zain, S.B.; Salim, M.; Chou, W.G.; Sajdel-Sulkowska, E.M.; Majocha, R.E.; Marotta, C.A.
Proc. Natl. Acad. Sci. U.S.A. 85, 929-933, 1988
A:Title: Molecular cloning of amyloid cDNA derived from mRNA of the Alzheimer disease bra
A:Reference number: A31087; MUID:88124954; PMID:2893379
A:Accession: A31087
A:Molecule type: mRNA
A:Residues: 507-770 <ZAI>
A:Cross-references: GB:M18734; NID:g178572; PIDN:AAA51726.1; PID:g178573
A:Note: the authors translated the codon GAA for residue 599 as Gly, ACC for residue 603
8 as Val, GTG for residue 609 as Asn, AAT for residue 610 as Gly, and GGT for residue 65
A:Note: the cited Genbank accession number, J03594, is not in release 101.0
R:Masters, C.L.; Multhaup, G.; Simms, G.; Pottgiesser, J.; Martins, R.N.; Beyreuther, K.

[illegible]

QY 223 GATATATGACGATGATGCCAGAGGCTGGCCCTGCTGGCTCATACACACTGGTGG 282
 Db : : : : :
 1 GluValCysSerGluGlnAlaGluThrGlyProCysArgAlaMetIleSerArgTrpTyr 20
 : : : : :
 QY 283 TACAATAAAAACTAAGATCTGTCCTCCAAATTCATCTATGCGGTGGCCAGGGGAACAAT 342
 Db : : : : :
 21 PheAspValThrGluGlyLysCysAlaProPhePheTyrGlyGlyCysGlyGlyAsnArg 40
 : : : : :
 QY 343 AACAACTTCCAACTGAAGCTATCTGCTGGTCACCTGC 381
 Db : : : : :
 41 AsnAsnPheAspThrGluGluTyrCysMetAlaValCys 53

RESULT 28
 S03607
 Alzheimer's disease amyloid A4 protein - rat (fragment)
 C:Species: Rattus norvegicus (Norway rat)
 C>Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 09-Jul-2004
 C:Accession: S03607
 R:Kang, J.; Mueller-Hill, B.
 Nucleic Acids Res. 17, 2130, 1989
 A:Title: The sequence of the two extra exons in rat preA4.
 A:Reference number: S03607; MUID:89183625; PMID:2648331
 A:Accession: S03607
 A:Molecule type: mRNA
 A:Residues: 1-76 <KAN>
 A:Cross-references: UNIPROT:P08592; EMBL:X14066; NID:g56957; PIDN:CAA32229.1; PID:g93026
 A:Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase
 C:Keywords: alternative splicing; serine proteinase inhibitor; transmembrane protein
 F:3-53/Domain: animal Kunitz-type proteinase inhibitor homology <BPI>

Alignment Scores:
 Pred. No.: 8.53e-07 Length: 76
 Score: 152.00 Matches: 24
 Percent Similarity: 58.4% Conservatives: 7
 Best Local Similarity: 45.2% Mismatches: 22
 Query Match: 19.9% Indels: 0
 DB: 2 Gaps: 0

US-10-807-204-11 (1-396) x S03607 (1-76)

QY 223 GATATATGACGATGATGCCAGAGGCTGGCCCTGCTGGCTCATACACACTGGTGG 282
 Db : : : : :
 1 GluValCysSerGluGlnAlaGluThrGlyProCysArgAlaMetIleSerArgTrpTyr 20
 : : : : :
 QY 283 TACAATAAAAACTAAGATCTGTCCTCCAAATTCATCTATGCGGTGGCCAGGGGAACAAT 342
 Db : : : : :
 21 PheAspValThrGluGlyLysCysAlaProPhePheTyrGlyGlyCysGlyGlyAsnArg 40
 : : : : :
 QY 343 AACAACTTCCAACTGAAGCTATCTGCTGGTCACCTGC 381
 Db : : : : :
 41 AsnAsnPheAspThrGluGluTyrCysMetAlaValCys 53

RESULT 29
 HCHU
 alpha-1-microglobulin/inter-alpha-trypsin inhibitor precursor [validated] - human
 N:Alternate names: bikunin; complex-forming glycoprotein heterogeneous in charge (HC) pH rich protein
 N:Contains: alpha-1-microglobulin (protein HC); inter-alpha-trypsin inhibitor
 C:Species: Homo sapiens (man)
 C>Date: 15-Oct-1982 #sequence_revision 30-Jun-1987 #text_change 09-Jul-2004
 C:Accession: S13433; S10778; A93642; A90074; A90225; A90686; P90450; B39079; A61580; B253217
 R:Vetr, H.; Gebhard, W.
 Biol. Chem. Hoppe-Seyler 371, 1185-1196, 1990
 A:Title: Structure of the human alpha(1)-microglobulin-bikunin gene.
 A:Reference number: S13433; MUID:91214554; PMID:1708673
 A:Accession: S13433
 A>Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-352 <VET1>
 A:Cross-references: UNIPROT:P02760; EMBL:X54816; NID:g24475; PIDN:CAA38585.1; PID:g82561
 R:Diarra-Mehrpour, M.; Bourguignon, J.; Sesbouee, R.; Salier, J.P.; Leveillard, T.; Mart
 Eur. J. Biochem. 191, 131-139, 1990

A:Title: Structural analysis of the human inter-alpha-trypsin inhibitor light-chain gene
 A:Reference number: S10778; MUID:90336621; PMID:1696200
 A:Accession: S10778
 A>Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-202 <DIA>
 R:Kaumeyer, J.F.; Polazzi, J.O.; Kotick, M.P.
 Nucleic Acids Res. 14, 7839-7850, 1986
 A:Title: The mRNA for a proteinase inhibitor related to the HI-30 domain of inter-alpha-
 A:Reference number: A93642; MUID:87040757; PMID:2430261
 A:Accession: A93642
 A:Molecule type: mRNA
 A:Residues: 1-352 <KAU>
 A:Cross-references: GB:X0494; NID:g24478; PIDN:CAA28182.1; PID:g24479
 R:Lopez Otin, C.; Grubb, A.O.; Mendez, E.
 Arch. Biochem. Biophys. 228, 544-554, 1984
 A:Title: The complete amino acid sequence of human complex-forming glycoprotein heteroge
 A:Reference number: A90074; MUID:84126849; PMID:6198962
 A:Accession: A90074
 A:Molecule type: protein
 A:Residues: 20-56,58-202 <LOP>
 A:Experimental source: individual with tubular proteinuria
 A>Note: no evidence of sequence heterogeneity could be found, in spite of persistent het
 R:Takagi, T.; Takagi, K.; Kawai, T.
 Biochem. Biophys. Res. Commun. 98, 997-1001, 1981
 A:Title: Complete amino acid sequence of human alpha-1-microglobulin.
 A:Reference number: A90225; MUID:81184038; PMID:6164372
 A:Accession: A90225
 A:Molecule type: protein
 A:Residues: 20-47,58-136,138-141,'T',143-144,146-198 <TAK>
 A:Experimental source: pooled urine of patients with tubular proteinuria
 R:Reisinger, P.; Hochstrasser, K.; Albrecht, G.J.; Lempert, K.; Salier, J.P.
 Biol. Chem. Hoppe-Seyler 366, 479-483, 1985
 A:Title: Human inter-alpha-trypsin inhibitor: localization of the kunitz-type domains in
 A:Reference number: A90686; MUID:85225968; PMID:2408638
 A:Accession: A90686
 A:Molecule type: protein
 A:Residues: 206-290,'VI',293-342,'E',344-350 <REI>
 R:Atmani, F.; Lacour, B.; Strecker, G.; Parvy, P.; Drueeke, T.; Daudon, M.
 Biochem. Biophys. Res. Commun. 191, 1158-1165, 1993
 A:Title: Molecular characteristics of uronic-acid-rich protein, a strong inhibitor of ca
 A:Reference number: P90450; MUID:93221481; PMID:8466493
 A:Accession: P90450
 A:Molecule type: protein
 A:Residues: 206-214,'X' <ATM1>
 R:Engchild, J.J.; Salvesen, G.; Hefta, S.A.; Thøgersen, I.B.; Rutherford, S.; Pizzo, S.V.
 J. Biol. Chem. 266, 747-751, 1991
 A:Title: Chondroitin 4-sulfate covalently cross-links the chains of the human blood prot
 A:Reference number: A39079; MUID:91093267; PMID:1898736
 A:Accession: A39079
 A:Molecule type: protein
 A:Residues: 206-225 <ENGL>
 R:Chirat, F.; Balduyck, M.; Mizon, C.; Laroui, S.; Sautiere, P.; Mizon, J.
 Int. J. Biochem. 23, 1201-1203, 1991
 A:Title: A chondroitin-sulfate chain is located on serine-10 of the urinary trypsin inhi
 A:Reference number: A61580; MUID:92175157; PMID:1794445
 A:Accession: A61580
 A:Molecule type: protein
 A:Residues: 214,'X',216-222,'X' <CHI>
 R:McKeehan, W.L.; Sakagami, Y.; Hoshi, H.; McKeehan, K.A.
 J. Biol. Chem. 261, 5378-5383, 1986
 A:Title: Two apparent human endothelial cell growth factors from human hepatoma cells a
 A:Reference number: A92583; MUID:86168278; PMID:3007499
 A:Accession: A92583
 A:Molecule type: protein
 A:Residues: 206-214,'X',216-230,'X',232-239,'X',241-248,'XX',251-252,'X',254 <MCK>
 R:Engchild, J.J.; Thøgersen, I.B.; Pizzo, S.V.; Salvesen, G.
 J. Biol. Chem. 264, 15975-15981, 1989
 A:Title: Analysis of inter-alpha-trypsin inhibitor and a novel trypsin inhibitor, pre-a
 A:Reference number: A92736; MUID:89380192; PMID:2476436
 A:Accession: A92736
 A:Molecule type: protein
 A:Residues: 206-225 <ENG2>

R;Traboni, C.; Cortese, R.
Nucleic Acids Res. 14, 6340, 1986
A;Title: Sequence of a full length cDNA coding for human protein HC (alpha-1-microglobulin)
A;Reference number: A25303; MUID:86312901; PMID:2428011
A;Accession: A25303
A;Molecule type: mRNA
A;Residues: 1-218,'HW' <TRA>
A;Note: this mRNA sequence appears to contain errors after residue 218
R;Calero, M.; Escibano, J.; Grubb, A.; Mendez, E.
J. Biol. Chem. 269, 384-389, 1994
A;Title: Location of a novel type of interpolypeptide chain linkage in the human protein
A;Reference number: A53110; MUID:94103241; PMID:7506257
A;Accession: A53110
A;Molecule type: protein
A;Residues: 45-57 <CAL1>
R;Vetr, H.; Koeglner, M.; Gebhard, W.
FEBS Lett. 245, 137-140, 1989
A;Title: The domain structure of the inhibitor subunit of human inter-alpha-trypsin inhibitor
A;Reference number: S03552; MUID:89171290; PMID:2466696
A;Accession: S03552
A;Status: nucleic acid sequence not shown
A;Molecule type: DNA
A;Residues: 206-352 <VET2>
R;Malik, N.; Balduyck, M.; Maes, P.; Capon, C.; Mizon, C.; Han, K.K.; Tartar, A.; Fournet
Biol. Chem. Hoppe-Seyler 373, 1009-1018, 1992
A;Title: The heavy chains of human plasma inter-alpha-trypsin inhibitor: their isolation
A;Reference number: S28928; MUID:93039735; PMID:1384548
A;Accession: S28930
A;Status: preliminary
A;Molecule type: protein
A;Residues: 206-215 <MAL>
R;Morelle, W.; Capon, C.; Balduyck, M.; Sautiere, P.; Kouach, M.; Michalski, C.; Fournet
Eur. J. Biochem. 221, 881-888, 1994
A;Title: Chondroisin sulphate covalently cross-links the three polypeptide chains of inter
A;Reference number: S43466; MUID:94229087; PMID:7513643
A;Accession: S43466
A;Status: preliminary
A;Molecule type: protein
A;Residues: 206-221 <WOR>
R;Wisniewski, H.G.; Burgess, W.H.; Oppenheim, J.D.; Vilcek, J.
Biochemistry 33, 7423-7429, 1994
A;Title: TSG-6, an arthritis-associated hyaluronan binding protein, forms a stable complex
A;Reference number: A53642; MUID:94271799; PMID:7516184
A;Accession: A53642
A;Status: preliminary
A;Molecule type: protein
A;Residues: 206-217 <WIS>
R;Calero, M.; Mendez, E.; Garcia, E.
Biochim. Biophys. Acta 1249, 91-99, 1995
A;Title: Expression of the human complex-forming glycoprotein HC (alpha-1-microglobulin)
A;Reference number: S55688; MUID:95284116; PMID:7533295
A;Accession: S55688
A;Molecule type: protein
A;Residues: 20-24 <CAL2>
R;Bourguignon, J.; Diarra-Mehrpor, M.; Sesboue, R.; Frain, M.; Sala-Trepat, J.M.; Marti
Biochem. Biophys. Res. Commun. 131, 1146-1153, 1985
A;Title: Human inter-alpha-trypsin-inhibitor: characterization and partial nucleotide sequence
A;Reference number: 152208; MUID:86025577; PMID:2413856
A;Accession: 152208
A;Status: translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 302-352 <BOU>
R;Wojcik, E.G.C.; van den Berg, M.; van der Linden, I.K.; Poort, S.R.; Cupers, R.; Berti
Biochem. J. 311, 753-759, 1995
A;Title: Factor IX Zuthphen: a Cys(18) -> Arg mutation results in formation of a heterodimer
A;Reference number: S59509; MUID:96067589; PMID:7487929
A;Accession: S59509
A;Molecule type: protein
A;Residues: 27-35,'Y' 37 <WOJ>
R;Atmani, F.; Mizon, J.; Khan, S.R.
Eur. J. Biochem. 236, 984-990, 1996
A;Title: Identification of uronic-acid-rich protein as urinary bikunin, the light chain

A;Reference number: S66434; MUID:96270753; PMID:8665922
A;Accession: S66434
A;Molecule type: protein
A;Residues: 206-214,'X',216-230 <ATM2>
R;Akerstroem, B.; Bratt, T.; Enghild, J.J.
FEBS Lett. 362, 50-54, 1995
A;Title: Formation of the alpha(1)-microglobulin chromophore in mammalian and insect cells
A;Reference number: S68728; MUID:95212582; PMID:7535251
A;Accession: S68728
A;Molecule type: protein
A;Residues: 89-100 <AKE>
R;Jessen, T.E.; Faarvang, K.L.; Ploug, M.
FEBS Lett. 230, 195-200, 1988
A;Title: Carbohydrate as covalent crosslink in human inter-alpha-trypsin inhibitor: a novel
A;Reference number: S02431; MUID:88167187; PMID:2450785
A;Accession: S02431
A;Molecule type: protein
A;Residues: 206-214,'X',216-217 <JES>
R;Lopez, C.; Grubb, A.; Mendez, E.
FEBS Lett. 144, 349-353, 1982
A;Title: Human protein HC displays variability in its carboxyl-terminal amino acid sequence
A;Reference number: A91304
A;Contents: annotation; variant of alpha-1-microglobulin
A;Note: pooled urine samples contained two forms of this protein, both lacking 57-Lys and
R;Hochstrasser, K.; Schonberger, O.L.; Rossmann, I.; Wachter, E.
Hoppe-Seyler's Z. Physiol. Chem. 362, 1357-1362, 1981
A;Title: Kunitz-type proteinase inhibitors derived by limited proteolysis of the inter-alpha-
by affinity chromatography.
A;Reference number: A91698; MUID:82074265; PMID:6171497
A;Contents: annotation; carboxylate binding sites
R;Morii, M.; Travis, J.
Biol. Chem. Hoppe-Seyler 366, 19-21, 1985
A;Title: The reactive site of human inter-alpha-trypsin inhibitor is in the amino-terminal
A;Reference number: A90882; MUID:85255940; PMID:3890890
A;Contents: annotation; inhibitory site
A;Note: in vitro, the first twelve residues of the amino end of the inhibitor appear to be
C;Comment: Alpha-1-microglobulin and inter-alpha-trypsin inhibitor are proteolytically pro-
C;Comment: Alpha-1-microglobulin occurs in many physiological fluids including plasma, u-
. It contains at least one brown-yellow chromophore.

Alignment Scores:
Pred. No.: 7,75e-07 Length: 352
Score: 152.00 Matches: 25
Percent Similarity: 58.93% Conservative: 8
Best Local Similarity: 44.64% Mismatches: 23
Query Match: 19.90% Indels: 0
DB: 1 Gaps: 0

US-10-807-204-11 (1-396) x HCHU (1-352)

Qy 217 AGAAAGGATATATGCAGTAGTGCACAGGAGCTGGCCCTTGCTGGCTCCATACCACAC 276
Db 227 LysGluAspSerCysGlnLeuGlyTyrSerAlaGlyProCysMetGlyMetThrSerArg 246
Qy 277 TGGTGGTACAAATAAAAAAATCAAGATCTGCTCCGAATTCATCTATGGCGGTGCGAGGG 336
Db 247 TyrPheTyrAsnGlyThrSerMetAlaCysGluThrPheGlnTyrGlyGlyCysMetGly 266
Qy 337 AACAAATAACAACCTCCAAACTGAAGCTATCTGTCTGTGTACCTGCAAA 384
Db 267 AsnGlyAsnAenPheValThrGluLysGluCysLeuGlnThrCysArg 282

RESULT 30
JC2556
alpha-1-microglobulin/inter-alpha-trypsin inhibitor precursor - Atlantic salmon (fragment
N;Alternate names: bikunin
C;Species: Salmo salar (Atlantic salmon)
C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 09-Jul-2004
C;Accession: JC2556
R;Hanley, S.; Powell, R.
Gene 147, 297-298, 1994
A;Title: Sequence of a cDNA clone encoding the Atlantic salmon alpha1-microglobulin/bikun

US-10-807-204-11 (1-396) x TIVIVC (1-65)

Qy	217	AGAAAGGATATATGTCAGTATGCCACAGGAGGTGGCCCTGCCTGGCTCCATACCCAC	276
		:	
Db	3	ArgProLysPheCysTyrLeuProAlaAspProGlyArgCysLeuAlaTyrMetProArg	22
		:	
Qy	277	TGTTGGTACAAATAAAAAATAAGATCTGCTCGAATTCATCTATGGCGGTTCACAGGG	336
		:	
Db	23	PheTyrTyrAsnProAlaSerAsnLysCysGluLysPheIleTyrGlyGlyCysArgGly	42
		:	

Qy 337 ACAATAACAACCTCCAAACTGAAGCTATCTGTCTGGTCACCTGC 381

Db 43 AsnAlaasnAsnPhelLysThrTrpAspGluCysArgHisThrCys 57

C;Date: 17-Aug-1989 #sequence_revision 17-Aug-1989 #text_change 09-Jul-2004

R; Yamada, T.; Sasaki, H.; Dohura, K.; Goto, I.; Sakaki, Y.

A:Title: Structure and expression of the alternatively-spliced forms of mRNA for

A:Reference Number: A32282, MOID:03143013, MID:2133333
A:Accession: A32282

A;status: preliminary
A:Molecule type: mRNA

A;Residue: I-100 <YAM>
A.Cross-references: INIPROT:P12023. GB:M24397. NTD:Q200350. PIDN:AAA39929.1: P12023

C;Supertfamily: Alzheimer's disease amyloid beta protein; animal knockout-type protein

F;11-61/Domain: animal Kunitz-type proteinase inhibitor homology <BPT>

Alignment Scores:

Score:	151.00	Matches:	24
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Best Local Similarity:	44.44%	Mismatches:	23
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DB:	2	GapB:	0
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US-10-807-204-11 (1-396) x A32282 (1-100)

QY 220 AAGGATATATGCAGTATGCCACAGGAGGCTGGCCCCCTGCCCTCCATACCACTGG 279

Db 8 ArqGluValCysSerGluGlnAlaGluThrGlyProCysArgAlaMetIleSerArgTrp 27

280 TGGTACAATAAAAAAAGATCTGCTCCGAATTCATCTATGGCGGTTGCCAGGGAAC 339

28 TyrpHeAspValThrGluGlyLvsCysValProPhePheTyrGlyGlyCysGlyGlyAsn 47

340 AATAACAAC TTCCAAACTGAAGCTATCTGTCTGGTCACCTGC 381

[illegible]

2
 2
 E
 E
 C
 E

T32497

C;Species: *Caenorhabditis elegans*

C;Accession: T32497

submitted to the EMBL Data Library, December 1997

A;Reference number: Z21179

A:Status: preliminary; translated from GB/EMBL/DBBJ

A;Cross-references: UNIPROT:P26228
A;Experimental source: hemolymph
C;Superfamily: basic proteinase inhibitor; animal Kunitz-type proteinase inhibitor homol
C;Keywords: serine proteinase inhibitor
F;6-56/Domain: animal Kunitz-type proteinase inhibitor homology <BPI>
F;6-56,15-39,31-52/Disulfide bonds: #status predicted
F;16/Inhibitory site: Arg (chymotrypsin) #status predicted

Alignment Scores:
Pred. No.: 1.71e-06 Length: 57
Score: 149.00 Matches: 26
Percent Similarity: 61.11% Conservatives: 7
Best Local Similarity: 48.15% Mismatches: 21
Query Match: 19.50% Indels: 0
DB: 1 Gaps: 0

US-10-807-204-11 (1-396) x TIFBHP (1-57)

QY 220 AAGGATATATGAGTATGCCAGAGGCTGGCCCTGCTGCCTCCATACCACACTGG 279
Db 3 LysSerAlaCysLeuGlnProLysGluValGlyProCysArgLysSerAspPheValPhe 22
QY 280 TGGTACATAAAAACTAAGATCTGCTCCGAATTCATCTATGGCGGTTGCCAGGGGAAC 339
Db 23 PheTyrAsnAlaAspThrLysAlaCysGluGluPheLeuTyrGlyGlyCysArgGlyAsn 42
QY 340 AATAACAACCTTCCAAACTGAAGCTATCTGCTGGTCACCTGC 381
Db 43 AspAsnArgPheAsnThrLysGluGlyCysGluLysLeuCys 56

RESULT 37

S04855
Alzheimer's disease amyloid A4 protein - mouse (fragment)
C;Species: Mus musculus domesticus (western European house mouse)
C;Date: 28-Feb-1990 #sequence_revision 28-Feb-1990 #text_change 09-Jul-2004
A;Accession: S04855
R;Fukuchi, K.I.; Martin, G.M.; Deeb, S.S.
Nucleic Acids Res. 17, 5396, 1989
A;Title: Sequence of the protease inhibitor domain of the A4 amyloid protein precursor
A;Reference number: S04855; MUID:89345111; PMID:2569710
A;Accession: S04855
A;Molecule type: mRNA
A;Residues: 1-76 <FUK>

A;Cross-references: UNIPROT:P12023; EMBL:X15210; NID:g49965; PIDN:CAA33280.1; PID:g993013
A;Note: the authors translated the codon GAT for residue 74 as Val
C;Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase i
C;Keywords: alternative splicing; serine proteinase inhibitor; transmembrane protein
F;3-53/Domain: animal Kunitz-type proteinase inhibitor homology <BPI>

Alignment Scores:
Pred. No.: 1.68e-06 Length: 76
Score: 149.00 Matches: 24
Percent Similarity: 56.60% Conservatives: 26
Best Local Similarity: 45.28% Mismatches: 23
Query Match: 19.50% Indels: 0
DB: 2 Gaps: 0

US-10-807-204-11 (1-396) x S04855 (1-76)

QY 223 GATATATGAGTATGCCAGAGGCTGGCCCTGCTGCCTCCATACCACACTGGTG 282
Db 1 GluValCysSerGluGlnAlaGluThrGlyProCysArgAlaMetIleSerArgTrpTyr 20
QY 283 TACNATAAAAACTAAGATCTGCTCCGAATTCATCTATGGCGGTTGCCAGGGGAACAT 342
Db 21 PheAspValThrGluGlyLysCysValProPhePheTyrGlyGlyCysGlyGlyAsnArg 40

QY 343 AACAACTTCCAAACTGAAGCTATCTGCTGGTCACCTGC 381
Db 41 AsnAsnPheAspThrGluGluTyrCysMetAlaValCys 53

RESULT 38

A29652

inter-alpha-trypsin inhibitor (BPI type) - sheep (fragment)
C;Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
C;Date: 31-Dec-1988 #sequence_revision 31-Dec-1988 #text_change 09-Jul-2004
C;Accession: A29652
R;Rasp, G.; Hochstrasser, K.; Wächter, E.; Reisinger, P.W.M.
Biol. Chem. Hoppe-Seyler 369, 727-731, 1987
A;Title: The amino-acid sequence of the trypsin-released inhibitor from sheep inter-alpha-trypsin inhibitor (XI).
A;Reference number: A29652; MUID:87299012; PMID:2441725
A;Accession: A29652
A;Molecule type: protein
A;Residues: 1-123 <RAS>
A;Cross-references: UNIPROT:P13371
C;Superfamily: alpha-1-microglobulin and inter-alpha-trypsin inhibitor light chain precu
C;Keywords: serine proteinase inhibitor
F;5-55/Domain: animal Kunitz-type proteinase inhibitor homology <BPI>
F;61-111/Domain: animal Kunitz-type proteinase inhibitor homology <BP2>

Alignment Scores:
Pred. No.: 1.63e-06 Length: 123
Score: 149.00 Matches: 24
Percent Similarity: 57.14% Conservatives: 8
Best Local Similarity: 42.86% Mismatches: 24
Query Match: 19.50% Indels: 0
DB: 2 Gaps: 0

US-10-807-204-11 (1-396) x A29652 (1-123)

QY 217 AGAAAGGATATATGAGTATGCCAGAGGCTGGCCCTGCTGCCTCCATACCACAC 276
Db 1 LysGluAspSerCysGlnLeuGlyTyrSerGlnGlyProCysLeuGlyMetPheLysArg 20
QY 277 TGGTGGTACAATAAAAACTAAGATCTGCTCCGAATTCATCTATGGCGGTTGCCAGGG 336
Db 21 TyrPheTyrAsnGlyThrSerMetAlaCysGluThrPheTyrTyrGlyGlyCysMetGly 40
QY 337 AACATAACAACCTTCCAAACTGAAGCTATCTGCTGGTCACCTGCAAA 384
Db 41 AsnGlyAsnAsnPheProSerGluLysGluCysLeuGlnThrCysArg 56

RESULT 39

S01803
chymotrypsin inhibitor II - silkworm
C;Species: Bombyx mori (silkworm)
C;Date: 30-Sep-1989 #sequence_revision 30-Sep-1989 #text_change 09-Jul-2004
C;Accession: S01803
R;Sasaki, T.
Biol. Chem. Hoppe-Seyler 369, 1235-1241, 1988
A;Title: Amino-acid sequences of two basic chymotrypsin inhibitors from silkworm larval
A;Reference number: S01802; MUID:89228538; PMID:3072972
A;Accession: S01803
A;Molecule type: protein
A;Residues: 1-62 <SAS>

A;Cross-references: UNIPROT:P10832
C;Superfamily: basic proteinase inhibitor; animal Kunitz-type proteinase inhibitor homol
C;Keywords: serine proteinase inhibitor
F;9-60/Domain: animal Kunitz-type proteinase inhibitor homology <BPI>

Alignment Scores:
Pred. No.: 1.91e-06 Length: 62
Score: 148.50 Matches: 30
Percent Similarity: 61.40% Conservatives: 5
Best Local Similarity: 52.63% Mismatches: 21
Query Match: 19.44% Indels: 1
DB: 2 Gaps: 1

US-10-807-204-11 (1-396) x S01803 (1-62)

QY 220 AAGGATATATGAGTATGCCA---CAGGAGGCTGGCCCTGCTGCCTCCATACCACAC 276
Db 6 LysProIleCysGluGlnAlaPheGlyAsnSerGlyProCysPheAlaTyrIleLysLeu 25
QY 277 TGGTGGTACAATAAAAACTAAGATCTGCTCCGAATTCATCTATGGCGGTTGCCAGGG 336

QY 179 GTTGCCCGTTCCAGCGTGGAAAGAAATGTTAGACTTC----- 216
 Db 197 ysValProGlyAspargGluValGluSerThrSerPheAlaargAlaValL 207
 QY 217 -----AGAA 220
 Db 207 euProGlnGluAenGluGlySerGlySerGluProLeuIleThrGlyThrLeuLysLysG 227
 QY 221 AGGATATATGATGATGATCCAGGAGGCTGCCCTGCTGCCTCCATACCACACTGGT 280
 Db 227 luAspSerCysGlnLeuAenTyrSerGluGlyProCysLeuGlyMetGlnGlnLysTyrIT 247
 QY 281 GGTCAATAAATAAATAAAGTCTGCTCGGAATTCATCTATGCGCGTGGCCAGGGGAACA 340
 Db 247 yTyrAsnGlnAlaSerMetAlaCysGluThrPheGlnTyrGlyGlyCysLeuGlyAenG 267
 QY 341 ATAACAACCTCCAACTGAAGTATCTGTGTGGTCACTGCACAA 384
 Db 267 lyAsnAsnPheAlaSerGluLysGluCysLeuGlnThrCysArg 281

RESULT 42

TIHOBI

Alpha-1-microglobulin/inter-alpha-trypsin inhibitor - horse (fragment)
 N:Alternate names: E1-14 (inhibitory fragment of ITI); ITI; trypsin inhibitor, E-UTI
 C:Species: Equus caballus (domestic horse)
 C:Date: 30-Jun-1987 #sequence_revision 04-Feb-2000 #text_change 09-Jul-2004
 C:Accession: A01210; A45653
 R:Hochstrasser, K.; Wächter, E.; Albrecht, G.J.; Reisinger, P.
 Biol. Chem. Hoppe-Seyler 366, 473-478, 1985
 A:Title: Kunitz-type proteinase inhibitors derived by limited proteolysis of the inter-
 A:Reference number: A90685; MUID:85225967; PMID:2408637
 A:Accession: A01210
 A:Molecule type: protein
 A:Residues: 3-125 <HOC>
 A:Cross-references: UNIPROT:P04365
 R:Veeraragavan, K.; Singh, K.; Wächter, E.; Hochstrasser, K.
 Biochem. Int. 26, 405-413, 1992
 A:Title: Characterization of a trypsin inhibitor from equine urine.
 A:Reference number: A45653; MUID:92328813; PMID:1627153
 A:Accession: A45653
 A>Status: preliminary
 A:Molecule type: protein
 A:Residues: 1-12, E', 14-33 <VEE>
 A:Cross-references: PIDN:AB22430.1; PID:G250858
 A:Experimental source: urine
 A>Note: sequence extracted from NCBI backbone (NCBIP:107966)
 C:Comment: This inhibitory fragment, released from native ITI after limited proteolysis
 first domain interacts weakly with PMN-granulocytic elastase and not at all with pancrea
 C:Comment: The amino acid at position p2' (19-Met) appears to determine the specificity
 d elastase; those with leucine interact strongly.
 C:Superfamily: alpha-1-microglobulin and inter-alpha-trypsin inhibitor light chain precu
 C:Keywords: duplication; glycoprotein; plasma; serine proteinase inhibitor
 F:7-57/Domain: animal Kunitz-type proteinase inhibitor homology <BP1>
 F:63-113/Domain: animal Kunitz-type proteinase inhibitor homology <BP2>
 F:7-57,16-40,32-53,63-113,72-96,88-109/disulfide bonds: #status predicted
 F:17/inhibitory site: leu (chymotrypsin, elastase) #status predicted
 F:26/Binding site: carbohydrate (asn) (covalent) #status experimental
 F:73/inhibitory site: Arg (trypsin) #status predicted

Alignment Scores:

Pred. No.:	2,57e-06	Length:	125
Score:	147.00	Matches:	24
Percent Similarity:	58.93%	Conservative:	9
Best Local Similarity:	42.86%	Mismatches:	23
Query Match:	19.24%	Indels:	0
DB:	1	Gaps:	0

US-10-807-204-11 (1-396) x TIHOBI (1-125)

QY 217 AGAAGGATATATGATGATGATCCAGGAGGCTGGCCCTGCTGCCTCCATACCACAC 276
 Db 3 LysGluAspSerCysGlnLeuAspHisAlaGlnGlyProCysLeuGlyMetIleSerArg 22

QY 277 TGGTGGTACATAAAAAAATAAGATCTGTCCGAATTCATCTATGCGGTTGCCAGGG 336
 Db 23 TyrPheTyrAenGlyThrSerMetAlaCysGluThrPheGlnTyrGlyCysLeuGly 42
 QY 337 AACAAATACAACTCCAAACTGAAGCTATCTGTGTGGTCACTGCACAA 384
 Db 43 AenGlyAsnAenPheAlaSerGlnLysGluCysLeuGlnThrCysArg 58

RESULT 43

TIHO

basic proteinase inhibitor precursor - bovine
 N:Alternate names: aprotinin; basic pancreatic trypsin inhibitor; BPTI; cationic kallikr
 C:Species: Bos primigenius taurus (cattle)
 C:Date: 24-Apr-1984 #sequence_revision 22-Jul-1994 #text_change 09-Jul-2004
 C:Accession: S00277; A30333; S10546; S02486; S28197; A90162; A92023; A90736; A90927; A34
 R:Creighton, T.E.; Charles, I.G.
 J. Mol. Biol. 194, 11-22, 1987
 A:Title: Sequences of the genes and polypeptide precursors for two bovine protease inhib
 A:Reference number: S00274; MUID:87283904; PMID:2441071
 A:Accession: S00277
 A:Molecule type: DNA; mRNA
 A:Residues: 1-100 <CR2>
 A:Cross-references: UNIPROT:P00974; GB:M20934; GB:X05274; NID:G162767; PIDN:AAD13685.1;
 R:Creighton, T.E.; Charles, I.G.
 Cold Spring Harb. Symp. Quant. Biol. 52, 511-519, 1987
 A:Title: Biosynthesis, processing, and evolution of bovine pancreatic trypsin inhibitor.
 A:Reference number: A90926; MUID:88295740; PMID:2456884
 A:Accession: A30333
 A:Molecule type: DNA
 A:Residues: 1-100 <CRE>
 A:Cross-references: GB:M20934; GB:X05274; NID:G162767; PIDN:AAD13685.1; PID:G162769
 R:Kingston, I.B.; Anderson, S.
 Biochem. J. 233, 443-450, 1986
 A:Title: Sequences encoding two trypsin inhibitors occur in strikingly similar genomic
 A:Reference number: S10546; MUID:86158754; PMID:2420326
 A:Accession: S10546
 A:Molecule type: DNA
 A:Residues: 34-97 <KIN>
 R:Fioretti, E.; Angeletti, M.; Fiorucci, L.; Barra, D.; Bossa, F.; Ascoli, F.
 Biol. Chem. Hoppe-Seyler 369(Suppl.), 37-42, 1988
 A:Title: Aprotinin-like isoinhibitors in bovine organs.
 A:Reference number: S02485; MUID:89076531; PMID:2462435
 A:Accession: S02486
 A:Molecule type: protein
 A:Residues: 36-93 <PIO>
 R:Ikeita, M.; Jones, C.S.; Kamo, M.; Taugita, A.; Kizuki, K.; Moriya, H.
 Protein Seq. Data Anal. 5, 7-11, 1992
 A:Title: Purification and characterization of the major cationic kallikrein inhibitor i
 A:Reference number: S28197; MUID:93150003; PMID:1283464
 A:Accession: S28197
 A:Molecule type: protein
 A:Residues: 36-93 <IKS>
 R:Kasell, B.; Laskowski, M.
 Biochem. Biophys. Res. Commun. 20, 463-468, 1965
 A:Title: The basic trypsin inhibitor of bovine pancreas. V. The disulfide linkages.
 A:Reference number: A90162; MUID:6083012; PMID:5860161
 A:Contents: annotation; disulfide bonds
 A:Accession: A90162
 A:Molecule type: protein
 A:Residues: 36-93 <KAS>
 R:Anderer, F.A.; Hornle, S.
 J. Biol. Chem. 241, 1568-1572, 1966
 A:Title: The disulfide linkages in kallikrein inactivator of bovine lung.
 A:Reference number: A92023; MUID:66171231; PMID:5296424
 A:Contents: annotation; disulfide bonds
 A:Accession: A92023
 A:Molecule type: protein
 A:Residues: 36-93 <AN2>
 R:Chauvet, J.; Acher, R.
 Bull. Soc. Chim. Biol. 49, 985-1000, 1967
 A:Title: La structure covalente d'un inhibiteur polypeptidique de la trypsine (inhibite
 A:Reference number: A90736; MUID:68012003; PMID:6053284

A;Contents: annotation; disulfide bonds

A;Accession: A90736
A;Molecule type: protein
A;Residues: 36-93 <CHA>
R;Diouha, V.; Pospisilova, D.; Meloun, B.; Sorm, F.
Collect. Czech. Chem. Commun. 33, 1363-1365, 1968
A;Title: Sequence of residues 18-20 in pancreatic trypsin inhibitor.
A;Reference number: A90927
A;Accession: A90927
A;Molecule type: protein
A;Residues: 36-93 <DIO>
R;Huber, R.; Kukla, D.; Ruhlmann, A.; Epp, O.; Formanek, H.
Naturwissenschaften 57, 389-392, 1970
A;Title: The basic trypsin inhibitor of bovine pancreas. I. Structure analysis and conformation.
A;Reference number: A93410; MUID:7025230; PMID:5447861
A;Contents: annotation; X-ray crystallography of basic protease inhibitor, 2.5 angstroms
R;Lewis, R.V.; Ray, P.; Coghill, R.; Kruggel, W.
Biochem. Biophys. Res. Commun. 167, 543-547, 1990
A;Title: Presence of pancreatic trypsin inhibitor in adrenal medullary chromaffin cells.
A;Reference number: A34658; MUID:90211226; PMID:2322242
A;Accession: A34658

A;Molecule type: protein
A;Residues: 36-53,55-81 <LEW>
R;Anderson, S.; Kingston, I.B.
Proc. Natl. Acad. Sci. U.S.A. 80, 6838-6842, 1983
A;Title: Isolation of a genomic clone for bovine pancreatic trypsin inhibitor by using a cDNA probe.
A;Reference number: A93977; MUID:84070725; PMID:6580617
A;Accession: A93977

A;Molecule type: DNA
A;Residues: 'PSLFNRDPPIPA',34-97,'GKTGGRAGEGKG' <AND>
A;Cross-references: GB:X03365; GB:X00966; NID:g142; PIDN:CAA27062.1; PID:g1364183
R;Stiekmann, J.; Wenzel, H.R.; Schroeder, W.; Tchesche, H.
Biol. Chem. Hoppe-Seyler 369, 157-163, 1988
A;Title: Characterization and sequence determination of six aprotinin homologues from bovine lung.
A;Reference number: S00371; MUID:88221840; PMID:2453200
A;Accession: S10062

A;Molecule type: protein
A;Residues: 36-66,'P',68-82,'S',84-93 <SIR>
A;Experimental source: lung
A;Note: the authors designated this protein as isoprotinin 2
C;Comment: Basic proteinase inhibitor is an intracellular polypeptide found in many tissues.
C;Genetics:

A;Introns: 34/1; 98/1
C;Superfamily: basic proteinase inhibitor; animal Kunitz-type proteinase inhibitor homolog
C;Keywords: serine proteinase inhibitor
F;1-20/Domain: signal sequence #status predicted <SIG>
F;21-35/Domain: propeptide #status predicted <PRO>
F;36-100/Product: basic proteinase inhibitor #status experimental <MAT>
F;40-90/Domain: animal Kunitz-type proteinase inhibitor homology <BPI>
F;40-90,49-73,65-86/Disulfide bonds: #status experimental
F;50/Inhibitory site: Lys (trypsin, chymotrypsin, kallikrein, plasmin) #status experimental

Alignment Scores:
Pred. No.: 3.27e-06 Length: 100
Score: 146.00 Matches: 24
Percent Similarity: 58.18% Conservative: 8
Best Local Similarity: 43.64% Mismatches: 23
Query Match: 19.11% Indels: 0
DB: 1 Gaps: 0

US-10-807-204-11 (1-396) x TIBO (1-100)

Qy 217 AGAAGGATATATGAGTATGCCACAGGAGCTGGCCCTCGCTCCATACCACAC 276

Db 36 ArgProaspPheCysLeuGluProProtyrThrGlyProCysLysAlaAArgileArg 55

Qy 277 TGGTGGTACATAAATAAAGTATGCTCCGAATTCATCTGCGGTTCGACGGG 336

Db 56 TyrPheTyraenAlaLysAlaGlyLeuCysGlnThrPheValTyGlyGlyCysArgAla 75

Qy 337 AACAAATCAACTCCAAAGCTATCTGTCTGTGTCACCTGC 381

Db 76 LysArgaenAenPheLysSerAlaGluAspCysMetArgThrCys 90

RESULT 44

C89114

protein C37C3.6a [imported] - Caenorhabditis elegans

C;Species: Caenorhabditis elegans

C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004

C;Accession: C89114

R;anonymous, The C. elegans Sequencing Consortium.

Science 282, 2012-2018, 1998

A;Title: Genome sequence of the nematode C. elegans: a platform for investigating biology

A;Reference number: A75000; MUID:99069613; PMID:9851916

A;Note: see websites genome.wustl.edu/gsc/C_elegans/ and www.sanger.ac.uk/Projects/C_elegans/

A;Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; and

A;Accession: C89114

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-1558 <STO>

A;Cross-references: UNIPROT:Q8I7I0; GB:chr_V; PIDN:AAC25867.1; PID:g3294501; GSPDB:GN00023

C;Genetics:

A;Gene: C37C3.6a

A;Map position: 5

Alignment Scores:

Pred. No.: 2.76e-06 Length: 1558
Score: 146.00 Matches: 22
Percent Similarity: 54.55% Conservative: 8
Best Local Similarity: 40.00% Mismatches: 25
Query Match: 19.11% Indels: 0
DB: 2 Gaps: 0

US-10-807-204-11 (1-396) x C89114 (1-1558)

Qy 226 ATATGAGTATGCCACAGGAGCTGGCCCTCGCTCCATACCACACTGGTGTAC 285

Db 1446 ValCysaspGluAlaLysAspThrGlyProCysThrAenPheValThrLysTrpTyr 1465

Qy 286 AATAAAAAAATAAGATCTGCTCGAATTTCATCTATGCGGTTCACAGGGGAAACAATAAC 345

Db 1466 AsnLysAlaaspGlyThrCysAenAArgPheHisTyGlyGlyCysGlnGlyThrAenAen 1485

Qy 346 AACTTCCAACTGAAGTATCTGTGTGTCACCTGCAAAAATAAC 390

Db 1486 ArgPheaspAenGluGlnGlnCysLysAlaAaCysGlnAenHis 1500

RESULT 45

T34395

hypothetical protein C37C3.6b - Caenorhabditis elegans

C;Species: Caenorhabditis elegans

C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 09-Jul-2004

C;Accession: T34395; T34394

R;Gisels, C.; Bradshaw, H.

submitted to the EMBL Data Library, July 1996

A;Description: The sequence of C. elegans cosmid C37C3.

A;Reference number: Z21518

A;Accession: T34395

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: DNA

A;Residues: 1-2167 <GEI>

A;Cross-references: UNIPROT:O76840; EMBL:U64857; PIDN:AAC25868.1; GSPDB:GN00023; CESP:C37C3

A;Experimental source: strain Bristol N2; clone C37C3

A;Accession: T34394

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: DNA

A;Residues: 1-1555, 'SKF' <GE2>

A;Cross-references: EMBL:U64857; PIDN:AAC25867.1; GSPDB:GN00023; CESP:C37C3.6a

A;Experimental source: strain Bristol N2; clone C37C3

C;Genetics:

A;Gene: CESP:C37C3.6b; CESP:C37C3.6a

A;Map position: 5

A;Introns: 32/3; 104/2; 156/2; 207/1; 459/2; 536/3; 577/2; 1105/3; 1367/1; 1438/1; 1556/1

Alignment Scores:

Pred. No.: 2.7e-06 Length: 2167

Score: 146.00 Matches: 22
Percent Similarity: 54.55% Conservative: 8
Best Local Similarity: 40.00% Mismatches: 25
Query Match: 19.11% Indels: 0
DB: 2 Gaps: 0

US-10-807-204-11 (1-396) x T34395 (1-2167)

QY 226 ATATGAGTATGCCACAGGAGCTGCGCCCTGCTGCCTCCATACACACTGGTGTAC 285
Db 1446 ValCysAspGluAlaLysAspThrGlyProCysThrAsnPheValThrLysTrpTyr 1465
QY 286 AATAAAAACTAAGATCTGTCGGAATCATCTATGGCGGTGCCAGGGAGCAATAAC 345
Db 1466 AsnLysAlaAspGlyThrCysAsnArgPheHisTyrGlyGlyCysGlnGlyThrAsnAsn 1485

QY 346 AACCTCCAACTGAAGCTATCTGCTGGTCACCTCCAAAATAAC 390
Db 1486 ArgPheAspAsnGluGlnCysLysAlaAlaCysGlnAsnHis 1500

RESULT 46
A55115
uterine plasmin/trypsin inhibitor - pig
C:Species: Sus scrofa domestica (domestic pig)
C>Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C:Accession: A55115
R:Stallings-Mann, M.L.; Burke, M.G.; Trout, W.E.; Roberts, R.M.
J. Biol. Chem. 269, 24090-24094, 1994
A:Title: Purification, characterization, and cDNA cloning of a Kunitz-type proteinase in
A:Reference number: A55115; MUID:95014140; PMID:7929061
A:Accession: A55115
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-122 <STA>
A:Cross-references: UNIPROT:Q29100; GB:U14282; NID:G682652; PIDN:AAAC2425.1; PID:G682653
A>Note: authors translated the codon GGC for residue 36 as Ala, AGC for residue 48 as Al
C:Superfamily: basic proteinase inhibitor; animal Kunitz-type proteinase inhibitor homol
C:Keywords: serine proteinase inhibitor
F:38-88/Domain: animal Kunitz-type proteinase inhibitor homology <BPI>

Alignment Scores:
Pred. No.: 4.05e-06 Length: 122
Score: 145.00 Matches: 24
Percent Similarity: 56.86% Conservative: 5
Best Local Similarity: 47.06% Mismatches: 22
Query Match: 18.98% Indels: 0
DB: 1 Gaps: 0

US-10-807-204-11 (1-396) x A55115 (1-122)

QY 229 TGCAGTATGCCACAGGAGCTGCGCCCTGCTGCCTCCATACACACTGGGTACAAT 288
Db 38 CysArgGluProGlyThrGlyProCysSerAlaHisPheValArgTyrPheThrAsn 57
QY 289 AAAAAAACTAAGATCTGTCGGAATCATCTATGGCGGTGCCAGGGAGCAATAACAC 348
Db 58 AlaThrThrGlyLeuCysGlnSerPheValTyrGlyGlyCysArgGlyLysGlnAsnAsn 77

QY 349 TTCCAAACCTGAAGCTATCTGCTGGTCACCTGC 381
Db 78 PheMetAspGluLysGluCysLeuHisThrCys 88

RESULT 47
T34212
hypotheical protein F10E7.4 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C>Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 09-Jul-2004
C:Accession: T34212
R:Pauley, A.
submitted to the EMBL Data Library, November 1995
A:Description: The sequence of C. elegans cosmid F10E7.
A:Reference number: Z21489
A:Accession: T34212

A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA
A:Residues: 1-805 <PAU>
A:Cross-references: UNIPROT:Q19305; EMBL:U41264; PIDN:AA82427.1; CESP:F10E7.4
C:Genetics:
A:Gene: CESP:F10E7.4
A:Introns: 9/1; 34/3; 57/1; 90/3; 128/3; 162/1; 205/1; 285/2; 417/1; 475/1; 606/1; 745/1

Alignment Scores:
Pred. No.: 3.6e-06 Length: 805
Score: 145.00 Matches: 27
Percent Similarity: 50.57% Conservative: 17
Best Local Similarity: 31.03% Mismatches: 29
Query Match: 18.98% Indels: 14
DB: 2 Gaps: 3

US-10-807-204-11 (1-396) x T34212 (1-805)

QY 124 GTGGAGNAATAGACCAGTGTACCAAAACCAGAGATTGCCAGAAAACATGAAGTGTGC 183
Db 585 LeuGlnGluLysAspThrCysVal-----MetGlnSerCys 596

QY 184 CGGTTCCGCCCTGGAGAAAGAAATGTTAGACTTCAGA---AAGGATATATGCAGTATGCCA 240
Db 597 -----ArgArgPheIleGluIleAsnSerGluGluIleCysGlnGluAsp 611

QY 241 CAGGAGGTGGCCCTGCTGCCTCCATACACACTGGTGTACAAATAAAAACTAAG 300
Db 612 LysGlnAlaGlyGlnCysAlaGlyAsnPheProArgTyrTrpTyrAsnHisGluLysThr 631

QY 301 ATCTGCTCCGAATCATCTATGGCGGTGCCAGGGAGCAATAACAACTTCCAAACTGAA 360
Db 632 GlnCysGluArgPheIlePheThrGlyCysLysGlyAsnArgAsnGlnPheGluThrGlu 651

QY 361 GCTATCTGCTGGTCACCTGC 381
Db 652 GluGluCysLysGlnIleCys 658

RESULT 48

B59399
short epsilon-dendrotoxin His55, subunit - Dendroaspis angusticeps

C:Species: Dendroaspis angusticeps
C>Date: 31-Dec-2001 #sequence_revision 31-Dec-2001 #text_change 09-Jul-2004
C:Accession: B59399
R:Sigle, R.; Hackett, M.; Aird, S.D.
Toxicol 40, 297-308, 2002
A:Title: Primary structure of four dendrotoxin E homologs from the venom of Dendroaspis
A:Reference number: A59399
A:Accession: B59399
A>Status: preliminary
A:Molecule type: protein
A:Residues: 1-57 <AIR>
A:Cross-references: UNIPROT:Q7LZE3
A>Note: trypsin inhibitor; K+ channel antagonist
C:Superfamily: basic proteinase inhibitor; animal Kunitz-type proteinase inhibitor homol
F:5-55/Disulfide bonds: #status experimental
F:14-38/Disulfide bonds: #status experimental
F:30-51/Disulfide bonds: #status experimental

Alignment Scores:
Pred. No.: 5.32e-06 Length: 57
Score: 144.00 Matches: 26
Percent Similarity: 57.41% Conservative: 5
Best Local Similarity: 48.15% Mismatches: 23
Query Match: 18.85% Indels: 0
DB: 2 Gaps: 0

US-10-807-204-11 (1-396) x B59399 (1-57)

QY 220 AAGGATATATGAGTATGCCACAGGCGTGGCCCTGCTGCCTCCATACACACTGG 279
Db 2 ArgThrPheCysLysLeuProAlaGluProGlyProCysLysAlaSerIleProAlaPhe 21

GenCore version 5.1.6
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OM nucleic - protein search, using frame_plus_n2p model

Run on: September 21, 2005, 16:50:21 ; Search time 87 Seconds

(without alignments)

4661.686 Million cell updates/sec

Title: US-10-807-204-11

Perfect score: 764

Sequence: 1 atgggactctcaggactctt.....cctgcaaaaaataaccattaa 396

Scoring table:

BLOSUM62
Xgapop 10.0, Xgapext 0.5
Ygapop 10.0, Ygapext 0.5
Fgapop 6.0, Fgapext 7.0
Delop 6.0, Delext 7.0

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 3224756

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 50 summaries

Command line parameters:

-MODE=frame_n2p.model -DEV=xlh
-Q=/cgn2_1/USPTO_spool/US10807204/runat_20092005_162900_29226/app_query.fasta_1.583
-DB=UniProt_03 -QFMT=fastan -SUFFIX=std.rup -MINMATCH=0.1 -LOOPEXT=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=1 -MATRIX=blsum62 -TRANS=human40.cdi -LIST=50
-DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=50 -MODE=LOCAL
-OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US10807204 @CGN_1_101 @runat_20092005_162900_29226 -NCPU=6 -ICPU=3
-NO MMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -HEADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : UniProt 03.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	693	90.7	131	1 WFD6 HUMAN	Q9bqv6 homo sapien
2	514	67.3	137	2 Q9BDL0	Q9bd10 oryctolagus
3	455	59.6	133	1 EPPI HUMAN	Q95925 homo sapien
4	455	59.6	143	2 Q86TF9	Q86tp9 homo sapien
5	450	58.9	182	2 Q8H245	Q86ie19 rattus norv
6	449	58.8	133	2 Q8H245	Q8h245 papio papio
7	441	57.7	133	1 EPPI MACMU	Q9bd11 macaca mula
8	386	50.5	134	1 EPPI MOUSE	Q9da01 mus musculus
9	219	28.7	77	2 Q8H244	Q8hz44 papio hamad
10	205	26.8	241	1 WFD8 HUMAN	Q8h1u0 homo sapien
11	189.5	24.8	759	2 Q8H191	Q8it91 ancylostoma
12	186	24.3	110	1 IBP CARCR	P00993 caretta car
13	185.5	24.3	988	2 Q22685	Q22685 caenorhabdi
14	182	23.8	2419	2 Q7PXZ1	Q7pxz1 anopheles g
15	181	23.7	2772	2 Q9VAV4	Q9vav4 drosophila
16	181	23.7	2776	2 Q869A0	Q869a0 drosophila

17	181	23.7	2894	2 Q7KRX2	Q7krx2 drosophila
18	181	23.7	2898	2 Q868Z9	Q868z9 drosophila
19	180.5	23.6	571	2 Q7TQN3	Q7tqn3 mus musculus
20	174.5	22.8	342	2 Q6P2V8	Q6p2v8 xenopus tro
21	174.5	22.8	342	2 Q7S246	Q7sz46 xenopus lae
22	174	22.8	515	2 Q6DRJ1	Q6drj1 brachydanio
23	173.5	22.7	1599	2 Q99983	Q99983 caenorhabdi
24	173	22.6	587	2 Q6AX20	Q6ax20 xenopus lae
25	173	22.6	751	2 Q708Z0	Q708z0 xenopus lae
26	172.5	22.6	750	2 Q6DJB6	Q6djb6 xenopus tro
27	172	22.5	67	1 IBPC BOVIN	P00976 bos taurus
28	171.5	22.4	576	2 Q8TEU8	Q8teu8 homo sapien
29	171.5	22.4	576	2 Q6UXZ9	Q6uxz9 homo sapien
30	171	22.4	1416	1 YN81 CABEL	Q03610 caenorhabdi
31	170	22.3	83	2 Q6ITB9	Q6itb9 pseudochis
32	170	22.3	516	2 Q7T363	Q7t363 brachydanio
33	169	22.1	83	2 Q6ITB5	Q6itb5 oxyuranus m
34	169	22.1	169	2 Q9N0X7	Q9n0x7 bos taurus
35	169	22.1	1297	2 Q9N343	Q9n343 caenorhabdi
36	168.5	22.1	750	2 Q708Y9	Q708y9 xenopus lae
37	168	22.0	86	2 Q9GP15	Q9gp15 ixodes ric
38	168	22.0	1743	2 Q9XW55	Q9xw55 caenorhabdi
39	168	22.0	3198	2 Q9U8G8	Q9u8g8 manduca sex
40	167.5	21.9	342	2 P70004	P70004 xenopus lae
41	167.5	21.9	922	2 Q21418	Q21418 caenorhabdi
42	167.5	21.9	1474	2 Q62504	Q62504 caenorhabdi
43	167	21.9	80	2 Q8T3S7	Q8t3s7 araneus ven
44	167	21.9	83	2 Q6ITB4	Q6itb4 oxyuranus m
45	167	21.9	83	2 Q6ITB6	Q6itb6 oxyuranus s
46	167	21.9	90	2 Q6T6S5	Q6t6s5 bitis gabon
47	166	21.7	83	2 Q90WAL	Q90wal pseudonaja
48	166	21.7	122	1 BTIA BOOMI	P83609 boophilus m
49	166	21.7	507	2 Q6I750	Q6i750 rattus norv
50	165.5	21.7	337	1 AMBP_PIG	P04366 sus scrofa

ALIGNMENTS

RESULT 1

WFD6_HUMAN
ID WFD6 HUMAN STANDARD; PRT; 131 AA.
AC Q9BQY6; Q8NFV6;
DT 10-OCT-2003 (Rel. 42, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE WAP four-disulfide core domain protein 6 precursor (Putative protease inhibitor WAP6).
DE inhibitor WAP6).
GN Name=WFD6; Synonyms=C20orf171, WAP6;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM 2).
RX MEDLINE=22304654; PubMed=12206714; DOI=10.1042/BJ20020869;
RA Claus A., Lilja H., Lundwall A.;
RT "A locus on human chromosome 20 contains several genes expressing protease inhibitor domains with homology to whey acidic protein."; Biochem. J. 368:233-242(2002).
RL [2]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RX MEDLINE=21638749; PubMed=11780052; DOI=10.1038/414865a;
RA Deloukas P., Matthews L.H., Ashurst J.L., Burton J., Gilbert J.G.R., Jones M., Stavridis G., Almeida J.P., Babbage A.K., Bagguley C.L., Bailey J., Barlow K.F., Bates K.N., Beard L.M., Beare D.M., Beasley O.P., Bird C.P., Blakey S.E., Bridgeman A.M., Brown A.J., Buck D., Burrill W.D., Butler A.P., Carder C., Carter N.P., Chapman J.C., Clamp M., Clark G., Clark L.N., Clark S.Y., Clee C.M., Clegg S., Cobley V.E., Collier R.E., Connor R.E., Corby N.R., Coulson A., Coville G.J., Deadman R., Dhani P.D., Dunn M., Ellington A.G., Frankland J.A., Fraser A., French L., Garner P., Graham D.V., Griffiths C., Griffiths M.N.D., Gwilliam R., Hall R.E., Hammond S., Harley J.L., Heath P.D., Ho S., Holden J.L., Howden P.J.,

```
RA Huckle E., Hunt A.R., Hunt S.E., Jekosch K., Johnson C.M., Johnson D.,
RA Kay M.P., Kimberley A.M., King A., Knights A., Laird G.K., Lawlor S.,
RA Leivaeslahti M.H., Leversha M.A., Lloyd C., Lloyd D.M., Lovell J.D.,
RA Mareh V.L., Martin S.L., McConachie L.J., McLay K., McMurray A.A.,
RA Milne S.A., Mistry D., Moore M.J.P., Mullikin J.C., Nickerson T.,
RA Oliver K., Parker A., Patel R., Pearce T.A.V., Peck A.I.,
RA Phillimore B.J.C.T., Prathalingam S.R., Plumb R.W., Ramsay H.,
RA Rice C.M., Ross M.T., Scott C.E., Sehra H.K., Showkneen R., Sims S.,
RA Skuce C.D., Smith M.L., Soderlund C., Steward C.A., Sulston J.E.,
RA Swann R.M., Sycamore N., Taylor R., Tee L., Thomas D.W., Thorpe A.,
RA Tracey A., Tromans A.C., Vaudin M., Wall M., Wallis J.M.,
RA Whitehead S.L., Whitaker P., Willey D.L., Williams L., Williams S.A.,
RA Wilming L., Wray P.W., Hubbard T., Durbin R.M., Bentley D.R., Beck S.,
RT Rogers J.;
RT "The DNA sequence and comparative analysis of human chromosome 20.";
RL Nature 414:865-871(2001).
CC -!- SUBCELLULAR LOCATION: Secreted (Potential).
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=1;
CC IsoId=Q9BQV6-1; Sequence=Displayed;
CC Name=2;
CC IsoId=Q9BQV6-2; Sequence=VSP_007550; VSP_007551;
CC -!- TISSUE SPECIFICITY: Ubiquitously expressed, but the highest levels
CC are found in epididymis, testis and trachea.
CC -!- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.
CC -!- SIMILARITY: Contains 1 WAP-type domain.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; AF411861; AA03684.1; -.
DR EMBL; AL031663; KAC36264.1; -.
DR HSSP; P02760; 1BIK.
DR Genew; HGNC:16164; WFDG6.
DR InterPro; IPR002223; Prot_Inh_Kunz-m.
DR InterPro; IPR008197; WAP.
DR Pfam; PF00014; Kunitz_BPTI; 1.
DR Pfam; PF00095; WAP; 1.
DR PRINTS; PR00759; BASICPTASE.
DR ProDom; PD000222; Prot_Inh_Kunz-m; 1.
DR SMART; SM00131; KU; 1.
DR SMART; SM00217; WAP; 1.
DR PROSITE; PS00317; 4_DISULFIDE_CORE; FALSE_NEG.
DR PROSITE; PS00280; BPTI_KUNITZ_1; FALSE_NEG.
DR PROSITE; PS50279; BPTI_KUNITZ_2; 1.
KW Alternative splicing; Serine protease inhibitor; Signal.
FT SIGNAL 1 25 Potential.
FT CHAIN 26 131 WAP four-disulfide core domain protein 6.
FT DOMAIN 31 69 WAP.
FT DOMAIN 70 128 BPTI/Kunitz inhibitor.
FT DISULFID 33 61 By similarity.
FT DISULFID 48 60 By similarity.
FT DISULFID 54 69 By similarity.
FT VARSPLIC 75 86 IYAVCHRRRLAFA -> VSLTLYHKEELE (in isoform
FT /FTId=VSP_007550.
FT VARSPLIC 87 131 Missing (in isoform 2).
FT /FTId=VSP_007551.
SQ SEQUENCE 131 AA; 14626 MW; 2F6D06EF43EB7564 CRC64;
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Alignment Scores:

Pred. No.:	1.28e-61	Length:	131
Score:	693.00	Matches:	129
Best Local Similarity:	97.73%	Conservative:	0
Query Match:	97.73%	Mismatches:	2
DB:	100.71%	Indels:	2
	1	Gaps:	0

```
US-10-807-204-11 (1-396) x WFD6_HUMAN (1-131)
QY 1 ATGGAGCTCTCAGGACTTCTGCCAATCTGGTACCATTATCCTTTTGGGGGATCCAG 60
Db 1 MetGlyLeuSerGlyLeuLeuProIleLeuValProPheIleLeuLeuGlyAspIleGln 20
QY 61 GAACCTGGGACGCTGAAGGATCCTTTGGCAAGCCGTGTCCCAAAATCAAAGTGGAAATGC 120
Db 21 GluProGlyHisAlaGluGlyIleLeuGlyIleLeuGlyIleLeuValGluCys 40
QY 121 GAAGTGGAGAAATAGACCACTGTACCAAAATCCAGAGATTGCCAGAAATCATGAAGTGT 180
Db 41 GluValGluGluIleAspGlnCysThrLysProArgAspCysProGluAsnMetLysCys 60
QY 181 TGGCCGTTTACCGCTGCAAAAGAAATGTTTAGACTTTCAGAAAGGATATATGCAAGTATGCCA 240
Db 61 CysProPheSerArgGlyIleLysCysLeuAspPheArgLys-IleTyrAlaValCysHi 80
QY 241 CAGGAGGCTGGCCCTCCCTGGCTCCATACCACTGGTGGTGTACAAAT-AAAAAACTAA 299
Db 80 sArgArgLeuAlaProAlaIleProProTyrHisThrGlyGlyThrIleLysIleThrLy 100
QY 300 GATCTGCTCCGAATTCATCTATGCGCGTTGCCAGGGGAACAATAACAACTTCCAAACTGA 359
Db 100 sileCysSerGluPheIleTyrGlyGlySerGlnGlyAsnAsnAsnAsnAsnAsnAsnAsn 120
QY 360 AGCTATCTGTCTGGTCCACCTGCAAAAATACCAT 393
Db 120 uAlaileCysLeuValThrCysLysIleTyrHis 131
RESULT 2
Q9BDL0 PRELIMINARY; PRT; 137 AA.
AC Q9BDL0;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Eppin.
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Testis.
RX MEDLINE=22791380; PubMed=12909348; DOI=10.1016/S0378-1119(03)00608-5;
RA Silvasammugam P., Hall S.H., Hamil K.G., French F.S., O'Rand M.G.,
RA Richardson R.T.;
RT "Characterization of mouse Eppin and a gene cluster of similar
RL Gene 312:125-134(2003).
CC -!- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.
DR EMBL; AF346415; AAK31337.1; -.
DR HSSP; Q16019; IAAP.
DR GO; GO:0004867; F:serine-type endopeptidase inhibitor activity; IEA.
DR InterPro; IPR002223; Prot_Inh_Kunz-m.
DR InterPro; IPR008197; WAP.
DR Pfam; PF00014; Kunitz_BPTI; 1.
DR Pfam; PF00095; WAP; 1.
DR PRINTS; PR00759; BASICPTASE.
DR ProDom; PD000222; Prot_Inh_Kunz-m; 1.
DR SMART; SM00131; KU; 1.
DR SMART; SM00217; WAP; 1.
DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
DR PROSITE; PS50279; BPTI_KUNITZ_2; 1.
SQ SEQUENCE 137 AA; 15773 MW; F397AF4E065D626B CRC64;
Alignment Scores:
Pred. No.: 2.09e-43 Length: 137
Score: 514.00 Matches: 90
Percent Similarity: 81.25% Conservative: 14
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DR Pfam; PF00014; Kunitz_BPTI; 1.
DR Pfam; PF00095; WAP; 1.
DR PRINTS; PR00003; 4DISULPHCORE.
DR PRINTS; PR00759; BASICPTASE.
DR ProDom; PD000222; Prot_Inh_Kunz-m; 1.
DR SMART; SM00131; KU; 1.
DR SMART; SM00217; WAP; 1.
DR PROSITE; PS00317; 4_DISULFIDE_CORE; 1.
DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
DR PROSITE; PS0279; BPTI_KUNITZ_2; 1.
KW Alternative splicing; Serine protease inhibitor; Signal.
FT SIGNAL 1 231
FT CHAIN 22 131
FT DOMAIN 29 73
FT DOMAIN 77 127
FT DISULFID 33 61
FT DISULFID 40 65
FT DISULFID 48 60
FT DISULFID 54 69
FT DISULFID 77 127
FT DISULFID 86 110
FT DISULFID 102 123
FT VARSPLIT 1 31
SQ SEQUENCE 133 AA; 15284 MW; F7831B203366D9DC CRC64;

Alignment Scores:
Pred. No.: 2.09e-37 Length: 133
Score: 455.00 Matches: 77
Percent Similarity: 74.22% Conservative: 18
Best Local Similarity: 60.16% Mismatches: 33
Query Match: 59.55% Indels: 0
DB: 1 Gaps: 0

US-10-807-204-11 (1-396) x EPPI_HUMAN (1-133)
Qy 1 ATGGGACTCTCAGGACTTCTGCCAATCCTGTGACCATTCATCCTTTTGGGGGACATCCAG 60
Db 1 MetGlySerGlyLeuSerGlyLeuValLeuPheValLeuLeuAlaAsnValGln 20

Qy 61 GAACCTGGGACGCTGAAGGATCCTTGGCAAGCGTGTCCCAAAATCAAAAGTGAATGC 120
Db 21 GlyProGlyLeuThrAspTyrLeuPheProArgCysProLysIleArgGluGluCys 40

Qy 121 GAATGGAGAAATAGACCATGTACCAACCCAGAGATTGCCAGAAACATGAAGTGT 180
Db 41 GluPheGlnGluArgAspValCysThrLysAspArgGlnCysGlnAspAsnLysCys 60

Qy 181 TGCCGCTTACGCCGTGGAAAGAAATGTTTAGACTTCAGAAAGGATATATGAGTATGCCA 240
Db 61 CysValPheSerCysGlyLysLysCysLeuAspLeuLysGlnAspValCysGluMetPro 80

Qy 241 CAGGAGGCTGCCCTCGCTGCCTCCATACACACACTGGTGGTACATAAATAAACTAAG 300
Db 81 LysGluThrGlyProCysLeuAlaTyrPheLeuHisTyrTyrAspLysLysAspAsn 100

Qy 301 ATCTGCTCGAATTCATCTATGGCGGTGGCAGGGGAAACAATAACAATCTTCCAACTGAA 360
Db 101 ThrCysSerMetPheValTyrGlyCysGlnGlyAsnAsnAsnAsnPheGlnSerLys 120

Qy 361 GCTATCTGCTGGTCACTGCCAAA 384
Db 121 AlaAsnCysLeuAsnThrCysLys 128

RESULT 4
ID Q86TP9 PRELIMINARY; PRT; 143 AA.
AC Q86TP9;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE SPINLWI protein (Fragment).

GN Name=SPINLWI;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins L.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skaleka U., Smallus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
RA Strausberg R.;
RA Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.
DR EMBL; BC044829; AAH4829.1; -.
DR HSSP; P00974; 1UUA.
DR GO; GO:0004867; F:serine-type endopeptidase inhibitor activity; IEA.
DR InterPro; IPR002223; Prot_Inh_Kunz-m.
DR InterPro; IPR008197; WAP.
DR Pfam; PF00014; Kunitz_BPTI; 1.
DR Pfam; PF00095; WAP; 1.
DR PRINTS; PR00003; 4DISULPHCORE.
DR PRINTS; PR00759; BASICPTASE.
DR ProDom; PD000222; Prot_Inh_Kunz-m; 1.
DR SMART; SM00131; KU; 1.
DR SMART; SM00217; WAP; 1.
DR PROSITE; PS00317; 4_DISULFIDE_CORE; 1.
DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
DR PROSITE; PS0279; BPTI_KUNITZ_2; 1.
FT NON_TER 1
FT NON_TER 1
SQ SEQUENCE 143 AA; 16506 MW; 92BF56C2B7977508 CRC64;

Alignment Scores:
Pred. No.: 2.1e-37 Length: 143
Score: 455.00 Matches: 77
Percent Similarity: 74.22% Conservative: 18
Best Local Similarity: 60.16% Mismatches: 33
Query Match: 59.55% Indels: 0
DB: 2 Gaps: 0

US-10-807-204-11 (1-396) x Q86TP9 (1-143)
Qy 1 ATGGGACTCTCAGGACTTCTGCCAATCCTGTGACCATTCATCCTTTTGGGGGACATCCAG 60
Db 11 MetGlySerGlyLeuSerGlyLeuValLeuPheValLeuLeuAlaAsnValGln 30

Qy 61 GAACCTGGGACGCTGAAGGATCCTTGGCAAGCGTGTCCCAAAATCAAAAGTGAATGC 120
Db 31 GlyProGlyLeuThrAspTyrLeuPheProArgCysProLysIleArgGluGluCys 50

Qy 121 GAATGGAGAAATAGACCATGTACCAACCCAGAGATTGCCAGAAACATGAAGTGT 180
Db 121 GAATGGAGAAATAGACCATGTACCAACCCAGAGATTGCCAGAAACATGAAGTGT 180
```



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Db      21 GlyProGlyLeuThrAspTrpLeuPheProArgCysProThrIleArgGluCys 40
      |||||      : : :      : : :      |||||      ||| : : :      |||||
Qy      121 GAAGTGGAGAAATAGACAGTGTACCAAAACCCAGAGATTGCCAGAAAACATGAAGTGT 180
      |||      |||      ||| : : :      |||      ||| : : :      |||||
Db      41 GluPheArgGluArgAspValCysThrArgHisArgGlnCysProAspAsnLysLysCys 60
      |||||      |||||      |||||      |||||      |||||      |||||
Qy      181 TGCCCGTTCAGCCGTGGGAAGAAATGTTAGACTTCAGAAAGGATATATGAGTATGCCA 240
      |||      |||||      |||||      |||||      |||||      |||||
Db      61 CysValPheSerCysGlyLysCysLeuAspLeuLysGlnAspValCysGluMetPro 80
      |||||      |||||      |||||      |||||      |||||      |||||
Qy      241 CAGGAGGCTGCCCTGCCTCCATACCACACTGCTGTACCAATAAAAAAACTAAG 300
      |||      |||||      |||||      |||||      |||||      |||||
Db      81 AsnGluThrGlyProCysLeuAlaPhePheIleArgTrpTrpTrpAspLysLysAsnAsn 100
      |||||      |||||      |||||      |||||      |||||      |||||
Qy      301 ATCTGCTCCGAATTCATCTATGCGGTGGCCAGGGAAACAATAACAACCTTCCAACTGAA 360
      |||||      |||||      |||||      |||||      |||||      |||||
Db      101 ThrCysSerThrPheValTyrGlyCysGlnGlyAsnAsnAsnAsnPheGlnSerGlu 120
      |||||      |||||      |||||      |||||      |||||      |||||
Qy      361 GCTATCTGCTGCTGCCTGCCTGCAAA 384
      |||      |||||      |||||      |||||      |||||      |||||
Db      121 AlaAsnCysLeuAsnThrCysLys 128
      |||||      |||||      |||||      |||||      |||||      |||||

RESULT 7
EPPI_MACMU
ID EPPI_MACMU STANDARD; PRT; 133 AA.
AC Q9BDL1;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Eppin precursor (Epididymal protease inhibitor) (Serine protease
DE inhibitor-like with Kunitz and WAP domains 1).
GN Name=SPINLW1;
OS Macaca mulatta (Rhesus macaque).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae;
OC Cercopitheciinae; Macaca.
OX NCBI_TaxID=9544;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Epididymis, and Testis;
RA Sivashanmugam P., Hall S.H., Hamil K.G., French F.S., O'Rand M.G.,
RA Richardson R.T.;
RT "Characterization of monkey and mouse Eppin, a protease inhibitor from
RT epididymis and testis.";
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
CC -!- SUBCELLULAR LOCATION: Secreted (Potential).
CC -!- TISSUE SPECIFICITY: Expressed in epididymis and testis.
CC -!- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.
CC -!- SIMILARITY: Contains 1 WAP-type domain.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
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CC entities requires a license agreement (see http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; AF346414; AAK31336.1; -.
DR HSSP; P00974; 1BPTI.
DR InterPro; IPR002223; Prot_Inh_Kunz-m.
DR InterPro; IPR008197; WAP.
DR Pfam; PF00014; Kunitz_BPTI; 1.
DR Pfam; PF00095; WAP; 1.
DR PRINTS; PR00759; BASICPTASE.
DR ProDom; PD000222; Prot_Inh_Kunz-m; 1.
DR SMART; SM00131; KU; 1.
DR SMART; SM00217; WAP; 1.
DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
DR PROSITE; PS02079; BPTI_KUNITZ_2; 1.
KW Serine protease inhibitor; Signal.
FT SIGNAL 1 21 Potential.

```

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FT CHAIN 22 133 Eppin.
FT DOMAIN 29 73 WAP.
FT DOMAIN 77 127 BPTI/Kunitz inhibitor.
FT DISULFID 33 61 By similarity.
FT DISULFID 40 65 By similarity.
FT DISULFID 48 60 By similarity.
FT DISULFID 54 69 By similarity.
FT DISULFID 77 127 By similarity.
FT DISULFID 86 110 By similarity.
FT DISULFID 102 123 By similarity.
SQ SEQUENCE 133 AA; 15279 MW; 433AB946E39A35B9 CRC64;

Alignment Scores:
Pred. No.: 5.56e-36 Length: 133
Score: 441.00 Matches: 76
Percent Similarity: 71.88% Conservative: 16
Best Local Similarity: 59.38% Mismatches: 36
Query Match: 57.72% Indels: 0
DB: 1 Gaps: 0

US-10-807-204-11 (1-396) x EPPI_MACMU (1-133)
Qy 1 ATGGGACTCTCAGGACTTCTGCCAATCTCGTACCATTCATCTTTGGGGACATCCAG 60
      |||||      |||||      |||||      |||||      |||||      |||||
Db 1 MetGlySerSerGlyLeuLeuSerLeuValLeuPheIleLeuLeuValAsnValGln 20
      |||||      |||||      |||||      |||||      |||||      |||||
Qy 61 GAACCTGGGCAGCTGAAGCATCTTGGCAAGCCGTGTCGCAAAATCAAAGTGGATGC 120
      |||||      |||||      |||||      |||||      |||||      |||||
Db 21 GlyProGlyLeuThrAspTrpLeuPheProArgCysProThrIleArgGluCys 40
      |||||      |||||      |||||      |||||      |||||      |||||
Qy 121 GAAGTGGAGAAATAGACAGTGTACCAAAACCCAGAGATTGCCAGAAAACATGAAGTGT 180
      |||||      |||||      |||||      |||||      |||||      |||||
Db 41 GluPheArgGluArgAspValCysThrArgHisArgGlnCysProAspAsnLysLysCys 60
      |||||      |||||      |||||      |||||      |||||      |||||
Qy 181 TGCCCGTTCAGCCGTGGGAAGAAATGTTAGACTTCAGAAAGGATATATGAGTATGCCA 240
      |||||      |||||      |||||      |||||      |||||      |||||
Db 61 CysValPheSerCysGlyLysCysLeuAspLeuLysGlnAspValCysGluMetPro 80
      |||||      |||||      |||||      |||||      |||||      |||||
Qy 241 CAGGAGGCTGCCCTGCCTCCATACCACACTGCTGTACCAATAAAAAAACTAAG 300
      |||||      |||||      |||||      |||||      |||||      |||||
Db 81 AsnGluThrGlyProCysLeuAlaPhePheIleArgTrpTrpTrpAspLysLysAsnAsn 100
      |||||      |||||      |||||      |||||      |||||      |||||
Qy 301 ATCTGCTCCGAATTCATCTATGCGGTGGCCAGGGAAACAATAACAACCTTCCAACTGAA 360
      |||||      |||||      |||||      |||||      |||||      |||||
Db 101 ThrCysSerThrPheValHisGlyCysGlnGlyAsnAsnAsnAsnPheGlnSerGlu 120
      |||||      |||||      |||||      |||||      |||||      |||||
Qy 361 GCTATCTGCTGCTGCCTGCCTGCAAA 384
      |||||      |||||      |||||      |||||      |||||      |||||
Db 121 AlaAsnCysLeuAsnThrCysLys 128
      |||||      |||||      |||||      |||||      |||||      |||||

RESULT 8
EPPI_MOUSE
ID EPPI_MOUSE STANDARD; PRT; 134 AA.
AC Q9DA01;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Eppin precursor (Epididymal protease inhibitor) (Serine protease
DE inhibitor-like with Kunitz and WAP domains 1).
GN Name=Spinlwl;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/c; TISSUE=Epididymis, and Testis;
RA Sivashanmugam P., Hall S.H., Hamil K.G., French F.S., O'Rand M.G.,
RA Richardson R.T.;
RT "Characterization of monkey and mouse Eppin, a protease inhibitor from
RT epididymis and testis.";
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
RN [2]

```


SEQUENCE FROM N.A.
 RP STRAIN=C57BL/6J; TISSUE=Testis; DOI=10.1038/nature01266;
 RC MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;
 RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
 RA Nikaide I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,
 RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,
 RA Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
 RA Schriml L.M., Kanapin A., Bataulda H., Batalov S., Beisel K.W.,
 RA Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S.,
 RA Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,
 RA Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,
 RA Grimmond S., Guscinich S., Hirokawa N., Jackson I.J., Jarvis E.D.,
 RA Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,
 RA Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
 RA Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,
 RA Nagashima T., Nunata K., Okido T., Pavan W.J., Perteza G., Pesole G.,
 RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,
 RA Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,
 RA Sandelin A., Schneider C., Sempile C.A., Setou M., Shimada K.,
 RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,
 RA Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,
 RA Wilming L.G., Wynshaw-Boris A., Yanagisawa M., Yang I., Yang L.,
 RA Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,
 RA Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,
 RA Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,
 RA Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,
 RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,
 RA Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
 RA Birney E., Hayashizaki Y.,
 RA "Analysis of the mouse transcriptome based on functional annotation of
 RT 60,770 full-length cDNAs";
 RL Nature 420:563-573 (2002).
 RN (3)
 RP SEQUENCE FROM N.A.
 RC TISSUE=Testis;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Munz D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahy J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywicki M.I., Skalska U., Smalilus D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,
 RA "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
 CC -|- SUBCELLULAR LOCATION: Secreted (Potential).
 CC -|- TISSUE SPECIFICITY: Expressed in epididymis and testis.
 CC -|- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.
 CC -|- SIMILARITY: Contains 1 WAP-type domain.
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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 CC -----
 CC EMBL; AF346413; AK31335.1; -
 CC EMBL; AK006296; BAB24514.1; -
 CC EMBL; BC048637; AAF48637.1; -
 CC HSP; P31713; 1SHP.

DR MGD; MGI:1922776; Spinlwl.
 DR GO; GO:0001689; C:cytosol; IDA.
 DR GO; GO:0005737; C:cytoplasm; IDA.
 DR InterPro; IPR002223; Prot_Inh_Kunz-m.
 DR InterPro; IPR008197; WAP.
 DR Pfam; PF00014; Kunitz_BPTI; 1.
 DR Pfam; PF00095; WAP; 1.
 DR PRINTS; PR00003; 4DISULPHORE.
 DR PRINTS; PR00759; BASICPTASE.
 DR ProDom; PD000222; Prot_Inh_Kunz-m; 1.
 DR PROSITE; PS00317; 4_DISULFIDE_CORE; 1.
 DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
 DR PROSITE; PS0279; BPTI_KUNITZ_2; 1.
 KW Serine protease inhibitor; Signal.
 FT SIGNAL 1 21 Potential.
 FT CHAIN 22 134 Eppin.
 FT DOMAIN 29 73 WAP.
 FT DOMAIN 77 127 BPTI/Kunitz inhibitor.
 FT DISULFID 33 61 By similarity.
 FT DISULFID 40 65 By similarity.
 FT DISULFID 48 60 By similarity.
 FT DISULFID 54 69 By similarity.
 FT DISULFID 77 127 By similarity.
 FT DISULFID 86 110 By similarity.
 FT DISULFID 102 123 By similarity.
 SQ SEQUENCE 134 AA; 15470 MW; DFE63D4D4C427F CRC64;
 Alignment Scores:
 Pred. No.: 2,19e-30 Length: 134
 Score: 386.00 Matches: 66
 Percent Similarity: 70.54% Conservative: 25
 Best Local Similarity: 51.16% Mismatches: 38
 Query Match: 50.52% Indels: 0
 DB: 1 Gaps: 0
 US-10-807-204-11 (1-396) x BPPI_MOUSE (1-134)
 QY 1 ATGGGACTCTCAGGACTTCTGCGCAATCTGTCATCTGTCATCTCTTTGGGGGACATCCAG 60
 Db 1 MetLysLeuSerGlyPheValSerLeuValLeuPheGlyLeuLeuAlaArgValGln 20
 QY 61 GAACCTGGGCGCAGCTGAAGGCATCTTGGCAAGCGCTGCCCAATCAAAGTGAATGC 120
 Db 21 GlyProSerLeuAlaAspLeuLeuPheProArgCysPheArgGluGluCys 40
 QY 121 GAAGTGGGAAGAAATAGACAGTGTACCAACCCAGAGATTGCCAGAAAACATGAAGTGT 180
 Db 41 GluHisGlnGluArgAspLeuCysThrArgAspArgAspCysProLysLysGluLysCys 60
 QY 181 TGCCCGTTTCAGCCGTGGAAAGAAATGTTTAGACTTTCAGAAAGGATATATGCAAGTATGCCA 240
 Db 61 CysValPheAsnGlyLysLysCysLeuAsnProGlnGlnAspIleCysSerLeuPro 80
 QY 241 CAGGAGGCTGCCCTGCTGCCCTCCATACCACACTGCTGCTACATAACCAATAAAAAA 300
 Db 81 LysAspSerGlyTyrCysMetAlaTyrPheArgArgTrpTrpPheAsnLysGluAsnSer 100
 QY 301 ATCTGCTCCGAATTCATCTATGCGCGTGGCCAGGGAACAATAACAACCTTCCAAACTGAA 360
 Db 101 ThrCysGlnValPheIleTyrGlyCysGlnGlyAsnAsnAsnAsnAsnAsnPheGlnSerGln 120
 QY 361 GCTATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 387
 Db 121 SerIleCysGlnAsnAlaCysGluLys 129
 RESULT 9
 Q8H244
 ID Q8H244 PRELIMINARY; PRT; 77 AA.
 AC Q8H244;
 DT 01-MAR-2003 (TrEMBLrel. 23, Created)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Epididymal protease inhibitor 2.

```
GN Name=Eppin;
OS Papio hamadryas (Hamadryas baboon);
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecinae; Papio.
OX NCBI_TaxID=9557;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Testis;
RA Shivashanmugam P., O'Rand M.G., Richardson R.T.;
RL Submitted (AUG-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY141975; AAN08509.1; -.
DR GO; GO:0008233; F:peptidase activity; IEA.
DR InterPro; IPR008197; WAP.
DR Pfam; PF00095; WAP; 1.
DR PRINTS; PR00003; 4DISULPHCORE.
DR SMART; SM00217; WAP; 1.
KW Protease.
SQ SEQUENCE 77 AA; 8787 MW; B86E5868C57CEBD0 CRC64;

Alignment Scores:
Pred. No.: 2.05e-13 Length: 77
Score: 219.00 Matches: 40
Percent Similarity: 68.92% Conservative: 11
Best Local Similarity: 54.95% Mismatches: 23
Query Match: 28.66% Indels: 0
DB: 2 Gaps: 0

US-10-807-204-11 (1-396) x Q8HZ44 (1-77)
QY 1 ATGGGACTCTCAGGACTTCTGCAATCCTGGTACCATTATCTTTGGGGGACATCCAG 60
DB 1 MetGlySerSerGlyLeuLeuSerLeuValLeuPheLeuLeuAlaAsnValGln 20
QY 61 GAACCTGGGACGCTGAGGACATCTTGGCAAGCGGTGTCACAAATCAAAAGTGGAAATGC 120
DB 21 GlyProGlyLeuThrAspValLeuPheProArgCysProThrIleArgGluGluCys 40
QY 121 GAAGTGGAGAAATAGACCACTGTACCAACCCAGAGNATGCCAGAGAAAACATGAAGTGT 180
DB 41 GluPheArgGluArgAspValCysThrArgHisArgGlnCysProAspAsnLysLysCys 60
QY 181 TGCCCGCTGACCGCTGGAAAGAAATGTTTAGACTTCAGAAAG 222
DB 61 CysValPheSerCysGlyLysCysLeuAspLeuLysGln 74

RESULT 10
WFD8 HUMAN
AC O81UÅO; O96A34; PRT; 241 AA.
DT 10-OCT-2003 (Rel. 42, Created)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE WAP four-disulfide core domain protein 8 precursor (Putative protease inhibitor WAP8).
GN Name=WFD8; Synonyms=C20orf170, WAP8;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Claus A., Lilja H., Lundwall A.;
RL MEDLINE=22304654; PubMed=12206714; DOI=10.1042/BJ20020869;
RT "A locus on human chromosome 20 contains several genes expressing protease inhibitor domains with homology to whey acidic protein.";
RL Biochem. J. 368:233-242(2002).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=21638749; PubMed=11780052; DOI=10.1038/414865a;
RA Deloukas P., Matthews L.H., Ashurst J.L., Burton J., Gilbert J.G.R.,
RA Jones M., Stavrides G., Almeida J.P., Babbage A.K., Bagguley C.L.,
RA Bailey J., Barlow K.F., Bates K.N., Beard L.M., Beare D.M.,
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RA Beasley O.P., Bird C.P., Blakey S.E., Bridgeman A.M., Brown A.J.,
RA Buck D., Burrill W.D., Butler A.P., Carder C., Carter N.P.,
RA Chapman J.C., Clamp M., Clark G., Clark L.N., Clark S.Y., Clee C.M.,
RA Clegg S., Cobley V.E., Collier R.E., Connor R.E., Corby N.R.,
RA Coulson A., Coville G.J., Deadman R., Dharm P.D., Dunn M.,
RA Ellington A.G., Frankland J.A., Fraser A., French L., Garner P.,
RA Grafham D.V., Griffiths C., Griffiths M.N.D., Gwilliam R., Hall P.E.,
RA Hammond S., Harley J.L., Heath P.D., Ho S., Holden J.L., Howden P.J.,
RA Huckle E., Hunt A.R., Hunt S.E., Jekosch K., Johnson C.M., Johnson D.,
RA Kay M.P., Kimberley A.M., King A., Knights A., Laird G.K., Lawlor S.,
RA Leivaeslahti M.H., Leversha M.A., Lloyd C., Lloyd D.M., Lovell J.D.,
RA Marsh V.L., Martin S.L., McConnachie L.J., McIay K., McMurray A.A.,
RA Milne S.A., Mistry D., Moore M.J.F., Mullikin J.C., Nickerson T.,
RA Oliver K., Parker A., Patel R., Pearce T.A.V., Peck A.I.,
RA Phillimore B.J.C.T., Prathalingam S.R., Plumb R.W., Ramsay H.,
RA Rice C.M., Ross M.T., Scott C.E., Sehra H.K., Shownkeen R., Sims S.,
RA Skuce C.D., Smith M.L., Soderlund C., Steward C.A., Sultston J.E.,
RA Swann R.M., Sycamore N., Taylor R., Tee L., Thomas D.W., Thorpe A.,
RA Tracey A., Tromans A.C., Vaudin M., Wall M., Wallis J.M.,
RA Whitehead S.L., Whittaker P., Willey D.L., Williams L., Williams S.A.,
RA Wilming L., Wray P.W., Hubbard T., Durbin R.M., Bentley D.R., Beck S.,
RA Rogers J.;
RA "The DNA sequence and comparative analysis of human chromosome 20.";
RT Nature 414:865-871(2001).
RL -!- SUBCELLULAR LOCATION: Secreted (Potential).
CC -!- TISSUE SPECIFICITY: Expressed ubiquitously, the highest levels are
CC found in the epididymis followed by testis and trachea.
CC -!- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.
CC -!- SIMILARITY: Contains 3 WAP-type domains.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC
CC EMBL; AF492015; AAN70997.1; -.
DR EMBL; AF492016; AAN70998.1; -.
DR EMBL; AL031663; CAB37634.2; -.
DR EMBL; AL591715; CAB39449.1; -.
DR HSP; P31713; ISHP.
DR Genew; HGNC:16163; WFD8.
DR InterPro; IPR002223; Prot_Inh_Kunz-m.
DR InterPro; IPR008197; WAP.
DR Pfam; PF00014; Kunitz_BPTI; 1.
DR Pfam; PF00095; WAP; 3.
DR PRINTS; PR00003; 4DISULPHCORE.
DR PRINTS; PR00759; BASICTPASE.
DR ProDom; PD000222; Prot_Inh_Kunz-m; 1.
DR SMART; SM00131; KU; 1.
DR SMART; SM00217; WAP; 3.
DR PROSITE; PS00317; 4 DISULFIDE CORE; 3.
DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
DR PROSITE; PS0279; BPTI_KUNITZ_2; 1.
DR Repeat; Serine protease inhibitor; Signal.
KW SIGNAL
FT CHAIN 1 38 Potential.
FT DOMAIN 39 241 WAP four-disulfide core domain protein 8.
FT DOMAIN 47 90 WAP 1.
FT DOMAIN 95 145 BPTI/Kunitz inhibitor.
FT DOMAIN 150 193 WAP 2.
FT DOMAIN 197 239 WAP 3.
FT DISULFID 51 79 By similarity.
FT DISULFID 58 83 By similarity.
FT DISULFID 66 78 By similarity.
FT DISULFID 95 145 By similarity.
FT DISULFID 104 128 By similarity.
FT DISULFID 120 141 By similarity.
FT DISULFID 72 87 By similarity.
FT DISULFID 154 182 By similarity.
FT DISULFID 165 186 By similarity.
FT DISULFID 169 181 By similarity.
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FT DISULFID 175 190 By similarity.
FT DISULFID 201 229 By similarity.
FT DISULFID 208 232 By similarity.
FT DISULFID 216 228 By similarity.
FT DISULFID 222 236 By similarity.
SQ SEQUENCE 241 AA; 27797 MW; 2566B54AF4BDC57B CRC64;

Alignment Scores:
Pred. No.: 5,91e-12 Length: 241
Score: 205.00 Matches: 39
Percent Similarity: 50.00% Conservative: 13
Best Local Similarity: 37.50% Mismatches: 48
Query Match: 26.83% Indels: 4
DB: 1 Gaps: 1

US-10-807-204-11 (1-396) x WFD8_HUMAN (1-241)
QY 70 CACGCTGAAGCATCTTGGCAGCGGTGCCAAATCAAGTGAATGCGAGTGGAA 129
Db 46 HisLysProGlyLeu-----CysProLysGluArgLeuThrCysThrThrGlu 61
QY 130 GAAATAGACCACTGTACCAACCCAGAGATTGCCAGAAACATCAAGTGTTCGCCGCTTC 189
Db 62 LeuProAspSerCysAsnThrAspPheAspCysLysGluTyrGlnLysCysCysPhePhe 81
QY 190 AGCCCGTGGAAAGAAATGTTTAGACTTCAGAAAGGATATATGAGTATGCCACAGGAGCT 249
Db 82 AlaCysGlnLysLysCysMetAspProPheGlnGluProCysMetLeuProValArgHis 101
QY 250 GGCCTCCGCTGCTCCATACCACTGCTGGTGGTACATATAAAACAACTAAGTCTGCTCC 309
Db 102 GlyAsnCysAsnHisGluAlaGlnArgTrpHisPheAspPheLysAsnTyrArgCysThr 121
QY 310 GAATTCATCTATGCGGTGGCGAGGAGCAATACAACTCCAACTGAAGCTATCTGT 369
Db 122 ProPheLysTyrArgGlyCysGluGlyAsnAlaAsnAsnPhenLeuSerGluAspAlaCys 141
QY 370 CTGCTCACCTCG 381
Db 142 ArgThrAlaCys 145

RESULT 11
Q8IT91 PRELIMINARY; PRT; 759 AA.
AC Q8IT91;
DT 01-WAR-2003 (TrEMBLrel. 23, Created)
DT 01-WAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Kunitz-like protease inhibitor precursor.
OS Ancylostoma caninum (Dog hookworm).
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Strongylida;
OC Ancylostomatoidae; Ancylostomatidae; Ancylostomatinae; Ancylostoma.
OX NCBI_TaxID=29170;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Baltimore;
RX MEDLINE=22645137; PubMed=12760667;
RA Hawdon J.M., Datu B., Crowell M.;
RT Inhibitor from the hookworm Ancylostoma caninum.;
RL J. Parasitol. 89:402-407(2003).
CC -!- SIMILARITY: Contains 12 BPTI/Kunitz inhibitor domains.
DR EMBL; AF533590; AAN10061.1; -.
DR HSSP; P31713; 1SHP.
DR GO; GO:008233; F:peptidase activity; IEA.
DR GO; GO:0004867; F:serine-type endopeptidase inhibitor activity; IEA.
DR InterPro; IPR002223; Prot Inh Kunz-m.
DR Pfam; PF00014; Kunitz BPTI; 12.
DR PRINTS; PR00759; BASICTPASE.
DR SMART; SM00131; KU; 12.
DR PROSITE; PS00280; BPTI_KUNITZ_1; 10.
DR PROSITE; PS0279; BPTI_KUNITZ_2; 12.
DR Protease; Signal.
KW

FT SIGNAL 1 16 Potential.
SQ SEQUENCE 759 AA; 84886 MW; C431A3C3F418F40A CRC64;

Alignment Scores:
Pred. No.: 2,42e-10 Length: 759
Score: 189.50 Matches: 42
Percent Similarity: 40.71% Conservative: 15
Best Local Similarity: 30.00% Mismatches: 30
Query Match: 24.80% Indels: 53
DB: 2 Gaps: 4

US-10-807-204-11 (1-396) x Q8IT91 (1-759)
QY 127 GAAGAATAGACCACTGTACCAA-----CCAGAGATTGCCAGAA 168
Db 496 GluSerMetGluGluCysThrArgThrCysLysLysAlaValProGluProGluProGlu 515
QY 169 AACATGAAGTCTTGC---CCGTTCCAGCGTGA----- 198
Db 516 LysGluThrCysSerGlnProIleGluAlaGlyProCysLysAlaMetValArgArgPhe 535
QY 199 -----AAGAAATGTTTAGACTTC----- 216
Db 536 AlaTyrAspAsnAlaLysGluLysCysValGluPhePheTyrGlyGlyCysLysGlyAsn 555
QY 216 ----- 216
Db 556 LysAsnAsnPheGluThrMetGluAspCysThrPheThrCysGluGlnArgLeuAlaLys 575
QY 217 -----ACAAAGGATATATGCGATGTCACAGGAGGCTGGCCCTGCTGCGCTCC 267
Db 576 ProGluLeuGluLysAspValCysSerGlnProIleThrAlaGlyProCysArgAlaSer 595
QY 268 ATACCACACTGCTGTACATAATAAAACTAAGATCTGCTCCGAATTCATCTATGCGCGT 327
Db 596 IleProArgTyrGlyTyrAspSerLysLysArgLysCysValLysPheThrThrGlyGly 615
QY 328 TGCCAGGGGAACAATAACAACCTTCCAAACTGAAGCTATCTGCTGCTGCTGCTGCAAAAA 387
Db 616 CysLysGlyAsnGlyAsnArgPheProThrLysAsnGluCysGluLysThrCysLysArg 635

RESULT 12
IBP_CARCR STANDARD; PRT; 110 AA.
AC P00993;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Chelonianin (Basic protease inhibitor) (RTPI).
OS Carretta caretta (Loggerhead).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Testudines; Cryptodira; Chelonioidea; Chelonidae; Carretta.
OX NCBI_TaxID=8467;
RN [1]
RP SEQUENCE.
RC TISSUE=Egg white;
RA Kato I., Tomimaga N.;
RT "Trypsin-subtilisin inhibitor from red sea turtle eggwhite consists of
RT two tandem domains -- one Kunitz -- one of a new family.";
RL Fed. Proc. 38:832-832(1979).
CC -!- FUNCTION: The first domain inhibits trypsin; the second one
CC inhibits subtilisin.
CC -!- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.
CC -!- SIMILARITY: Contains 1 WAP-type domain.
CC -!- CAUTION: As the paper only indicates the species as "red sea
CC turtle", the species indicated here is therefore an inference.
DR PIR; A01224; TITROR.
DR HSSP; P00974; 1K09.
DR InterPro; IPR002223; Prot Inh Kunz-m.
DR InterPro; IPR008197; WAP.
DR Pfam; PF00014; Kunitz_BPTI; 1.
DR Pfam; PF00095; WAP; 1.
DR PRINTS; PR00003; 4DISULPHCORE.

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NCBI_TaxID=180454;
[1]
SEQUENCE FROM N.A.
STRAIN=PEST;
RA Anopheles Genome Sequencing Consortium;
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: Contains 9 BPTI/Kunitz inhibitor domains.
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; AAB01008987; EAA01339.1; -.
DR HSP; P10646; IIRH.
DR GO; GO:0004867; F:serine-type endopeptidase inhibitor activity; IEA.
DR InterPro; IPR010294; F:serine-type endopeptidase inhibitor activity.
DR InterPro; IPR006209; EGF like.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR010909; PLAC.
DR InterPro; IPR002223; Prot_Inh_Kunz-m.
DR InterPro; IPR000884; TSP1.
DR InterPro; IPR008197; WAP.
DR Pfam; PF05986; ADAM_spacer1; 1.
DR Pfam; PF00014; Kunitz_BPTI; 9.
DR Pfam; PF00090; TSP1; 7.
DR Pfam; PF00095; WAP; 1.
DR PRINTS; PR00003; 4DISULPHCORE.
DR PRINTS; PR00759; BASICTPASE.
DR ProDom; PD000222; Prot_Inh_Kunz-m; 9.
DR PROSITE; PS00317; 4 DISULFIDE CORE; 1.
DR PROSITE; PS00280; BPTI_KUNITZ_1; 8.
DR PROSITE; PS00279; BPTI_KUNITZ_2; 9.
DR PROSITE; PS00022; EGF_1; UNKNOWN_1.
DR PROSITE; PS00835; IG LIKE; 2.
DR PROSITE; PS00900; PLAC; 1.
DR PROSITE; PS00902; TSP1; 5.
FT NON_TER 1
SQ SEQUENCE 2419 AA; 260249 MW; 58078660983CR946 CRC64;

Alignment Scores:
Pred. No.: 1-52e-09 Length: 2419
Score: 182.00 Matches: 39
Percent Similarity: 44.35% Conservative: 12
Best Local Similarity: 33.91% Mismatches: 32
Query Match: 23.82% Indels: 32
DB: Gaps: 4

US-10-807-204-11 (1-396) x Q7PXZ1 (1-2419)
QY 136 GACAGTGTACCAACCCAGA----- 156
Db 1515 AspValCysHisLeuProLysIleSerGlyProCysThrGlyHisTrpAsnMetTrpTyr 1534
QY 157 ----GATTGCCCGAAGAACATGAAGTGTTCGCCGTCAGCCGCGGA----- 198
Db 1535 TyrAspAlaGluArgAsnMet---CysAlaGlnPheThrTyrGlyCysLeuGlyAsn 1553
QY 199 -----AAGAAATGT-----TTAGACTTCAGAAAG 222
Db 1554 AlaAsnArgPheGluSerGlnGluCysLysAlaLeuCysSerValAspSerLys 1573
QY 223 GATATATGCAGTATGCCACAGGAGGTGGCCCTGCTGCCTCCATACACACTGTGTG 282
Db 1574 ProProCysGluGlnProMetGluAlaGlyProCysAsnGlyThrPheGluArgTrpTyr 1593
QY 283 TACATAAAAAAATAAGATCTCTCGAATTCATCTATGCGGTGGCCAGGGACACAT 342
Db 1594 TyrAspLysGluThrAspAlaCysHisProPheThrPheGlyCysLysGlyAsnLys 1613
QY 343 AACAACTTCCAACTGAAGTATCTCTGTGTGGTCCACCTGCAGAAAAA 387
Db 1614 AsnAsnTyrProThrGluAlaSerCysGlyTyrHisCysAlaLys 1628

RESULT 15
Q9VAV4
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ID AC Q9VAV4 PRELIMINARY; PRT; 2772 AA.
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE CG33103-PB.
OS Name=fpn; ORFNames=CG33103;
GN Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OC NCBI_TaxID=7227;
RN [1]
SEQUENCE FROM N.A.
MEDLINE=20196006; PubMed=10731132; DOI=10.1126/science.287.5461.2185;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.H., Blazer E.G., Champ O., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Gabor G.B.,
RA Abril J.F., Agbayani A., An H.J., Andrews-Pfannkoch C., Baldwin D.,
RA Balow R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brotter P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferrier S., Fleischmann W.,
RA Fostler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.H., Ibegwam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai X.,
RA Lascko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Mirkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusakern D.R., Pacleb J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.Y., Waasman D.A., Weinstein G.M., Weissenbach J.,
RA Williams S.M., Woodgett, Worley K.C., Wu D., Yang S., Yao Q.A., Ye J.,
RA Yeh R.F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster.";
RL Science 287:2185-2195(2000).
RN [2]
SEQUENCE FROM N.A.
MEDLINE=22426065; PubMed=12537568;
RA Celniker S.E., Wheeler D.A., Krommiller B., Carlson J.W., Halpern A.,
RA Patel S., Adams M., Champagne M., Dugan S.P., Frise E., Hodgson A.,
RA George R.A., Hoskins R.A., Lavery T., Muzny D.M., Nelson C.R.,
RA Pacleb J.M., Park S., Pfeiffer B.D., Richards S., Sodergren E.J.,
RA Svirskas R., Tabor P.E., Wan K., Stapleton M., Sutton G.G., Venter C.,
RA Weinstein G., Scher S.E., Myers E.W., Gibbs R.A., Rubin G.M.;
RT "Finishing a whole-genome shotgun: Release 3 of the Drosophila
RT melanogaster euchromatic genome sequence.";
RL Genome Biol. 3:RESEARCH0079-RESEARCH0079(2002).
RN [3]
SEQUENCE FROM N.A.
MEDLINE=22426070; PubMed=12537573;
RA Kaminker J.S., Bergman C.M., Krommiller B., Carlson J., Svirskas R.,
RA Patel S., Frise E., Wheeler D.A., Lewis S.E., Rubin G.M.,
RA Ashburner M., Celniker S.E.;
RT "The transposable elements of the Drosophila melanogaster euchromatin:
RT a genomics perspective.";
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DR PROSITE, PS50092; TSP1; 5.
KW Matrix protein.
SQ SEQUENCE 2776 AA; 299741 MW; 92D38A17360D2D42 CRC64;
Alignment Scores:
Pred. No.: 1.95e-09 Length: 2776
Score: 181.00 Matches: 36
Percent Similarity: 42.98% Conservative: 13
Best Local Similarity: 31.58% Mismatches: 35
Query Match: 23.65% Indels: 30
DB: 2 Gaps: 3
US-10-807-204-11 (1-396) x Q869A0 (1-2776)
QY 136 GACCACTGTACCAACACCAGCA-----GATTGCCCCAGAAAACATGAAGTGTGCCCCG 186
Db 1788 AspArgCysAlaLeuProGlySerGlnThrGlyAspCysSerGluGlyLeuAlaLysTrpHis 1807
QY 187 TTCAGCCGTGGA---AAGAAATGTTTACACTTC----- 216
Db 1808 PheSerGluSerGluGlyArgCysValProPheTyrSerGlyCysGlyGlyAsnLys 1827
QY 217 -----AGAAAGCAT 225
Db 1828 AsnAsnPheProThrLeuGluSerCysGluAspHisCysProArgGlnValAlaLysAsp 1847
QY 226 ATATCCAGTATGCCAGAGGAGCGCCCTGCTCCATCCACACTGGTGGTAC 285
Db 1848 IleCysGluIleProAlaGluValGlyGluCysAlaAsnTyrValThrSerTrpTyr 1867
QY 286 AATAAAAACTAAGATCTCCGAATTCATCTATGCGGTGCGAGGGGAACATAAC 345
Db 1868 AspThrGlnAspGlnAlaCysArgGlnPheTyrTyrGlyGlyCysGlyGlyAsnGluAen 1887
QY 346 AACTTCCAACTGAAGCATCTCTGTCGTACCTGCAGAAAAA 387
Db 1888 ArgPheProThrGluGluSerCysAlaAlaArgCysAspArg 1901
RESULT 17
Q7KRX2 PRELIMINARY; PRT; 2894 AA.
AC Q7KRX2
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE CG33103-PA.
GN Name=Ppn; ORFNames=CG33103;
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20196006; PubMed=10731132; DOI=10.1126/science.287.5461.2185;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.H., Blazer R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Gabor G.L.,
RA Abril J.F., Agbayani A., An H.J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brotter P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferrier W.M., Glasser K.,
RA Foeller C., Gabrielian A.E., Garg N.S., Gelbart W.M., Harris M.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,

RA Hostin D., Houston K.A., Howland T.J., Wei M.H., Ibegwam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasok P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milhina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nuskern D.R., Pacleb J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri F., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirskaas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.Y., Wassarman D.A., Weisbrock G.M., Weissenbach J.,
RA Williams S.M., Woodage, Worley K.C., Wu D., Yang S., Yao Q.A., Ye J.,
RA Yeh R.P., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.,
RA "Finishing a whole-genome shotgun: Release 3 of the Drosophila
RT melanogaster euchromatic genome sequence."
RL Genome Biol. 3:RESEARCH0079-RESEARCH0079(2002).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=22426065; PubMed=12537568;
RA Celniker S.E., Wheeler D.A., Kronmiller B., Carlson J.W., Halpern A.,
RA Patel S., Adams M., Champe M., Dugan S.P., Frise E., Hodgeson A.,
RA George R.A., Hoskins R.A., Lavery T., Muzny D.M., Nelson C.R.,
RA Pacleb J.M., Park S., Pfeiffer B.D., Richards S., Sodergren E.J.,
RA Svirskaas R., Tabor P.E., Wan K., Stapleton M., Sutton G.G., Venter C.,
RA Weinstock G., Scherer S.E., Myers E.W., Gibbs R.A., Rubin G.M.,
RT "Finishing a whole-genome shotgun: Release 3 of the Drosophila
RT melanogaster euchromatic genome sequence."
RL Genome Biol. 3:RESEARCH0079-RESEARCH0079(2002).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=22426070; PubMed=12537573;
RA Kaminker J.S., Bergman C.M., Kronmiller B., Carlson J., Svirskaas R.,
RA Patel S., Frise E., Wheeler D.A., Lewis S.E., Rubin G.M.,
RA Ashburner M., Celniker S.E.,
RT "The transposable elements of the Drosophila melanogaster euchromatin:
RT a genomics perspective."
RL Genome Biol. 3:RESEARCH0084-RESEARCH0084(2002).
RN [4]
RP SEQUENCE FROM N.A.
RX MEDLINE=22426069; PubMed=12537572;
RA Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
RA Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochuk S.E.,
RA Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Berman B.P.,
RA Bettencourt B.R., Celniker S.E., de Grey A.D., Drysdale R.A.,
RA Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,
RA Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
RA Lewis S.E.,
RT "Annotation of the Drosophila melanogaster euchromatic genome: a
RT systematic review."
RL Genome Biol. 3:RESEARCH0083-RESEARCH0083(2002).
RN [5]
RP SEQUENCE FROM N.A.
RG FlyBase;
RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
RN [6]
RP SEQUENCE FROM N.A.
RG FlyBase;
RL Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Contains 12 BPTI/Kunitz inhibitor domains.
EMBL: AE003765; AAF56795.3; -
HSSP: PA0646; 1A2Z.
GO: GO:0004867; F:serine-type endopeptidase inhibitor activity; IEA.
InterPro: IPR010294; ADAM_spacer1.
InterPro: IPR006209; EGF_like.
InterPro: IPR003599; Ig_
InterPro: IPR007110; Ig-like.
InterPro: IPR003598; Ig_C2.
InterPro: IPR010909; PLAC.
InterPro: IPR002223; Prot_Inh_Kunz-m.

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DR InterPro; IPR000884; TSP1.
DR InterPro; IPR008197; WAP.
DR Pfam; PF05986; ADAM_spacer1.
DR Pfam; PF00047; Ig_2.
DR Pfam; PF00014; Kunitz_BPTI; 12.
DR Pfam; PF00090; TSP_1; 5.
DR Pfam; PF00095; WAP; 1.
DR PRINTS; PR00003; 4DISULPHCORE.
DR PRINTS; PR00759; BASICPTASE.
DR ProDom; PD000222; Prot_Inh_Kunz-m; 12.
DR SMART; SM00409; IG; 3.
DR SMART; SM00408; IGC2; 3.
DR SMART; SM00131; KU; 12.
DR SMART; SM00209; TSP1; 7.
DR SMART; SM00217; WAP; 1.
DR PROSITE; PS00317; 4_DISULFIDE_CORE; 1.
DR PROSITE; PS00280; BPTI_KUNITZ_1; 11.
DR PROSITE; PS02079; BPTI_KUNITZ_2; 12.
DR PROSITE; PS00022; EGF_1; UNKNOWN_1.
DR PROSITE; PS00835; IG LIKE; 3.
DR PROSITE; PS09000; PLAC; 1.
DR PROSITE; PS00092; TSP1; 5.
SQ SEQUENCE 2894 AA; 312663 MW; A1BFE1BAD9B214BC CRC64;

Alignment Scores:
Pred. No.: 1.95e-09 Length: 2894
Score: 181.00 Matches: 36
Percent Similarity: 42.98% Conservative: 13
Best Local Similarity: 31.58% Mismatches: 35
Query Match: 23.69% Indels: 30
DB: 2 Gaps: 3

US-10-807-204-11 (1-396) x Q7KRX2 (1-2894)
Qy 136 GACCAGTGTACCAACCCAGA-----GATTGCCAGAAAACATGAAGTGTGCCCG 186
Db 1788 AspArgCysAlaLeuProLysGlnThrGlyAspCysSerGluLysLeuAlaLysTrpHis 1807
Qy 187 TTCAGCCGTGGA---AAGAAATGTTAGACTTC----- 216
Db 1808 PheSerGluSerGluLysArgCysValProPheTyrTyrSerGlyGlyAsnLys 1827
Qy 217 -----AGAAAGGAT 225
Db 1828 AsnAsnPheProThrLeuGluSerCysGluAspHisCysProArgGlnValAlaLysAsp 1847
Qy 226 ATATGCAGTATGCCACAGAGGCTGGCCCTCGCTCCATACACACTGGTGTGAC 285
Db 1848 IleCysGluIleProAlaGluValGlyGluCysAlaAsnTyrValThrSerTyrTyr 1867
Qy 286 AATAAAAAAACTAAGATCTGCTCGAATTTCATCTATGCGGTTCGCGGGAACAATAAC 345
Db 1868 AspThrGlnAspGlnAlaCysArgGlnPheTyrTyrGlyGlyCysGlyGlyAsnGluAsn 1887
Qy 346 AACTTCCAACTGAAGCTATCTGTCTGCTACCTGCACAAAAA 387
Db 1888 ArgPheProThrGluGluSerCysLeuAlaArgCysAspArg 1901

RESULT 18
Q868Z9 ID Q868Z9 PRELIMINARY; PRT; 2898 AA.
AC Q868Z9;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Extracellular matrix protein papilin 3.
GN Name=Ppn;
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
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RP SEQUENCE FROM N.A.
RX MEDLINE=2252133; PubMed=12666201; DOI=10.1002/dvdy.10265;
RA Kramerova I.A., Kramerov A.A., Fessler J.H.;
RT "Alternative splicing of papilin and the diversity of Drosophila
RL extracellular matrix during embryonic morphogenesis.";
RL Dev. Dyn. 226:634-642(2003).
RN [2]

RP SEQUENCE FROM N.A.
RA Kramerova I., Fessler J.H.;
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: Contains 12 BPTI/Kunitz inhibitor domains.
DR EMBL; AF529180; ARO84908.1; -.
DR HSSP; P12111; 1KTH.
DR FlyBase; FBgn0003137; Ppn.
DR GO; GO:0005604; C:basement membrane; IDA.
DR InterPro; IPR010294; ADAM_spacer1.
DR InterPro; IPR006209; EGF_Like.
DR InterPro; IPR007110; Ig-Like.
DR InterPro; IPR003598; IG_C2.
DR InterPro; IPR010909; PLAC.
DR InterPro; IPR002223; Prot_Inh_Kunz-m.
DR InterPro; IPR000884; TSP1.
DR InterPro; IPR008197; WAP.
DR Pfam; PF05986; ADAM_spacer1; 1.
DR Pfam; PF00047; Ig; 2.
DR Pfam; PF00014; Kunitz_BPTI; 12.
DR Pfam; PF00090; TSP_1; 5.
DR Pfam; PF00095; WAP; 1.
DR PRINTS; PR00003; 4DISULPHCORE.
DR PRINTS; PR00759; BASICPTASE.
DR ProDom; PD000222; Prot_Inh_Kunz-m; 12.
DR SMART; SM00408; IGC2; 3.
DR SMART; SM00131; KU; 12.
DR SMART; SM00209; TSP1; 7.
DR SMART; SM00217; WAP; 1.
DR PROSITE; PS00317; 4_DISULFIDE_CORE; 1.
DR PROSITE; PS00280; BPTI_KUNITZ_1; 11.
DR PROSITE; PS02079; BPTI_KUNITZ_2; 12.
DR PROSITE; PS00022; EGF_1; UNKNOWN_1.
DR PROSITE; PS00835; IG LIKE; 3.
DR PROSITE; PS09000; PLAC; 1.
DR PROSITE; PS00092; TSP1; 5.
DR Matrix protein.
SQ SEQUENCE 2898 AA; 313250 MW; 2F992742F2D64A00 CRC64;

Alignment Scores:
Pred. No.: 1.95e-09 Length: 2898
Score: 181.00 Matches: 36
Percent Similarity: 42.98% Conservative: 13
Best Local Similarity: 31.58% Mismatches: 35
Query Match: 23.69% Indels: 30
DB: 2 Gaps: 3

US-10-807-204-11 (1-396) x Q868Z9 (1-2898)
Qy 136 GACCAGTGTACCAACCCAGA-----GATTGCCAGAAAACATGAAGTGTGCCCG 186
Db 1788 AspArgCysAlaLeuProLysGlnThrGlyAspCysSerGluLysLeuAlaLysTrpHis 1807
Qy 187 TTCAGCCGTGGA---AAGAAATGTTAGACTTC----- 216
Db 1808 PheSerGluSerGluLysArgCysValProPheTyrTyrSerGlyGlyAsnLys 1827
Qy 217 -----AGAAAGGAT 225
Db 1828 AsnAsnPheProThrLeuGluSerCysGluAspHisCysProArgGlnValAlaLysAsp 1847
Qy 226 ATATGCAGTATGCCACAGAGGCTGGCCCTCGCTCCATACACACTGGTGTGAC 285
Db 1848 IleCysGluIleProAlaGluValGlyGluCysAlaAsnTyrValThrSerTyrTyr 1867
Qy 286 AATAAAAAAACTAAGATCTGCTCGAATTTCATCTATGCGGTTCGCGGGAACAATAAC 345
Db 1868 AspThrGlnAspGlnAlaCysArgGlnPheTyrTyrGlyGlyCysGlyGlyAsnGluAsn 1887
Qy 346 AACTTCCAACTGAAGCTATCTGTCTGCTACCTGCACAAAAA 387
Db 1888 ArgPheProThrGluGluSerCysLeuAlaArgCysAspArg 1901
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Db 182 AenAenGlyGluCysSerProGlyGluileGlu-----ValArgProArgArgThrGln 199
QY 160 -----TGCCACAGAA-----AACATGAAGTGTTCGCCCGTTCAGCCGT 195
Db 200 ArgAlaValLeuProGluGluGluCysGlyMetGluAenSerProPheSerLys 219
QY 196 GGAAGAATAATTAGATTCTCAGAAAGATATATGCAAGATATGCAAGAGAGGCTGCCCC 255
Db 220 AenLys-----ValGluSerCysArgLeuAlaProAlaSerGlyPro 233
QY 256 TGCTGGCTCCATACACACTGGTGGTACATAAATAAATAAGATCTGCTCCGAATTC 315
Db 234 CysLeuGlyAenHisAenArgTyrPheTyrAenSerSerThrMetAlaCysGluThrPhe 253
QY 316 ATCTATGGCGGTTCGAGGGGAACATAAACAACATTCACAACTGAAAGTATCTGTCTGCTC 375
Db 254 GlnTyrGlyGlyCysLeuGlyAenAenAenAenPheHisSerGluLysGluCysLeuGln 273
QY 376 ACCTGCAAA 384
Db 274 ThrCysArg 276

RESULT 22
Q6DRJ1 PRELIMINARY; PRT; 515 AA.
AC Q6DRJ1;
DT 25-OCT-2004 (TReMBLrel. 28, Created)
DT 25-OCT-2004 (TReMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TReMBLrel. 28, Last annotation update)
DE Serine protease inhibitor HGFA1.
OS Brachydanio vario (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Osteichthyes; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RX PubMed=15256591; DOI=10.1073/pnas.0403929101;
RA Amsterdam A., Nissen R.M., Sun Z., Swindell E.C., Farrington S.,
RA Hopkins N.
RT "Identification of 315 genes essential for early zebrafish
development."
RL Proc. Natl. Acad. Sci. U.S.A. 101:12792-12797(2004).
CC -!- SIMILARITY: Contains 2 BPTI/Kunitz inhibitor domains.
DR EMBL; AY648768; AAT68086.1; -.
DR GO; GO:0008233; F:peptidase activity; IEA.
DR GO; GO:0004867; F:serine-type endopeptidase inhibitor activity; IEA.
DR InterPro; IPR002048; EF-hand.
DR InterPro; IPR002172; LDL receptor_A.
DR InterPro; IPR011106; MANSC_N.
DR InterPro; IPR00601; PKD.
DR InterPro; IPR002223; Prot_Inh_Kunz-m.
DR Pfam; PF00014; Kunitz_BPTI; 2.
DR Pfam; PF00057; Ldl_recept_a; 1.
DR Pfam; PF07502; MANSC; 1.
DR PRINTS; PR00759; BASICPTASE.
DR ProDom; PD000222; Prot_Inh_Kunz-m; 2.
DR SMART; SM00131; KU; 2.
DR SMART; SM00192; Ldla; 1.
DR SMART; SM00089; PKD; 1.
DR PROSITE; PS00280; BPTI_KUNITZ_1; 2.
DR PROSITE; PS0279; BPTI_KUNITZ_2; 2.
DR PROSITE; PS00018; EF_HAND; UNKNOWN_1.
DR PROSITE; PS01209; LDLRA_1; 1.
DR PROSITE; PS50088; LDLRA_2; 1.
DR PROSITE; PS50093; PKD; 1.
KW Protease.
SQ SEQUENCE 515 AA; 57579 MW; AF948A7B0EB46DB4 CRC64;

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Alignment Scores:
Pred. No.: 8.89e-09 Length: 515
Score: 174.00 Matches: 43
Percent Similarity: 38.51% Conservative: 19

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Best Local Similarity: 26.71% Mismatches: 57
Query Match: 22.77% Indels: 42
DB: 2 Gaps: 5

US-10-807-204-11 (1-396) x Q6DRJ1 (1-515)

QY 13 GGATCTTGCCAAATCCTGGTACCATTTCATCTTTGGGGACATCCAGAA----- 63
Db 271 GlyCysValProAenArgAenAenTyrLeuAlaLeuAenGluCysGlnSerAlaCysAen 290
QY 64 -----CCTGGGCACGCTGAAGGATCCTTGSC--- 90
Db 291 LysValSerValSerAenIleGlySerProProHisProSerGlyArgIleGlyPro 310
QY 91 -----AAGCCGTGTCCTCCAAAATCAAGTGAATGCGAAGTG 126
Db 311 IleAspAlaValGluGlnCysAspArgProCysSerProGluHisPheThrCysAsp--- 329
QY 127 GAAGAAATAGACCACTGTACCAACCCAGAGAT-----TGCCAGAAAAACATGAAGTG 180
Db 330 -----AenLysCysCysIleGlyLysAspLeuValCysAspLysGluLysGlnCys 346
QY 181 TGCCCGTTGACGCGTGGAAAGAAATGT----- 207
Db 347 SerAspGlySerAspGluLysGluCysAspLysTyrAspLysLeuLysLeuArg 366
QY 208 -----TTAGACTTCAGAAAGATATATGCACTATGCCACAGAGGCTGGCCCTGC 258
Db 367 GlyIleSerProAenValSerLysAlaArgCysValLysProProValThrGlyThrCys 386
QY 259 CTGGCTTCATACCACTGTGGTGTACATAAATAAATAAGATCTGCTCGAATTCATC 318
Db 387 ProGlySerGlnThrLysTyrTyrAsnProAenLysArgLeuCysTyrArgPheAen 406
QY 319 TATGCGGTGTCAGGGGAAACAATAACAATTCCTCAAGTATCTGCTGCTGCACC 378
Db 407 TyrGlyGlyCysGluGlyAsnGlnAsnArgPheGluThrGluAlaGlyCysMetThrPhe 426
QY 379 TGC 381
Db 427 Cys 427

RESULT 23
Q09983 PRELIMINARY; PRT; 1599 AA.
AC Q09983;
DT 01-NOV-1996 (TReMBLrel. 01, Created)
DT 01-NOV-1996 (TReMBLrel. 01, Last sequence update)
DT 01-MAR-2004 (TReMBLrel. 26, Last annotation update)
DE Hypothetical protein F30H5.3.
GN Name=F30H5.3; ORFNames=F30H5.3;
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=Bristol N2;
RX MEDLINE=99069613; PubMed=9851916;
RG WormBase Consortium;
RT "Genome sequence of the nematode C. elegans: a platform for
investigating biology. The C. elegans Sequencing Consortium."
RL Science 282:2012-2018(1998).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RA -Pauley A., Stellyes L.;
RT "The sequence of C. elegans cosmid F30H5."
RL Submitted (JUN-1995) to the EMBL/GenBank/DDAJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RA Waterston R.;

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RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RG WormBase Consortium;
RL Submitted (SEP-2004) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Contains 5 BPTI/Kunitz inhibitor domains.
DR EMBL; U29096; AAA68408.1; -.
DR PIR; T16210; T16210.
DR HSSP; P10646; IADZ.
DR IntAct; Q09983; -.
DR WormBase; WBGene0017937; F30H5.3.
DR WormPep; F30H5.3; CS01927.
DR CO; GO:0004867; F:serine-type endopeptidase inhibitor activity; IEA.
DR InterPro; IPR002198; ADH_short.
DR InterPro; IPR006149; EB_region.
DR InterPro; IPR006210; IEGF.
DR InterPro; IPR002223; Prot_Inh_Kunz-m.
DR InterPro; IPR006150; Worm_repeat_1.
DR Pfam; PF01683; EB; 3.
DR Pfam; PF00014; Kunitz_BPTI; 5.
DR PRINTS; PR00759; BASICPTASE.
DR SMART; SM00181; EGF; 1.
DR SMART; SM00131; KU; 5.
DR SMART; SM00289; WR1; 15.
DR PROSITE; PS00061; ADH_SHORT; UNKNOWN_1.
DR PROSITE; PS00280; BPTI_KUNITZ_1; 2.
DR PROSITE; PS02079; BPTI_KUNITZ_2; 5.
KW Hypothetical protein.
SQ SEQUENCE 1599 AA; 171658 MW; AB5B6A1D86E9880D CRC64;

Alignment Scores:
Pred. No.: 1.08e-08 Length: 1599
Score: 173.50 Matches: 35
Percent Similarity: 48.48% Conservatives: 13
Best Local Similarity: 35.35% Mismatches: 42
Query Match: 22.71% Indels: 9
DB: 2 Gaps: 2

US-10-807-204-11 (1-396) x Q09983 (1-1599)

Qy 109 AAGTGGAAATCGAAGTGTG-----GAAGAAATAGACAGTGATCC 147
Db |||:|||||:|||||:
518 LysLeuGlnCysLysTyGlyThrProLeuLysIleGlySerSerAsnGlnArgCysSer 537
Qy 148 AAACCCAGAGATGCCAGAAACATGAAGTGTGCGCGTTCAGCCGTGGAAAGAAATGT 207
Db |||:|||||:|||||:
538 AlaSerAlaAspCysProSerThrHisGluCys-----GlnSerAspHisAsnValCys 555
Qy 208 TTAGACTTCAGAAAGGATATATGAGTATGACAGAGGAGTGGCCCTGCTGGCTCC 267
Db |||:|||||:|||||:
556 CysProArgProGlnAlaIleCysSerGlnProLeuArgLeuGlyAspCysLysGlnSer 575
Qy 268 ATACACACTGGTGTGATACAAATAAAACTAAGATCTGCTCCGAATTCATCTATGGCGGT 327
Db |||:|||||:|||||:
576 ValargargTyTrpTyAsnAlaValThrArgAlaCysGluIlePheAspTyThrGly 595
Qy 328 TGCCAGGGAACAATAACAATTCGAACTGAAAGCTATCTCTGTGGTCACCTGCAAA 384
Db |||:|||||:|||||:
596 CysGlnGlyAsnAspAsnAsnPheGluThrLeuLeuGluCysGlnAsnThrCysGlu 614

RESULT 24
Q6AX20 ID Q6AX20 PRELIMINARY; PRT; 587 AA.
AC Q6AX20;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Aip2 A protein.
GN Name=aip2 A;
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;
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OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Kidney;
RX MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;
RA Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
RA Richardson P.,
RA "Genetic and genomic tools for Xenopus research: The NIH Xenopus
RA Dev. Dyn. 225:384-391(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Kidney;
RX PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Halle S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalek U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Kidney;
RA Klein S., Gerhard D.S.;
RL Submitted (AUG-2004) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.
DR EMBL; BC079801; AAH79801.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0005488; F:binding; IEA.
DR GO; GO:0004867; F:serine-type endopeptidase inhibitor activity; IEA.
DR InterPro; IPR008155; A4_APP.
DR InterPro; IPR008154; A4_extra.
DR InterPro; IPR02223; Prot_Inh_Kunz-m.
DR Pfam; PF02177; A4_EXTRA; 1.
DR Pfam; PF00014; Kunitz_BPTI; 1.
DR PRINTS; PR00203; AMYLOIDA4.
DR PRINTS; PR00759; BASICPTASE.
DR PRODOM; PD000222; Prot_Inh_Kunz-m; 1.
DR SMART; SM00006; A4_EXTRA; 1.
DR SMART; SM00131; KU; 1.
DR PROSITE; PS00320; A4_INTRA; 1.
DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
DR PROSITE; PS02079; BPTI_KUNITZ_2; 1.
SQ SEQUENCE 587 AA; 66870 MW; 7DF224C2138B94BF CRC64;

Alignment Scores:
Pred. No.: 1.13e-08 Length: 587
Score: 173.00 Matches: 29
Percent Similarity: 58.73% Conservatives: 8
Best Local Similarity: 46.03% Mismatches: 26
Query Match: 22.64% Indels: 0
DB: 2 Gaps: 0

US-10-807-204-11 (1-396) x Q6AX20 (1-587)

Qy 196 GGAAGAAATGTTTACAGTATGCAGAGGATATGCACAGGAGGTGGCCCC 255
Db |||:|||||:|||||:
273 GlyLysAspIleThrAspValLysSerValCysSerGlnGluAlaIleThrGlyPro 292
```



```
DR PROSITE; PS50279; BPTI_KUNITZ_2; 1.
SQ SEQUENCE 750 AA; 84927 MW; -4222350843147CAF CRC64;

Alignment Scores:
Pred. No.: 1.3e-08 Length: 750
Score: 172.50 Matches: 35
Percent Similarity: 45.71% Conservative: 13
Best Local Similarity: 33.33% Mismatches: 42
Query Match: 22.58% Indels: 15
DB: 2 Gaps: 1

US-10-807-204-11 (1-396) x Q6DJB6 (1-750)
QY 112 GTGAATCGAGTGGAGAAATAGACCACTGATACCAACCAGAGATTGCCAGAAAC 171
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
235 ValGluValGluGluGluGluGluGluGluGluGluGluGluGluGluGluGlu 254
QY 172 ATGAAGTGTGCCCGTTCAGCGCTGGA----- 198
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
255 GluProGluGluProTyTyGluGluAlaThrGluArgThrThrSerIleAlaThrThr 274
QY 199 -----AGAAATGTTAGACTTCAGAAAGGATATATGACGATGCCACAGAG 246
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
275 ThrThrThrThrGluSerValGluGluValValArgGluValCysSerGluGluAlaGlu 294
QY 247 GCTGCCCCCTGCTGCTCCATCCACACCTGGTGGTACATAAATAAATAAAGATCTGC 306
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
295 ThrGlyProCysArgAlaMetIleProArgTrpTyTyArgPvalThrGluArgLysCys 314
QY 307 TCCGAATTCATCTATGCGCGTTGCCAGGGGGAACATAACAATTCACAACTGAACTATC 366
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
315 AlaGlnPheIleTyGlyGlyCysGlyGlyAsnArgAsnAsnPheAspSerGluAspTyr 334
QY 367 TGCTGTGTCACCTGC 381
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
335 CysMetalValCys 339

RESULT 27
IBPC_BOVIN
ID IBPC_BOVIN STANDARD; PRT; 67 AA.
AC P00976;
DT 21-JUL-1986 (Rel. 01, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Colostrum trypsin inhibitor (Colostrum BPI).
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE.
RA Cechova D., Jonakova V., Sorm F.;
RT "Primary structure of trypsin inhibitor from cow colostrum (component B2).";
RL Collect. Czech. Chem. Commun. 36:3342-3357 (1971).
RN [2]
RP DISULFIDE BONDS.
RA Cechova D., Ber E.;
RT "Disulfide bonds of trypsin inhibitor from cow colostrum.";
RL Collect. Czech. Chem. Commun. 39:680-688 (1974).
RN [3]
RP CHARACTERIZATION.
RX PubMed=11947537;
RA Cechova D., Muszynska G.;
RT "Role of lysine 18 in active center of cow colostrum trypsin inhibitor.";
RL FEBS Lett. 8:84-86 (1970).
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.
DR PIR; A01207; TIBOC.
DR HSSP; P02760; 1BIK.
DR InterPro; IPR002223; Prot_Inh_Kunz-m.

Pfam; PF00014; Kunitz_BPTI; 1.
PRINTS; PR00759; BASICTPASE.
ProDom; PD000222; Prot_Inh_Kunz-m; 1.
SMART; SM00131; KU; 1.
DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
DR PROSITE; PS0279; BPTI_KUNITZ_2; 1.
KW Direct protein sequencing; Glycoprotein; Serine protease inhibitor.
FT SITE 18 19 Reactive bond for trypsin.
FT DISULFID 8 58
FT DISULFID 17 41
FT DISULFID 33 54
FT CARBOHYD 27 27 N-linked (GlcNAc...).
SQ SEQUENCE 67 AA; 7511 MW; E2B2093B7CD207CD CRC64;

Alignment Scores:
Pred. No.: 1.23e-08 Length: 67
Score: 172.00 Matches: 26
Percent Similarity: 68.52% Conservative: 11
Best Local Similarity: 48.15% Mismatches: 17
Query Match: 22.51% Indels: 0
DB: 1 Gaps: 0

US-10-807-204-11 (1-396) x IBPC_BOVIN (1-67)
QY 223 GATATATGTCAGTATGCCACAGAGGCTGCCCTGCTGCCTCCATACCACACTGGTGG 282
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
6 AspleucysGlnIueProGlnAlaArgGlyProCysLysAlaAlaLeuLeuArgTyrPhe 25
QY 283 TACAATAAAAACTAAGATCTGCTCGAATTCAATTCATCTATGCGGTTGCCAGGGAACAAT 342
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
26 TyrAsnSerThrSerAsnAlaCysGluProPheThrTyrGlyGlyCysGlnGlyAsnAsn 45
QY 343 AACAACTTCCAACTGAAGCTATCTGCTGTCACCTGCAAA 384
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
46 ***AsnPheGluThrThrGluMetCysLeuArgIleCysGlu 59

RESULT 28
Q8TEU8
ID Q8TEU8 PRELIMINARY; PRT; 576 AA.
AC Q8TEU8;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Multivalent protease inhibitor protein.
GN Name=WF1KXNP;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21173622; PubMed=11274388; DOI=10.1073/pnas.061028398;
RA Trexler M., Banyai L., Patthy L.;
RT "A human protein containing multiple types of protease-inhibitory modules.";
RL proc. Natl. Acad. Sci. U.S.A. 98:3705-3709 (2001).
RN [2]
RP SEQUENCE FROM N.A.
RA Trexler M., Banyai L., Patthy L.;
RT "Distinct expression pattern of two related human proteins containing multiple types of protease-inhibitory modules.";
RL Biol. Chem. 383:0-0 (2002).
CC -1- SIMILARITY: Contains 2 BPTI/Kunitz inhibitor domains.
DR EMBL; AF468657; AAL77058.1; -.
DR HSSP; P00974; 1K09.
DR GO; GO:0008233; F:peptidase activity; IEA.
DR GO; GO:0004867; F:serine-type endopeptidase inhibitor activity; IEA.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003598; Ig_c2.
DR InterPro; IPR001134; Netrin_C.
DR InterPro; IPR002350; Prot_inh_Kazal.
DR InterPro; IPR011497; Prot_inh_Kazal_2.
DR InterPro; IPR002223; Prot_inh_Kunz-m.
```

DR InterPro; IPR008993; TIMP_like.
DR InterPro; IPR008197; WAP.
DR Pfam; PF07648; Kazal_2; 1.
DR Pfam; PF00014; Kunitz_BPTI; 2.
DR Pfam; PF00095; WAP; 1.
DR PRINTS; PR00003; 4DISULPHCORE.
DR PRINTS; PR00759; BASICPTASE.
DR ProDom; PD000222; Prot_Inh_Kunz-m; 2.
DR SMART; SM00408; IGC2; 1.
DR SMART; SM00280; KAZAL; 1.
DR SMART; SM00131; KU; 2.
DR SMART; SM00217; WAP; 1.
DR PROSITE; PS00317; 4_DISULFIDE_CORE; 1.
DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
DR PROSITE; PS0279; BPTI_KUNITZ_2; 2.
DR PROSITE; PS00835; IG_LIKE; 1.
DR PROSITE; PS0189; NTR; 1.
KW Protease.
SQ SEQUENCE 576 AA; 63941 MW; 08B4F2EDBE121F81 CRC64;

Alignment Scores:
Pred. No.: 1,61e-08 Length: 576
Score: 171.50 Matches: 35
Percent Similarity: 40.91% Conservative: 10
Best Local Similarity: 31.82% Mismatches: 36
Query Match: 22.45% Indels: 29
DB: 3 Gaps: 3

US-10-807-204-11 (1-396) x Q8TEU8 (1-576)
QY 139 CAGTGTACCAACCC-----AGAGATTGCCAGAAACATG----- 174
Db 327 GluCysLeuLysProAspSerGluAspCysGlyGluGlnThrArgTrpHisPhe 346
QY 175 -----AAGTGTGCCCGTTCAGCCGTGGAAG----- 201
Db 347 AspAlaGlnAlaAsnAsnCysLeuThrPheThrPheGlyHisCysHisArgAsnLeuAsn 366
QY 202 -----AAATGTTTAGACTTCAGAAAGGATATATGC 231
Db 367 HisPheGluThrTyrrGluAlaCysMetLeuAlaCysMetSerGlyProLeuAlaAlaCys 386
QY 232 AGTATGCCACAGAGGCTGGCCCTCCATACACACACTGGTGGTACATAAA 291
Db 387 SerLeuProAlaLeuGlnGlyProCysAlaTyrrAlaProArgTrpAlaTyrrAsnSer 406
QY 292 AAAACTAAGATCTGCTCCGAATTCTATGCGCGTTCAGCGGGAACAATCAACTTC 351
Db 407 GlnThrGlyGlnCysGlnSerPheValTyrrGlyGlyCysGluGlyAsnGlyAsnAsnPhe 426
QY 352 CAAACTGAAGCTATCTGCTGTCACCTGC 381
Db 427 GluSerArgGluAlaCysGluGluSerCys 436

RESULT 29
Q6UXZ9
ID Q6UXZ9 PRELIMINARY; PRT; 576 AA.
AC Q6UXZ9;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Bikunin hlg.
GN ORFNames=UNQ9235;
OS Homo sapiens (human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22887296; PubMed=12975309; DOI=10.1101/gr.1293003;
RA Clark H.F., Gurney A.B., Abaya E., Baker K., Baldwin D., Brush J.,
RA Chen J., Chow B., Chui C., Crowley C., Currell B., Deuel B., Dowd P.,
RA Eaton D., Foster J., Grimaldi C., Gu Q., Hass P.E., Heldens S.,

RA Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J.,
RA Lewis L., Liao D., Mark M., Robble E., Sanchez C., Schoenfeld J.,
RA Seshagiri S., Simmons L., Singh J., Smith V., Stinson J., Vagts A.,
RA Wadlen R., Watanabe C., Wleand D., Woods K., Xie M.H., Yansura D.,
RA Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A., Wood W.I.,
RA Godowski P.;
RT "The secreted protein discovery initiative (SPDI), a large-scale
RT effort to identify novel human secreted and transmembrane proteins: a
RT bioinformatics assessment.";
RL Genome Res. 13:2265-2270(2003).
CC -1- SIMILARITY: Contains 2 BPTI/Kunitz inhibitor domains.
DR EMBL; AY358142; AAQ88509.1; -.
DR HSPF; P00974; IK09.
DR GO; GO:0004867; F:serine-type endopeptidase inhibitor activity; IEA.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG_LIKE.
DR InterPro; IPR003598; IG_c2.
DR InterPro; IPR001134; Netrin C.
DR InterPro; IPR002223; Prot_Inh_Kunz-m.
DR InterPro; IPR008993; TIMP_like.
DR InterPro; IPR008197; WAP.
DR Pfam; PF00014; Kunitz_BPTI; 2.
DR Pfam; PF00095; WAP; 1.
DR PRINTS; PR00003; 4DISULPHCORE.
DR PRINTS; PR00759; BASICPTASE.
DR ProDom; PD000222; Prot_Inh_Kunz-m; 2.
DR SMART; SM00408; IGC2; 1.
DR SMART; SM00131; KU; 2.
DR SMART; SM00217; WAP; 1.
DR PROSITE; PS00317; 4_DISULFIDE_CORE; 1.
DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
DR PROSITE; PS0279; BPTI_KUNITZ_2; 2.
DR PROSITE; PS00835; IG_LIKE; 1.
DR PROSITE; PS0189; NTR; 1.
SQ SEQUENCE 576 AA; 63912 MW; 08B42DD50C3CF81 CRC64;

Alignment Scores:
Pred. No.: 1,61e-08 Length: 576
Score: 171.50 Matches: 35
Percent Similarity: 40.91% Conservative: 10
Best Local Similarity: 31.82% Mismatches: 36
Query Match: 22.45% Indels: 29
DB: 3 Gaps: 3

US-10-807-204-11 (1-396) x Q6UXZ9 (1-576)
QY 139 CAGTGTACCAACCC-----AGAGATTGCCAGAAACATG----- 174
Db 327 GluCysLeuLysProAspSerGluAspCysGlyGluGlnThrArgTrpHisPhe 346
QY 175 -----AAGTGTGCCCGTTCAGCCGTGGAAG----- 201
Db 347 AspAlaGlnAlaAsnAsnCysLeuThrPheThrPheGlyHisCysHisArgAsnLeuAsn 366
QY 202 -----AAATGTTTAGACTTCAGAAAGGATATATGC 231
Db 367 HisPheGluThrTyrrGluAlaCysMetLeuAlaCysMetSerGlyProLeuAlaAlaCys 386
QY 232 AGTATGCCACAGAGGCTGGCCCTCCATACACACACTGGTGGTACATAAA 291
Db 387 SerLeuProAlaLeuGlnGlyProCysAlaTyrrAlaProArgTrpAlaTyrrAsnSer 406
QY 292 AAAACTAAGATCTGCTCCGAATTCTATGCGCGTTCAGCGGGAACAATCAACTTC 351
Db 407 GlnThrGlyGlnCysGlnSerPheValTyrrGlyGlyCysGluGlyAsnGlyAsnAsnPhe 426
QY 352 CAAACTGAAGCTATCTGCTGTCACCTGC 381
Db 427 GluSerArgGluAlaCysGluGluSerCys 436

RESULT 30
YN81_CABEL

ID AC Q03610; YN81_CAEEL STANDARD; PRT; 1416 AA.
DT 01-FEB-1994 (Rel. 28, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Hypothetical protein ZC84.1 in chromosome III.
GN ORFNames=ZC84.1;
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OK NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RX MEDLINE=94150718; PubMed=7906398; DOI=10.1038/368032a0;
RA Wilson R., Ainscough R., Anderson K., Baynes C., Berks M., Boulton A.,
RA Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson A.,
RA Craxton M., Dear S., Du Z., Durbin R., Favell A., Fraser A.,
RA Fulton L., Gardner A., Green P., Hawkins T., Hillier L., Jier M.,
RA Johnston L., Jones M., Kerhaw J., Kirsten J., Laisler N.,
RA Latreille P., Lightning J., Lloyd C., Mortimore B., O'Callaghan M.,
RA Parsons J., Percy C., Rifkin L., Roopra A., Saunders D., Shownkeen R.,
RA Sims M., Smaldon N., Smith A., Smith M., Sonnhammer E., Staden K.,
RA Sulston J., Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K.,
RA Waterston R., Watson A., Weinstock L., Wilkinson-Sproat J.,
RA Wohldman P.;
RT "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
RT elegans.";
RL Nature 368:32-38 (1994).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RX MEDLINE=93069613; PubMed=9851916;
RG The C. elegans sequencing consortium;
RT "Genome sequence of the nematode C. elegans: a platform for
RT investigating biology.";
RL Science 282:2012-2018 (1998).
RN [3]
RP REVISIONS
RA Jones S.J.M.;
RL Submitted (NOV-1997) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Contains 5 BPTI/Kunitz inhibitor domains.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; Z19157; CAA79569.1; -.
DR PIR; E88550; E88550.
DR PIR; S28291; S28291.
DR HSSP; P00981; 1DTK.
DR WormBase; WBGene00013846; ZC84.1.
DR WormPep; ZC84.1; CE15020.
DR InterPro; IPR006149; EB_region.
DR InterPro; IPR002223; Prot_inh_Kunz-m.
DR InterPro; IPR006150; Worm_repeat_1.
DR Pfam; PF01683; EB; 3.
DR Pfam; PF00014; Kunitz BPTI; 5.
DR PRINTS; PR00759; BASICTPTASE.
DR ProDom; PD000222; Prot_inh_Kunz-m; 5.
DR SMART; SM00131; KU; 5.
DR SMART; SM00289; WRI; 13.
DR PROSITE; PS00280; BPTI_KUNITZ_1; 3.
DR PROSITE; PS02079; BPTI_KUNITZ_2; 5.
KW Hypothetical protein; Repeat; Serine protease inhibitor.
FT DOMAIN 212 266 BPTI/Kunitz inhibitor 1.
FT DOMAIN 337 387 BPTI/Kunitz inhibitor 2.
FT DOMAIN 434 484 BPTI/Kunitz inhibitor 3.
FT DOMAIN 538 590 BPTI/Kunitz inhibitor 4.

FT DOMAIN 646 698 BPTI/Kunitz inhibitor 5.
SQ SEQUENCE 1416 AA; 152986 MW; 531CACE1CB22F70D CRC64;

Alignment Scores:
Pred. No.: 1.99e-08 Length: 1416
Score: 171.00 Matches: 35
Percent Similarity: 46.30% Conservative: 15
Best Local Similarity: 32.41% Mismatches: 40
Query Match: 22.38% Indels: 18
DB: 1 Gaps: 3

US-10-807-204-11 (1-396) x YN81_CAEEL (1-1416)

QY 109 AAGTGAATGCGAAGTG----- 126
DB 380 LyHisGluCysGluMetTyrCysAlaArgLeuGlnCysGluArgGlySerProLeuArg 399
QY 127 -----GAAGAAATAGACCACTGTACAAACCAGAGATGCCCAGAAAAACATGAAGTGT 180
DB 400 IleGlyGluGluAlaGlnArgCysGlnAsnAlaGlnCysProSerSerHisGlu--- 418
QY 181 TGCCCGTTCAGCCGTGGAAAGAATGTTTACACTTCAGAAAGGATATATCAGTATGCCA 240
DB 419 CysLysAlaAspGlnGly---ValCysCysProArgLysGlnThrIleCysAlaGlnPro 437
QY 241 CAGGAGGCTGCGCCCTGCCTGCCTCCATACACACTGGTGGTACATAAATAAAACCTAAG 300
DB 438 LeuArgIleGlyAspCysThrGluAsnValLysArgTyrTrpTyrAsnAlaArgThrArg 457
QY 301 ATCTGCTCGAATTCATCTATGCGGTTGCGAGGGGAACAATAACAACATTCCTCAAACTGAA 360
DB 458 GlnCysGlnMetPheGluTyrThrGlyCysGlnGlyAsnAspAsnAenPheAspSerIle 477
QY 361 GCTATCTGCTGTCACCTGCAAA 384
DB 478 MetAspCysGlnAsnPheCysLys 485

RESULT 31
Q6ITB9 PRELIMINARY; PRT; 83 AA.
AC Q6ITB9
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Mulgin-3.
OS Pseudechis australis (Mulga snake) (King brown snake).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC Elapidae; Acanthophiinae; Pseudechis.
OX NCBI_TaxID=8670;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Venom Gland;
RA Filippovich I.V., Sorokina N.I.;
RL Submitted (MAY-2004) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.
DR EMBL; AY626926; AAT45402.1; -.
DR HSSP; Q16019; IAAp.
DR GO; GO:0004867; F:serine-type endopeptidase inhibitor activity; IEA.
DR InterPro; IPR002223; Prot_inh_Kunz-m.
DR Pfam; PF00014; Kunitz BPTI; 1.
DR PRINTS; PR00759; BASICTPTASE.
DR ProDom; PD000222; Prot_inh_Kunz-m; 1.
DR SMART; SM00131; KU; 1.
DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
DR PROSITE; PS02079; BPTI_KUNITZ_2; 1.
SQ SEQUENCE 83 AA; 9103 MW; 315C361D8EC89221 CRC64;

Alignment Scores:
Pred. No.: 1.99e-08 Length: 83
Score: 170.00 Matches: 29
Percent Similarity: 61.82% Conservative: 5
Best Local Similarity: 52.73% Mismatches: 21


```
Query Match: 22.25% Indels: 0
DB: 2 Gaps: 0
US-10-807-204-11 (1-396) x Q6ITB9 (1-83)
QY 217 AGAAGGATATATGACAGTATGCCACAGAGGAGGCTGCCCTGCTGCCCTCCATACCACAC 276
Db 27 ArgProAspPheCysGluLeuProAlaAspThrGlyProCysArgValGlyPheProSer 46
QY 277 TGGTGTACAAATAAAAACTAAGATCTGCTCCGAATTCATCTATGGCGGTGGCCAGGGG 336
Db 47 PheTyrTyrAsnProAspGluLysCysLeuGluPheLeuTyrGlyGlyCysGlyGly 66
QY 337 AACAAATCAACTTCCAACTGAAGCTATCTCTGCTGTCACCTGC 381
Db 67 AsnAlaAsnAsnPheIleThrLysGluGluCysGluSerThrCys 81
Zgc:64075.
ORFNames=zgc:64075;
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Kidney.
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Donald M.F., Casavant T.L., Schetz T.E.,
RA Brownstein M.J., Udell T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Green E.D., Dickson M.C.,
RA Blakesley R.W., Touchman J.W., Shevchenko Y., Bouffard G.G.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalek U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RA "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Kidney.
RA Strausberg R.;
RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Contains 2 BPTI/Kunitz inhibitor domains.
DR EMBL; BC053239; AAH53239.1; -.
DR HSSP; P10646; 1ADZ.
DR ZFIN; ZDB-GENE-040426-2169; zgc:64075.
DR GO; GO:0004867; F:serine-type endopeptidase inhibitor activity; IEA.
DR InterPro; IPR002048; EF-hand.
DR InterPro; IPR002172; LDL receptor_A.
DR InterPro; IPR011106; MANSC_N.
DR InterPro; IPR000601; PKD.
DR InterPro; IPR002223; Prot_Inh_Kunz-m.
DR Pfam; PF00014; Kunitz_BPTI; 2.
DR Pfam; PF00057; Ldl_recept_a; 1.
DR Pfam; PF07502; MANSC; 1.

DR ProDom; PD000222; Prot_Inh_Kunz-m; 2.
DR SMART; SMO0131; KU; 2.
DR SMART; SMO0192; LDLa; 1.
DR SMART; SMO0089; PKD; 1.
DR PROSITE; PS00280; BPTI_KUNITZ_1; 2.
DR PROSITE; PS0279; BPTI_KUNITZ_2; 2.
DR PROSITE; PS00018; EF_HAND; UNKNOWN_1.
DR PROSITE; PS01209; LDLRA_1; 1.
DR PROSITE; PS00068; LDLRA_2; 1.
SQ SEQUENCE 516 AA; 57695 MW; 2080A4C5B270DE16 CRC64;

Alignment Scores:
Pred. No.: 2,27e-08 Length: 516
Score: 170.00 Matches: 40
Percent Similarity: 41.43% Conservative: 18
Best Local Similarity: 28.57% Mismatches: 52
Query Match: 22.25% Indels: 30
DB: 2 Gaps: 5

US-10-807-204-11 (1-396) x Q7T363 (1-516)
QY 40 ATCTTTTGGGGGACATCCAGAACCTGGG---CACGCTGAAGGCATCTTGGC----- 90
Db 292 ValSerValSerAsnIleGlySerProAlaProHisProSerGlyArgIleGlyProIle 311
QY 91 -----AAGCGTGTCCCAAAATCAAAGTGGGAATCGAAGTGGAA 129
Db 312 AspAlaValGluGlnCysAspArgProCysSerProGluHisPheThrCysAsp----- 329
QY 130 GAATAGACCACTGTACCAACCCAGACAT-----TGCCAGAAACATGAAGTGTTC 183
Db 330 -----AsnLysCysCysIleGlyLysAspLeuValCysAspLysGlnCysSer 347
QY 184 CGTTCAGCGCTGGAAAGAAATGT----- 207
Db 348 AspGlySerAspGluLysGluCysAspLysTyrPheTyrAspLeuValLysLeuArgGly 367
QY 208 -----TTAGACTTCAGAAAGATATATGCAGTATGCCACAGGAGGCTGGCCCTGCCTG 261
Db 368 IleSerProAspValSerLysAlaArgCysValLysProProValThrGlyThrCysPro 387
QY 262 GCCTCCATACCACTGCTGGTGTACATAAAAACTAAGATCTGCTCCGAATTCATCTAT 321
Db 388 GlySerGlnThrLysIleTyrTyrAsnProAsnLysArgLysCysTyrArgPheAsnTyr 407
QY 322 GCGGTTGCCAGGGGAACAATAACAACTTCCAAACTGAAGCTATCTGTCTGCTCACTGC 381
Db 408 GlyGlyCysGluGlyAsnGlnAsnArgPheGluThrGluAlaGlyCysMetThrPheCys 427

RESULT 33
Q6ITB5 PRELIMINARY; PRT; 83 AA.
AC Q6ITB5;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Microlepidin-1.
OS Oxyuramus microlepidotus (Inland taipan).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidodonta; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC Elapidae; Acanthophiinae; Oxyuramus.
NCBI_TaxID=111177;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Venom gland;
RA Filippovich I.V., Sorokina N.I.;
RL Submitted (MAY-2004) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.
DR EMBL; AY626930; AAT45406.1; -.
DR HSSP; P10646; 1ADZ.
DR GO; GO:0004867; F:serine-type endopeptidase inhibitor activity; IEA.
DR InterPro; IPR002223; Prot_Inh_Kunz-m.
DR Pfam; PF00014; Kunitz_BPTI; 1.
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QY 163 -----CCAGAAACATGAAGTGTGCGCTCAGCCGT-----GGAAAG 201
Db 262 GluAspTyrAsnAspGluAsnProThrGluProProAsnGluArgGlnLeuSerGlyLys 281
QY 202 AAATGTTTACAGCTTCAGAAAGGATATATGACAGTATGCCACAGGAGGCTGGCCCTCGCTG 261
Db 282 AspilelleThrAspValLysSerValCysSerGlnGluAlaValThrGlyProCysArg 301
QY 262 GCCTCCATACACACTGTGTGTGTACAAATAAATAAAGTGTGTCCGAATTCATCAT 321
Db 302 AlaMetMetProArgTyrPheAspLeuGlyGlnLysCysValArgPheIleTyr 321
QY 322 GCGGTTCAGGAGGGAACAATAACAACTCCAACTGAAGTATCTGTCTGTGTCACCTGC 381
Db 322 GlyGlyCysGlyGlyAsnArgAsnPheGluSerAlaAspTyrCysMetAlaValCys 341
QY 382 AAA 384
Db 342 Lys 342

RESULT 37
Q9GP15 PRELIMINARY; PRT; 86 AA.
AC Q9GP15;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein.
OS Ixodes ricinus (Sheep tick).
OC Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Acari;
OC Parasitiformes; Ixodida; Ixodidae; Ixodes.
OX NCBI_TaxID=34613;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Salivary glands;
RX MEDLINE=22134277; PubMed=12139212;
RA Lebouille G., Rochez C., Louahed J., Rutti B., Brossard M., Bollen A.,
RA Godfroid E.;
RT "Isolation of Ixodes ricinus salivary gland mRNA encoding factors
RT induced during the blood feeding process.";
RL Am. J. Trop. Med. Hyg. 66:225-233(2002).
CC -1- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.
DR EMBL; AJ269641; CAB55816.1; -.
DR HSSP; P12111; 1KNT.
DR GO; GO:0004867; F:serine-type endopeptidase inhibitor activity; IEA.
DR InterPro; IPR002223; Prot_inh_Kunz-m.
DR Pfam; PF00014; Kunitz_BPTI; 1.
DR PRINTS; PR00759; BASICTPASE.
DR ProDom; PD000222; Prot_inh_Kunz-m; 1.
DR SMART; SM00131; KU; 1.
DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
DR PROSITE; PS50279; BPTI_KUNITZ_2; 1.
KW Hypothetical protein.
SQ SEQUENCE 86 AA; 9727 MW; 9473B17974A055F0 CRC64;

Alignment Scores:
Pred. No.: 3.19e-08 Length: 86
Score: 168.00 Matches: 25
Percent Similarity: 69.23% Conservative: 11
Best Local Similarity: 48.08% Mismatches: 16
Query Match: 21.99% Indels: 0
DB: 2 Gaps: 0

US-10-807-204-11 (1-396) x Q9GP15 (1-86)
QY 229 TGCAGTAGCCACAGGAGCTGGCCCTGCTGCCTCCATACACACTGGTGTGTAACAT 288
Db 31 CysLysLeuProProAspAspGlyProCysArgAlaArgIleProSerTyrTyrPheAsn 50
QY 289 AAAAAAATAAGATCTGCTCCGAATTCATCTATGCGGTTCGCCAGGGGAAACAATAACAC 348
Db 51 ArgLysThrLysThrCysLysGluPheMetTyrGlyGlyCysGluGlyAsnGluAsn 70

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QY 349 TTCCAAACTGAGCTATCTGTCTGGTCACTCCTGCAGAA 384
Db 71 PheGluAsnIleThrThrCysGlnGluGluCysArg 82

RESULT 38
Q9XWX5 PRELIMINARY; PRT; 1743 AA.
AC Q9XWX5;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Hypothetical protein Y43P8B.3.
GN ORENAMES=Y43P8B.3;
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidae;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RX MEDLINE=99069613; PubMed=9851916;
RA none;
RT "Genome sequence of the nematode C.elegans: A platform for
RT investigating biology.";
RL Science 282:2012-2018(1998).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RX Ainscough R.;
RL Submitted (OCT-1998) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Contains 15 BPTI/Kunitz inhibitor domains.
DR EMBL; AL032623; CAA21511.1; -.
DR PIR; T26859; T26859.
DR HSSP; Q16019; 1AAP.
DR WormBase; WBGene00012814; Y43P8B.3.
DR WormPep; Y43P8B.3; CE21888.
DR GO; GO:0004867; F:serine-type endopeptidase inhibitor activity; IEA.
DR InterPro; IPR002223; Prot_inh_Kunz-m.
DR Pfam; PF00014; Kunitz_BPTI; 15.
DR PRINTS; PR00759; BASICTPASE.
DR SMART; SM00131; KU; 15.
DR SMART; SM00289; WR1; 10.
DR PROSITE; PS00280; BPTI_KUNITZ_1; 2.
DR PROSITE; PS50279; BPTI_KUNITZ_2; 15.
KW Hypothetical protein.
SQ SEQUENCE 1743 AA; 191111 MW; B93C163556433C2A CRC64;

Alignment Scores:
Pred. No.: 3.96e-08 Length: 1743
Score: 168.00 Matches: 37
Percent Similarity: 39.32% Conservative: 9
Best Local Similarity: 31.62% Mismatches: 49
Query Match: 21.99% Indels: 22
DB: 2 Gaps: 2

US-10-807-204-11 (1-396) x Q9XWX5 (1-1743)
QY 97 TGTCCCAAAATCAAAGTGGAAATGCGAAGTGGAAAGAAATAGACCAGTGTACCAACCAGCA 156
Db 1621 CysProHisGlyLysProAspValThrAspHisSerLeuThrThrCysGlyIleAspThr 1640
QY 157 GATTGCCCAAAAACATGAAGTGTTCGCCCTTCAGCGTGGGAAGAAA-----TGTTTA 210
Db 1641 GlyCysProArgAspHisValCysHisValSerLysArgGlySerLysThrValCysCys 1660
QY 211 GACTTCAGAAAGGATATATGACAGTATGCCACAGAGGCTGCCCTCGCTGGCTCCATA 270
Db 1661 ProAspProAlaSerPheCysLeuValArgAlaAspProGlyProCysAsnArgGluIle 1680
QY 271 CCACACTGGTGTACATAAAAAAATAAGATCTGCTCCGAATTCATCTATGCGGTTC 330
Db 271 CCACACTGGTGTACATAAAAAAATAAGATCTGCTCCGAATTCATCTATGCGGTTC 330

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Db 1681 ProArgTrrpAlaTyAspLysAlaSerGlySerCysLysLysPheIlePheGlyCys 1700
QY 331 CAGGGGAACAATAACAACCTTCCAAACTGAA----- 360
Db 1701 GlnGlyAsnLeuAsnAsnAsnPheAspThrAsnGlnCysValAlaPheGluTyThrGlyCys 1720
QY 361 -----GCTATCTGTCGTGGTCACTGC 381
Db 1721 GlyGlyAsnLeuAsnAsnPheValSerIleAlaAspCysGlnAlaThrCys 1737

RESULT 39
Q9UG8 PRELIMINARY; PRT; 3198 AA.
AC Q9UG8;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAY-2000 (TrEMBLrel. 26, Last annotation update)
DE Lacunin precursor.
OS Manduca sexta (Tobacco hawkmoth) (Tobacco hornworm).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia; Sphingioidea;
OC Sphingidae; Sphinginae; Manduca.
OX NCBI_TaxID=7130;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99457716; PubMed=10528409; DOI=10.1016/S0965-1748(99)00064-8;
RA Nardi J.B., Martos R., Walden K.K., Lampe D.J., Robertson H.M.;
RT "Expression of lacunin, a large multidomain extracellular matrix
RT protein, accompanies morphogenesis of epithelial monolayers in Manduca
RT sexta.";
RL Insect Biochem. Mol. Biol. 29:883-897(1999).
RN [2]

SEQUENCE FROM N.A.
RA Nardi J., Martos R., Walden K., Lampe D., Robertson H.;
RL Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: Contains 10 BPTI/Kunitz inhibitor domains.
DR EMBL; AF078161; AAF04457.1; -.
DR HSP; P12111; 1KTH.
DR GO; GO:0004867; F:serine-type endopeptidase inhibitor activity; IEA.
DR InterPro; IPR010294; ADAM spacer1.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003598; Ig_c2.
DR InterPro; IPR010909; PLAC.
DR InterPro; IPR004094; Prot inh antiatn.
DR InterPro; IPR002223; Prot Inh_Kunz-m.
DR InterPro; IPR000884; TSP1.
DR InterPro; IPR008197; WAP.
DR Pfam; PF05986; ADAM spacer1; 1.
DR Pfam; PF02822; Antistatin; 4.
DR Pfam; PF00014; Kunitz BPTI; 10.
DR Pfam; PF00090; TSP_1-5.
DR Pfam; PF00095; WAP; 1.
DR PRINTS; PR00003; 4DISULPHCORE.
DR PRINTS; PR00759; BASICPTASE.
DR SMART; SM00408; IGC2; 2.
DR SMART; SM00131; KU; 10.
DR SMART; SM00209; TSP1; 7.
DR SMART; SM00217; WAP; 1.
DR PROSITE; PS00317; 4 DISULFIDE CORE; 1.
DR PROSITE; PS00280; BPTI_KUNITZ_1; 8.
DR PROSITE; PS0279; BPTI_KUNITZ_2; 10.
DR PROSITE; PS0835; IG LIKE; 2.
DR PROSITE; PS0900; PLAC; 1.
DR PROSITE; PS00092; TSP1; 5.
KW Signal.
FT SIGNAL
SQ SEQUENCE 3198 AA; 349366 MW; AB4ACD459CD9134 CRC64;

Alignment Scores:
Pred. No.: 4.13e-08 Length: 3198
Score: 168.00 Matches: 39
Percent Similarity: 43.88% Conservative: 22
Best Local Similarity: 28.06% Mismatches: 51

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Query Match: 21.99% Indels: 27
DB: Gaps: 4
US-10-807-204-11 (1-396) x Q9UG8 (1-3198)
QY 9 CTCAGGACTCTGCGCAATCTCTGGTACCATTCATCTTTTGGGGACATC----- 57
Db 2190 ILeThrThrValArgProThrGluAlaHisPro-LeuThrGluMetCysPheMetG1 2209
QY 58 -CAGGAACCTGGGACGCTGAAGGCATCTTTGGCAAGCGGTGCCAAATCAAGTG-- 114
Db 2209 uLysAspProGly-----ProCysThrAspThrGluThrAr 2221
QY 115 -----GAATGGAAGTGGAGAAATAGACACAGTGTACCAA 149
Db 2221 gTrrpValTyAspTyLysLeuGlyLysCysValThrPheGluTyGlyGlyG1 2241
QY 150 ACCCAGAGATTGCCCAGAAACATGAAGTGTGGCCGTTCAGCCGTGAAGAAATGTTT 209
Db 2241 yAsnArgAsnAsnPheProThrGluGluTyCysGlnTyTyTyCysGlyThr----- 2258
QY 210 AGACTTCAGAAAGATATATGCAGTATGCCACAGAGAGCTGGCCCTCCCTGGCCTCCAT 269
Db 2259 -----AlaGlnAspIleCysGlnLeuProMetArgSerGlyProCysThrGluSerLe 2276
QY 270 ACCACACTGGTGTACAAATAAATAAATAAGATCTGTCGAATTCATCTATGGCGGTG 329
Db 2276 uMetArgTrpPheTyAspProSerSerAspSerCysSerGlnPheThrTyTyGlyGlyCy 2296
QY 330 CCAGGGGAACATACACACTTCCAACTGAGAGTATCTGTCTGGTGCACCTGCAAA 384
Db 2296 sAspGlyAsnAspAsnArgPheGluThrArgAspAspCysGluSerArgCysArg 2314

RESULT 40
P70004 PRELIMINARY; PRT; 342 AA.
AC P70004;
DT 01-FEB-1997 (TrEMBLrel. 02, Created)
DT 01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Alaphal-microglobulin/bikunin precursor (AMBP).
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Piploidea; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RA Kawahara A., Hikosaka A., Sasado T., Hirota K.;
RT "Thyroid hormone-dependent repression of alaphal-microglobulin/bikunin
RT (AMBP) gene expression during amphibian metamorphosis.";
RL Dev. Genes Evol. 206:355-362(1997).
CC -!- SIMILARITY: Belongs to the lipocalin family.
CC -!- SIMILARITY: Contains 2 BPTI/Kunitz inhibitor domains.
DR EMBL; D87752; BAA13453.1; -.
DR HSP; P02760; 1BIK.
DR GO; GO:0004867; F:serine-type endopeptidase inhibitor activity; IEA.
DR GO; GO:0005215; P:transporter activity; IEA.
DR GO; GO:0008810; P:transport; IEA.
DR InterPro; IPR002968; Al-microgloblin.
DR InterPro; IPR011038; Calycin.
DR InterPro; IPR002345; Lipocalin.
DR InterPro; IPR000566; Lipocln_cytFABP.
DR InterPro; IPR002223; Prot inh_Kunz-m.
DR Pfam; PF00014; Kunitz_BPTI; 2.
DR Pfam; PF00061; Lipocalin; 1.
DR PRINTS; PR01215; ALMCGLOBULIN.
DR PRINTS; PR00759; BASICPTASE.
DR PRINTS; PR00179; LIPOCALIN.
DR ProDom; PD000222; Prot_Inh_Kunz-m; 2.
DR SMART; SM00131; KU; 2.
DR PROSITE; PS00280; BPTI_KUNITZ_1; 2.

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DR PROSITE; PS50279; BPTI_KUNITZ_2; 2.
 DR PROSITE; PS00213; LIPOCALIN; 1.
 KW Lipocalin; Signal. 17 Potential.
 FT SIGNAL 18 342 Potential.
 SQ CHAIN 18 342 Potential.
 SQ SEQUENCE 342 AA; 38558 MW; 3050508BDFDC5C47B CRC64;

Alignment Scores:
 Pred. No.: 3.96e-08 Length: 342
 Score: 167.50 Matches: 47
 Percent Similarity: 46.15% Conservative: 19
 Best Local Similarity: 32.87% Mismatches: 46
 Query Match: 21.92% Indels: 31
 DB: 2 Gaps: 7

US-10-807-204-11 (1-396) x P70004 (1-342)

Qy 7 CTCTCAGGACTTCGCCAATCCTGTGATCCATTCTCTTTGGGGACATCCAGGAACCT 66
 Db 148 LeuTyrGlyArgSerProAspLeuArgPro---ThrLeuValAspGluPheArgGlnPhe 166
 Qy 67 GGGCAGCGTGAAGCATCCTTTGGCAGCGGTGTCCCAAAATCAAAGTG----- 114
 Db 167 AlaLeuAlaGlnGlyIle-----ProGluAspSerIleValMetLeuPro 181
 Qy 115 -----GAATCGAAGTGGAGAAATAGACCATGCTACCAACCCAGAGAT----- 159
 Db 182 AsnAsnGlyGluCysSerProGlyGluIleGlu-----ValArgProArgGlyThrGln 199
 Qy 160 -----TGCCCGAGAA-----AACATGAAGTGTGGCCCTTCAGCCGT 195
 Db 200 ArgAlaValLeuProGluGluGluCysSerGlyMetGluAsnSerProPheSerIlys 219
 Qy 196 GGAAGAAATGTTAGACTTCAGAAAGATATATGTCAGTATGCCACAGGAGGCTGGCCCC 255
 Db 220 AsnIlys-----GlyGluSerCysArgLeuAlaProAlaSerGlyPro 233
 Qy 256 TGCTGGCGCTCATACCATCAGTGTGGTACATAAATAAATAAGATCTGCTCCGAATTC 315
 Db 234 CysLeuGlyAlaHisAsnArgTyrPheTyrAsnSerSerMetAlaCysGluThrPhe 253
 Qy 316 ATCTATGCGGTGTGCGAGGGAACAATAACAACTTCCAACTTGAAGCTATCTGCTGTC 375
 Db 254 GlnTyrGlyGlyCysLeuGlyAsnAsnAsnAsnAsnAsnAsnAsnAsnAsnAsnAsn 375
 Qy 376 ACCTGCAAA 384
 Db 274 AspCysArg 276

RESULT 41

Q21418 ID Q21418 PRELIMINARY; PRT; 922 AA.
 AC Q21418;
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Hypothetical protein K10D3.4.
 GN ORFNames=K10D3.4;
 OS Caenorhabditis elegans.
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
 OC Rhabditidae; Peloderinae; Caenorhabditis.
 OX NCBI_TaxID=6239;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Bristol N2;
 RX MEDLINE=99069613; PubMed=9851916;
 RA none;
 RT "Genome sequence of the nematode C. elegans: A platform for
 RT investigating biology.";
 RL Science 282:2012-2018(1998).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Bristol N2;

RA McMurray A.A.;
 RL Submitted (JUN-1996) to the EMBL/GenBank/DBJ databases.
 CC -!- SIMILARITY: Contains 5 BPTI/Kunitz inhibitor domains.
 DR EMBL; Z75545; CAA99886.1; -.
 DR PIR; T23573; T23573.
 DR HSSP; P31713; 1SHP.
 DR InTact; Q21418; -.
 DR WormBase; WSGene00010738; K10D3.4.
 DR WormPep; K10D3.4; CE06173.
 DR GO; GO:0004867; F:serine-type endopeptidase inhibitor activity; IEA.
 DR InterPro; IPR006149; EB region.
 DR InterPro; IPR002223; Prot_Inh_Kunz-m.
 DR InterPro; IPR006150; Worm_repeat_1.
 DR Pfam; PF01683; EB; 1.
 DR Pfam; PF00014; Kunitz_BPTI; 5.
 DR PRINTS; PR00759; BASICTPASE.
 DR ProDom; PD000222; Prot_Inh_Kunz-m; 5.
 DR SMART; SM00131; KU; 5.
 DR SMART; SM00289; WR1; 6.
 DR PROSITE; PS00280; BPTI_KUNITZ_1; 2.
 DR PROSITE; PS00279; BPTI_KUNITZ_2; 5.
 KW Hypothetical protein.
 SQ SEQUENCE 922 AA; 99995 MW; 0CCBEC0AE2524CFD CRC64;

Alignment Scores:
 Pred. No.: 4.25e-08 Length: 922
 Score: 167.50 Matches: 42
 Percent Similarity: 39.72% Conservative: 14
 Best Local Similarity: 29.79% Mismatches: 56
 Query Match: 21.92% Indels: 29
 DB: 2 Gaps: 5

US-10-807-204-11 (1-396) x Q21418 (1-922)

Qy 31 GTACATTATCTCTTTGGGGACATCCAGAACTGGGCACGCTGAAGCATCTCTTGGC 90
 Db 328 IleglnPheSerTyrLeuGly-----GlnGlyGlyAsnAsnAsnAsnAsnAsn 344
 Qy 91 AAGCG---TGTCCTCAAAATC-----AAAGTGAATGCCAAGTGGGAAGAAATAGACCAG 141
 Db 345 GlnAspHisCysGluIysPheCysSerArgIleLeuCysSerAlaGlyGlu----- 361
 Qy 142 TGTACCAACCCAGAGATTGCCAGAAACATCAAGTGTTCGCCGTTTCAGCCGCTGGAAG 201
 Db 362 ProLeuIysAspSerSerGlyGluArgAsnMetGluCysSerProThrGlySerGlyAla 381
 Qy 202 AAA----- 204
 Db 382 AsnSerCysProSerThrHisSerCysGluSerThrSerGlySerThrThrPheGlyGly 401
 Qy 205 ---TGTTAGACTTCAGAAAGGATATATGCAGTATGCCACAGGAGCTGGCCCTGCCTG 261
 Db 402 ValCysCysProArgProGlnTyrValCysLeuLeuProArgGluGlnGlyAsnCysGly 421
 Qy 262 GCCTCCATACACACTCTGGTACATAAATAAATAAAGATCTGCTCCGAATTCATCTAT 321
 Db 422 ThrTyrSerAsnArgTyrPheAsnAlaIysThrGlyAsnCysGluGluPheIleTyr 441
 Qy 322 GCGGTTGCCAGGGAACAATAACAATCTCCAACTGAAGCTATCTGCTGTGGTCACCTGC 381
 Db 442 SerGlyCysGlnGlyAsnAlaAsnAsnAsnAsnAsnAsnAsnAsnAsnAsnAsnAsn 461
 Qy 382 AAA 384
 Db 462 Arg 462

RESULT 42
 O62504 ID O62504 PRELIMINARY; PRT; 1474 AA.
 AC O62504;
 DT 01-AUG-1998 (TrEMBLrel. 07, Created)
 DT 01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)


```
OC Elapidae; Acanthophiinae; Oxyuranus.
OX NCBI_TaxID=111177;
RN [1]
RP SEQUENCE FROM N.A.
RC Tissue=venom gland;
RA Filipovich I.V., Sorokina N.I.;
RL Submitted (MAY-2004) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.
DR EMBL; AY626931; AAT45407.1; -.
DR HSSP; P10646; 1ADZ.
DR GO; GO:0004867; F:serine-type endopeptidase inhibitor activity; IEA.
DR InterPro; IPR002223; Prot_Inh_Kunz-m.
DR Pfam; PF00014; Kunitz BPTI; 1.
DR PRINTS; PR00759; BASICTPASE.
DR ProDom; PD000222; Prot_Inh_Kunz-m; 1.
DR SMART; SM00131; KU; 1.
DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
DR PROSITE; PS02079; BPTI_KUNITZ_2; 1.
SQ SEQUENCE 83 AA; 9074 MW; 3145E51757014221 CRC64;

Alignment Scores:
Pred. No.: 4.02e-08 Length: 83
Score: 167.00 Matches: 28
Percent Similarity: 61.82% Conservative: 6
Best Local Similarity: 50.91% Mismatches: 21
Query Match: 21.86% Indels: 0
DB: 2 Gaps: 0

US-10-807-204-11 (1-396) x Q6ITB6 (1-83)
Qy 217 AGAAGATATATGCGAGTATGCCACAGGAGGCTGCGCCCTCGCTGCATACACAC 276
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 27 ArgProaspPheCysGluLeuProAlaAspThrGlyProCysArgValGlyPheProSer 46
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 277 TGGTGGTACATAAAAACTAGATCTGCTCCGAATTCATCTATGCGGTGCCAGGG 336
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 47 PheTyrTyrAsnProaspGluLysCysLeuGluPheIleTyrGlyGlyCysGluGly 66
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 337 AACATAACAACTCCAACTGAAGCTATCTGTCTGTGCACCTGC 381
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 67 AsnAlaAsnAsnPheIleThrLysGluGluCysGluSerThrCys 81

RESULT 45
Q6ITB6 PRELIMINARY; PRT; 83 AA.
AC Q6ITB6
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Scutellin-2.
OS Oxyuranus scutellatus.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC Elapidae; Acanthophiinae; Oxyuranus.
OX NCBI_TaxID=8668;
RN [1]
RP SEQUENCE FROM N.A.
RC Tissue=venom gland;
RA Filipovich I.V., Sorokina N.I.;
RL Submitted (MAY-2004) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.
DR EMBL; AY626929; AAT45405.1; -.
DR HSSP; P10646; 1ADZ.
DR GO; GO:0004867; F:serine-type endopeptidase inhibitor activity; IEA.
DR InterPro; IPR002223; Prot_Inh_Kunz-m.
DR Pfam; PF00014; Kunitz BPTI; 1.
DR PRINTS; PR00759; BASICTPASE.
DR ProDom; PD000222; Prot_Inh_Kunz-m; 1.
DR SMART; SM00131; KU; 1.
DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
DR PROSITE; PS02079; BPTI_KUNITZ_2; 1.
SQ SEQUENCE 83 AA; 9074 MW; 3145E51757014221 CRC64;

Alignment Scores:
Pred. No.: 4.02e-08 Length: 83
Score: 167.00 Matches: 28
Percent Similarity: 61.82% Conservative: 6
Best Local Similarity: 50.91% Mismatches: 21
Query Match: 21.86% Indels: 0
DB: 2 Gaps: 0

US-10-807-204-11 (1-396) x Q6ITB4 (1-83)
Qy 217 AGAAGATATATGCGAGTATGCCACAGGAGGCTGCGCCCTCGCTGCATACACAC 276
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 27 ArgProaspPheCysGluLeuProAlaAspThrGlyProCysArgValGlyPheProSer 46
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 277 TGGTGGTACATAAAAACTAGATCTGCTCCGAATTCATCTATGCGGTGCCAGGG 336
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 47 PheTyrTyrAsnProaspGluLysCysLeuGluPheIleTyrGlyGlyCysGluGly 66
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 337 AACATAACAACTCCAACTGAAGCTATCTGTCTGTGCACCTGC 381
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 67 AsnAlaAsnAsnPheIleThrLysGluGluCysGluSerThrCys 81

RESULT 45
Q6ITB6 PRELIMINARY; PRT; 83 AA.
AC Q6ITB6
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Scutellin-2.
OS Oxyuranus scutellatus.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC Elapidae; Acanthophiinae; Oxyuranus.
OX NCBI_TaxID=8668;
RN [1]
RP SEQUENCE FROM N.A.
RC Tissue=venom gland;
RA Filipovich I.V., Sorokina N.I.;
RL Submitted (MAY-2004) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.
DR EMBL; AY626929; AAT45405.1; -.
DR HSSP; P10646; 1ADZ.
DR GO; GO:0004867; F:serine-type endopeptidase inhibitor activity; IEA.
DR InterPro; IPR002223; Prot_Inh_Kunz-m.
DR Pfam; PF00014; Kunitz BPTI; 1.
DR PRINTS; PR00759; BASICTPASE.
DR ProDom; PD000222; Prot_Inh_Kunz-m; 1.
DR SMART; SM00131; KU; 1.
DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
DR PROSITE; PS02079; BPTI_KUNITZ_2; 1.
SQ SEQUENCE 83 AA; 9074 MW; 3145E51757014221 CRC64;

Alignment Scores:
Pred. No.: 4.02e-08 Length: 83
Score: 167.00 Matches: 28
Percent Similarity: 61.82% Conservative: 6
Best Local Similarity: 50.91% Mismatches: 21
Query Match: 21.86% Indels: 0
DB: 2 Gaps: 0

US-10-807-204-11 (1-396) x Q6ITB6 (1-83)
Qy 217 AGAAGATATATGCGAGTATGCCACAGGAGGCTGCGCCCTCGCTGCATACACAC 276
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 27 ArgProaspPheCysGluLeuProAlaAspThrGlyProCysArgValGlyPheProSer 46
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 277 TGGTGGTACATAAAAACTAGATCTGCTCCGAATTCATCTATGCGGTGCCAGGG 336
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 47 PheTyrTyrAsnProaspGluLysCysLeuGluPheIleTyrGlyGlyCysGluGly 66
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 337 AACATAACAACTCCAACTGAAGCTATCTGTCTGTGCACCTGC 381
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 67 AsnAlaAsnAsnPheIleThrLysGluGluCysGluSerThrCys 81

RESULT 46
Q6T6S5 PRELIMINARY; PRT; 90 AA.
AC Q6T6S5
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Kunitz protease inhibitor 2.
OS Bitis gabonica (Gaboon adder) (Gaboon viper).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC Viperidae; Viperinae; Bitis.
OX NCBI_TaxID=8694;
RN [1]
RP SEQUENCE FROM N.A.
RC PubMed=15276202; DOI=10.1016/j.jgene.2004.03.024;
RA Francischetti I.M., My-Pham V., Harrison J., Garfield M.K.,
RA Ribeiro J.M.;
RT "Bitis gabonica (Gaboon viper) snake venom gland: toward a catalog for
    the full-length transcripts (cdna) and proteins.";
RL Gene 337:55-69(2004).
RN [2]
RP SEQUENCE FROM N.A.
RA Francischetti I.M.B., Pham V.M., Garfield M.K., Ribeiro J.M.C.;
RL Submitted (OCT-2003) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.
DR EMBL; AY430413; AAR24535.1; -.
DR HSSP; Q16019; IAAp.
DR GO; GO:0008233; F:peptidase activity; IEA.
DR GO; GO:0004867; F:serine-type endopeptidase inhibitor activity; IEA.
DR InterPro; IPR002223; Prot_Inh_Kunz-m.
DR Pfam; PF00014; Kunitz BPTI; 1.
DR PRINTS; PR00759; BASICTPASE.
DR ProDom; PD000222; Prot_Inh_Kunz-m; 1.
DR SMART; SM00131; KU; 1.
DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
DR PROSITE; PS02079; BPTI_KUNITZ_2; 1.
KW Protease.
SQ SEQUENCE 90 AA; 10006 MW; 2BEDC1D2020852AF CRC64;

Alignment Scores:
Pred. No.: 4.05e-08 Length: 90
Score: 167.00 Matches: 28
Percent Similarity: 61.29% Conservative: 10
Best Local Similarity: 45.16% Mismatches: 20
Query Match: 21.86% Indels: 4
DB: 2 Gaps: 1

US-10-807-204-11 (1-396) x Q6T6S5 (1-90)
Qy 196 GAAAGAAATGTTTAGACTTCAGAAAGGATATATGCAGTATGCCACAGGAGGCTGCCCC 255
```


RESULT	48
BTIA	BOOMI
ID	_BTIA_BOOMI
STANDARD;	PRT; 122 AA.
AC	P83609;
DT	05-JUL-2004 (Rel. 44, Created)
DT	05-JUL-2004 (Rel. 44, Last sequence update)
DT	05-JUL-2004 (Rel. 44, Last annotation update)
DE	Kunitz-type serine protease inhibitor Bmt1-A (Fragments).
OS	Boophilus microplus (cattle tick).
OC	Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Acari;
OC	Parasitiformes; Ixodida; Ixodoidea; Ixodidae; Boophilus.
NBI_TaxID=6941;	
[1]	
RN	
RP	SEQUENCE, AND FUNCTION.

13305=header,
RX PubMed=10613008; DOI=10.1016/S0162-3109(99)00074-0;
RA Tanaka A.S., Andreotti R., Gomes A., Torquato R.J.S., Sampaio M.U.,
RA Sampaio C.A.M.;
RT "A double headed serine proteinase inhibitor-human plasma kallikrein
RT and elastase inhibitor-from *Boophilus microplus* larvae."
RL Immunopharmacology 45:171-177(1999).
CC -I- FUNCTION: Inhibits bovine trypsin, bovine chymotrypsin, human
CC plasmin, human plasma kallikrein and human neutrophil elastase,
CC but not bovine thrombin, human factor Xa or porcine pancreatic
CC kallikrein. May play a role in blocking blood coagulation during
CC the larvae fixation on cattle.
CC -I- SUBCELLULAR LOCATION: Secreted.
CC -I- SIMILARITY: Contains 2 BPTI/Kunitz inhibitor domains.
DR InterPro: IPR002223; Kunitz BPTI.

Percent Similarity:	52.94%	Conservative:	9
Best Local Similarity:	42.35%	Mismatches:	22
Query Match:	21.73%	Indels:	18
DB:	1	Gaps:	4

US-10-807-204-11 (1-396) x BTIA_BOONI (1-122)

Qy	136	GACCAGTGTACCAAAACCAGAGATTGCCAGAAAAACATGAAGTGTGGCCGTTCCAGC----	192
		:::	
Db	54	GlucInCys-----	-----lybAlaSerCysLysProGluThrGlu 65
Qy	193	---CGTGGAGAAATGTTTACGTTCAGAAAGGATATATGCAGATATGCCACAGAGGCT	249
Db	66	TyrGluAlaLysLysCysLeu-----	-----AlaArgPro---GluSer 77

```
QY 370 CTGGTCACCTGCAGAA 384
||| :|||
Db 118 LeuylsSerCysLys 122

RESULT 49
Q6I750 PRELIMINARY; PRT; 507 AA.
AC Q6I750;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hepatocyte growth factor activator inhibitor-1.
GN Name=HAI-1;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RA Tezuka S.;
RL Submitted (DEC-2003) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Contains 2 BPTI/Kunitz inhibitor domains.
DR EMBL; AB154834; BAD23971.1; -.
DR GO; GO:0004867; F:serine-type endopeptidase inhibitor activity; IEA.
DR InterPro; IPR002172; LDL receptor_A.
DR InterPro; IPR011106; MANSC_N.
DR InterPro; IPR002223; Prot_inh_Kunz-m.
DR Pfam; PF00014; Kunitz_BPTI; 2.
DR Pfam; PF00057; Ldl_recept_a; 1.
DR Pfam; PF07502; MANSC; 1.
DR PRINTS; PR00759; BASICPTASE.
DR ProDom; PD000222; Prot_inh_Kunz-m; 2.
DR SMART; SM00131; KU; 2.
DR SMART; SM00192; LDLA; 1.
DR PROSITE; PS00280; BPTI_KUNITZ_1; 2.
DR PROSITE; PS02079; BPTI_KUNITZ_2; 2.
DR PROSITE; PS01209; LDLRA_1; 1.
DR PROSITE; PS0068; LDLRA_2; 1.
SQ SEQUENCE 507 AA; 56465 MW; 810043AE28C47AF3 CRC64;

Alignment Scores:
Pred. No.: 5,79e-08 Length: 507
Score: 166.00 Matches: 33
Percent Similarity: 51.55% Conservative: 17
Best Local Similarity: 34.02% Mismatches: 39
Query Match: 21.73% Indels: 8
DB: 2 Gaps: 3

US-10-807-204-11 (1-396) x Q6I750 (1-507)

QY 118 TGCAGTGGAGAAATAGACAGTGTAACCAACCCAGAGATTGCCCA-----GAA 168
||| :|||
Db 324 CysCysIleAspGlyPheLeuGluCysAspThrProAspCysProAspGlySerAsp 343
||| :|||

QY 169 AACATGAAGTGTGCCCGTTCAGCCGTGGA-----AGAAATGTTTAGACTTCAGA 219
||| :|||
Db 344 GluAlaThrCysGluLysTySerSerGlyPheAspGluLeuGlnSerIleHisPheLeu 363
||| :|||

QY 220 AAGGAT-----ATATGAGTATGATGCACAGAGGCTGCCCTGCTGCCCTCCATACCA 273
||| :|||
Db 364 SerAspLysGlyTyCysAlaGluLeuProAspThrGlyPheCysLysGluAsnIlePro 383
||| :|||

QY 274 CACTGGTGGTACATAAATAAATAAGATCTGCTCCGAATTCATCTATGGGGTGGCAG 333
||| :|||
Db 384 ArgTrpTyArgAsnProPheSerGluArgCysAlaArgPheThrTyThrGlyGlyCysTyr 403
||| :|||

QY 334 GGGAAACAATACAACTCCAACTGAAGCTATCTGCTGGTCACCTGCAGAA 384
||| :|||
Db 404 GlyAsnLysAsnAsnPheGluLysGluGlnGlnCysLeuGluSerCysArg 420
||| :|||

RESULT 50
AMBP_PIG
```

```
ID AC P04356; P34954; STANDARD; PRT; 337 AA.
DT 20-MAR-1987 (Rel. 04, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE AMBP protein precursor [Contains: Alpha-1-microglobulin; Inter-alpha-
DE trypsin inhibitor light chain (ITI-LC) (Bikunin) (HI-30) (EI-14)]
DE (Fragment).
DE Name=AMBP; Synonyms=ITIL;
GN Sub scrofa (Pig).
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=90353595; PubMed=1696914; DOI=10.1016/0014-5793(90)91112-2;
RA Gebhard W., Schreitmuller T., Vetr H., Wächter E., Hochstrasser K.;
RA "Complementary DNA and deduced amino acid sequences of porcine alpha
RA 1-microglobulin and bikunin.";
RA FEBS Lett. 269:32-36(1990).
RL [2]
RN [2]
RP SEQUENCE OF 2-337 FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=91113729; PubMed=1703444; DOI=10.1016/0167-4781(91)90152-C;
RA Tavakkol A.;
RT "Molecular cloning of porcine alpha 1-microglobulin/HI-30 reveals
RT developmental and tissue-specific expression of two variant messenger
RT ribonucleic acids.";
RL Biochim. Biophys. Acta 1088:47-56(1991).
RN [3]
RP SEQUENCE OF 212-334.
RX MEDLINE=85225967; PubMed=2408637;
RA Hochstrasser K., Wächter E., Albrecht G.J., Reisinger P.;
RA "Kunitz-type proteinase inhibitors derived by limited proteolysis of the
RA inter-alpha-trypsin inhibitor, X. The amino-acid sequences of the
RA trypsin-released inhibitors from horse and pig inter-alpha-trypsin
RA inhibitors.";
RL Biol. Chem. Hoppe-Seyler 366:473-478(1985).
CC -1- FUNCTION: Alpha-1-microglobulin occurs in many physiological
CC fluids including plasma, urine, and cerebrospinal fluid. It
CC appears not only as a free monomer but also in complexes with IgA
CC and albumin.
CC -1- FUNCTION: Inter-alpha-trypsin inhibitor, present in plasma and
CC urine, inhibits trypsin, plasmin, and lysosomal granulocytic
CC elastase.
CC -1- SUBUNIT: I-alpha-I plasma protease inhibitors are assembled from
CC one or two heavy chains (H1, H2 or H3) and one light chain,
CC bikunin. Inter-alpha-inhibitor (I-alpha-I) is composed of H1, H2
CC and bikunin, inter-alpha-like inhibitor (I-alpha-LI) of H2 and
CC bikunin, and pre-alpha-inhibitor (P-alpha-I) of H3 and bikunin (By
CC similarity).
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- TISSUE SPECIFICITY: Expressed by the liver and secreted in plasma.
CC -1- PTM: The precursor is proteolytically processed into two
CC separately functioning proteins.
CC -1- PTM: Alpha-1-microglobulin contains covalently linked brown-yellow
CC chromophores (By similarity).
CC -1- SIMILARITY: In the N-terminal section; belongs to the lipocalin
CC family.
CC -1- SIMILARITY: Contains 2 BPTI/Kunitz inhibitor domains.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (see http://www.ebi.ac.uk/ebis/
CC or send an email to license@ebi.ac.uk).
CC -----
CC EMBL; X53685; CAA37725.1; -.
CC PIR; S11066; TIFGBI.
CC HSSP; P02760; 1BIK.
CC -----
DR EMBL; X53685; CAA37725.1; -.
DR PIR; S11066; TIFGBI.
DR HSSP; P02760; 1BIK.
```


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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 21, 2005, 16:37:09 ; Search time 107 Seconds
(without alignments)
473.510 Million cell updates/sec

Title: US-10-807-204-1
Perfect score: 131
Sequence: 1 MGLSGLPILVFFILGDIQ.....GNNNFQTEAICLVTCCKYH 131

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 2105692 seqs, 386760381 residues

Word size : 0

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 50 summaries

Database : A_Geneseq_16Dec04:*
1: Geneseqp1980s:*
2: Geneseqp1990s:*
3: Geneseqp2000s:*
4: Geneseqp2001s:*
5: Geneseqp2002s:*
6: Geneseqp2003as:*
7: Geneseqp2003bs:*
8: Geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	131	100.0	131	7 ADA19800	Adal19800 Engineere
2	131	100.0	131	7 ADA19811	Adal19811 Engineere
3	106	80.9	106	7 ADA19801	Adal19801 Mature fo
4	64	48.9	86	5 ABP69809	Abp69809 Human pol
5	64	48.9	86	6 ABJ26667	Abj26667 Human pro
6	64	48.9	98	7 ADA19808	Adal19808 Engineere
7	64	48.9	101	4 ABB12236	Abb12236 Human epp
8	64	48.9	131	7 ADA19814	Adal19814 Human DJ1
9	33	25.2	43	7 ADA19804	Adal19804 Engineere
10	33	25.2	179	8 ABM85103	Abm85103 Human dia
11	30	22.9	30	7 ADA19803	Adal19803 Engineere
12	24	18.3	24	7 ADA19805	Adal19805 Engineere
13	21	16.0	33	7 ADA19806	Adal19806 Engineere
14	21	16.0	33	7 ADA19809	Adal19809 Engineere
15	14	10.7	134	7 ADA19813	Adal19813 Mouse Epp
16	12	9.2	43	4 AAE13036	Aae13036 Human ser
17	12	9.2	51	2 AAU75257	Aau75257 Fragment
18	12	9.2	51	5 AAU75257	Aau75257 Human gen
19	12	9.2	51	5 AAU75257	Aau75257 Human gen
20	12	9.2	51	8 ADG98845	Adg98845 Human sec
21	12	9.2	58	4 AAE13084	Aae13084 Human ser
22	12	9.2	58	4 AAE13084	Aae13084 Human ser
23	12	9.2	58	7 ADF41997	Adf41997 Human CAB
24	12	9.2	58	8 ADL16838	Adl16838 Human Kun
25	12	9.2	58	8 ADR89980	Adr89980 Human CAB

26	12	9.2	64	4 AAE13093	Aae13093 Human ser
27	12	9.2	102	5 AAE27095	Aae27095 Human sec
28	12	9.2	102	5 AAE28009	Aae28009 Human gen
29	12	9.2	102	6 ABU65039	Abu65039 Human sec
30	12	9.2	102	8 ADG89848	Adg89848 Human sec
31	12	9.2	117	5 AAE27094	Aae27094 Human sec
32	12	9.2	117	5 AAE27165	Aae27165 Human gen
33	12	9.2	117	6 ABU65038	Abu65038 Human sec
34	12	9.2	117	8 ADG89847	Adg89847 Human sec
35	12	9.2	133	2 AAU75219	Aau75219 Human sec
36	12	9.2	133	5 AAE26982	Aae26982 Human gen
37	12	9.2	133	5 AAE27120	Aae27120 Human gen
38	12	9.2	133	6 ABU64993	Abu64993 Human sec
39	12	9.2	133	7 ADA19812	Ada19812 Human EPP
40	12	9.2	133	8 ADG89802	Adg89802 Human pro
41	12	9.2	164	3 AAU70010	Aay70010 Human pro
42	11	8.4	54	4 AAE13092	Aae13092 Trypsin i
43	10	7.6	136	7 ADA19815	Ada19815 Mouse DJ1
44	9	6.9	58	2 AAR78401	Aar78401 Human LAC
45	8	6.1	126	7 ADE64021	Ade64021 Human pro
46	8	6.1	140	5 AAU79498	Aau79498 Mouse par
47	8	6.1	140	5 AAU80150	Aau80150 Mouse par
48	8	6.1	166	4 AAM18394	Aam18394 Peptide #
49	8	6.1	166	4 ABB37425	Abb37425 Peptide #
50	8	6.1	175	5 AAU79499	Aau79499 Mouse par

ALIGNMENTS

RESULT 1
ADA19800
ID ADA19800 standard; protein; 131 AA.
XX AC ADA19800;
XX AC
DT 20-NOV-2003 (first entry)
XX DE Engineered human DJ11 protein SEQ ID NO:1.
XX KW DJ11; Kunitz-type protease inhibitor domain; antiinflammatory;
KW antiallergic; thrombolytic; anticoagulant; cardiant; vasotropic;
KW antibacterial; immunosuppressive; antirheumatic; antiarthritic;
KW nephrotropic; antipsoaratic; vulnery; protease inhibitor; gene therapy;
KW acute pancreatitis; pulmonary injury; allergy-induced protease release;
KW deep vein thrombosis; myocardial infarction; shock; septic shock;
KW hyperfibrinolytic haemorrhage; inflammatory disorder; emphysema;
KW idiopathic pulmonary fibrosis; rheumatoid arthritis; glomerulonephritis;
KW chronic inflammatory bowel disease; psoriasis.
XX OS Synthetic.
XX OS Homo sapiens.
XX Key Location/Qualifiers
FT Misc-difference 1..131 /note= "eppin-like precursor"
FT Peptide 1..25 /label= signal
FT Protein 26..131 /note= "mature DJ11 protein"
FT Disulfide-bond 33..61 /note= predicted disulfide bond
FT Disulfide-bond 40..65 /note= predicted disulfide bond
FT Disulfide-bond 48..60 /note= predicted disulfide bond
FT Disulfide-bond 54..69 /note= predicted disulfide bond
FT Domain 77..127 /note= Kunitz domain predicted by pfscan
FT Disulfide-bond 77..127 /note= predicted disulfide bond
FT Disulfide-bond 86..110 /note= predicted disulfide bond

FT Disulfide-bond 102..123 /note = predicted disulfide bond
 FT Disulfide-bond 102..123 /note = predicted disulfide bond
 XX WO2003070770-A2.
 XX 28-AUG-2003.
 XX 18-FEB-2003; 2003WO-EP001629.
 XX 21-FEB-2002; 2002US-0358683P.
 XX (GENE-) GENEPROT INC.
 XX Bougueleret L, Bairoch A, Niknejad A;
 XX WPI; 2003-663849/62.
 DR N-ESDB; ADA19810.
 XX New engineered human Kunitz-type protease inhibitor for diagnosing,
 PT preventing or treating conditions associated with excessive proteinase
 PT activity, e.g. inflammation, pulmonary injuries, myocardial infarction or
 PT hemorrhage.
 XX Claim 5; Page 69-70; 87pp; English.
 XX The present invention describes an isolated, purified or recombinant DJ11
 CC polypeptide comprising a Kunitz-type protease inhibitor domain or its
 CC biologically active portion. The polypeptide comprises at least 98 %
 CC identity to residues 77-127 of a 131 amino acid sequence (S1, see
 CC ADA19800), or to residues 52-102 of a 106 amino acid sequence (S2, see
 CC ADA19801). DJ11 has antiinflammatory, antiallergic, thrombolytic,
 CC anticoagulant, cardiant, vasotropic, antibacterial, immunosuppressive,
 CC antineumatic, antiarthritic, nephrotropic, antipsoriatic and vulnary
 CC activities, and can be used as a protease inhibitor and in gene therapy.
 CC Composition and methods from the present invention can be used in
 CC diagnosing, preventing or treating conditions associated with excessive
 CC proteinase activity, such as acute pancreatitis, pulmonary injury,
 CC allergy-induced protease release, deep vein thrombosis, myocardial
 CC infarction, shock (including septic shock), hyperfibrinolytic
 CC haemorrhage, and especially, inflammatory disorders (e.g. emphysema,
 CC idiopathic pulmonary fibrosis, rheumatoid arthritis, glomerulonephritis,
 CC chronic inflammatory bowel disease or psoriasis). The DJ11 proteins may
 CC be used in preserving platelet function, organ preservation or in wound
 CC healing. The polynucleotide sequence encoding DJ11 may be used as
 CC hybridisation probes, in chromosome and gene mapping, in the generation
 CC of antisense RNA and DNA, and as targets for pharmaceutical intervention.
 CC The present sequence represents an engineered human DJ11 protein from the
 CC present invention.
 XX SQ Sequence 131 AA;
 Query Match 100.0%; Score 131; DB 7; Length 131;
 Best Local Similarity 100.0%; Pred. No. 8.3e-131;
 Matches 131; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 MGLSGLLPILVPFILLGDIQEPGHAEGILGKPCPKIKVECEVEEIDQCTKPRDCPENMKC 60
 Db 1 MGLSGLLPILVPFILLGDIQEPGHAEGILGKPCPKIKVECEVEEIDQCTKPRDCPENMKC 60
 Qy 61 CPFSGCKKCLDFRDKICSMPOEAGPCLASIPHWYNNKTKICSEFIYGGCGGNNNNFQTE 120
 Db 61 CPFSGCKKCLDFRDKICSMPOEAGPCLASIPHWYNNKTKICSEFIYGGCGGNNNNFQTE 120
 Qy 121 AICLVTKKYYH 131
 Db 121 AICLVTKKYYH 131
 RESULT 2
 ADA19811
 ID ADA19811 standard; protein; 131 AA.
 XX

AC ADA19811;
 XX 20-NOV-2003 (first entry)
 XX Engineered human DJ11 protein SEQ ID NO:12.
 DE DJ11; Kunitz-type protease inhibitor domain; antiinflammatory;
 KW antiallergic; thrombolytic; anticoagulant; cardiant; vasotropic;
 KW antibacterial; immunosuppressive; antirheumatic; antiarthritic;
 KW nephrotropic; antipsoriatic; vulnary; protease inhibitor; gene therapy;
 KW acute pancreatitis; pulmonary injury; allergy-induced protease release;
 KW deep vein thrombosis; myocardial infarction; shock; septic shock;
 KW hyperfibrinolytic haemorrhage; inflammatory disorder; emphysema;
 KW idiopathic pulmonary fibrosis; rheumatoid arthritis; glomerulonephritis;
 KW chronic inflammatory bowel disease; psoriasis.
 XX Synthetic.
 OS Homo sapiens.
 XX WO2003070770-A2.
 PN 28-AUG-2003.
 PD 18-FEB-2003; 2003WO-EP001629.
 XX 21-FEB-2002; 2002US-0358683P.
 PR (GENE-) GENEPROT INC.
 XX Bougueleret L, Bairoch A, Niknejad A;
 XX WPI; 2003-663849/62.
 XX New engineered human Kunitz-type protease inhibitor for diagnosing,
 PT preventing or treating conditions associated with excessive proteinase
 PT activity, e.g. inflammation, pulmonary injuries, myocardial infarction or
 PT hemorrhage.
 XX Disclosure; Page 84; 87pp; English.
 XX The present invention describes an isolated, purified or recombinant DJ11
 CC polypeptide comprising a Kunitz-type protease inhibitor domain or its
 CC biologically active portion. The polypeptide comprises at least 98 %
 CC identity to residues 77-127 of a 131 amino acid sequence (S1, see
 CC ADA19800), or to residues 52-102 of a 106 amino acid sequence (S2, see
 CC ADA19801). DJ11 has antiinflammatory, antiallergic, thrombolytic,
 CC anticoagulant, cardiant, vasotropic, antibacterial, immunosuppressive,
 CC antineumatic, antiarthritic, nephrotropic, antipsoriatic and vulnary
 CC activities, and can be used as a protease inhibitor and in gene therapy.
 CC Composition and methods from the present invention can be used in
 CC diagnosing, preventing or treating conditions associated with excessive
 CC proteinase activity, such as acute pancreatitis, pulmonary injury,
 CC allergy-induced protease release, deep vein thrombosis, myocardial
 CC infarction, shock (including septic shock), hyperfibrinolytic
 CC haemorrhage, and especially, inflammatory disorders (e.g. emphysema,
 CC idiopathic pulmonary fibrosis, rheumatoid arthritis, glomerulonephritis,
 CC chronic inflammatory bowel disease or psoriasis). The DJ11 proteins may
 CC be used in preserving platelet function, organ preservation or in wound
 CC healing. The polynucleotide sequence encoding DJ11 may be used as
 CC hybridisation probes, in chromosome and gene mapping, in the generation
 CC of antisense RNA and DNA, and as targets for pharmaceutical intervention.
 CC The present sequence represents an engineered human DJ11 protein from the
 CC present invention.
 XX SQ Sequence 131 AA;
 Query Match 100.0%; Score 131; DB 7; Length 131;
 Best Local Similarity 100.0%; Pred. No. 8.3e-131;
 Matches 131; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 MGLSGLLPILVPFILLGDIQEPGHAEGILGKPCPKIKVECEVEEIDQCTKPRDCPENMKC 60
 Db 1 MGLSGLLPILVPFILLGDIQEPGHAEGILGKPCPKIKVECEVEEIDQCTKPRDCPENMKC 60

QY 61 CPFCGKCLDFRKDCSMPQAGPCLASIPHHWYNNKTKICSEFIYGGCGQNNNFOTE 120
DB 61 CPFCGKCLDFRKDCSMPQAGPCLASIPHHWYNNKTKICSEFIYGGCGQNNNFOTE 120

QY 121 AICLVTCCKYH 131
DB 121 AICLVTCCKYH 131

RESULT 3
ADA19801
ID ADA19801 standard; protein; 106 AA.
AC ADA19801;
XX
DT 20-NOV-2003 (first entry)
XX
DE Mature form of engineered human DJ11 protein SEQ ID NO:2.
XX
KW DJ11; Kunitz-type protease inhibitor domain; antiinflammatory;
KW antiallergic; thrombolytic; anticoagulant; cardiant; vasotropic;
KW antibacterial; immunosuppressive; antirheumatic; antiarthritic;
KW nephrotropic; antiporiatic; vulnary; protease inhibitor; gene therapy;
KW acute pancreatitis; pulmonary injury; allergy-induced protease release;
KW deep vein thrombosis; myocardial infarction; shock; septic shock;
KW hyperfibrinolytic haemorrhage; inflammatory disorder; emphysema;
KW idiopathic pulmonary fibrosis; rheumatoid arthritis; glomerulonephritis;
KW chronic inflammatory bowel disease; psoriasis.
XX
OS Synthetic.
OS Homo sapiens.
XX
XX
FH Key Location/Qualifiers
FT Disulfide-bond 8..36 /note = predicted disulfide bond
FT Disulfide-bond 15..40 /note = predicted disulfide bond
FT Disulfide-bond 23..35 /note = predicted disulfide bond
FT Disulfide-bond 29..44 /note = predicted disulfide bond
FT Disulfide-bond 52..102 /note = predicted disulfide bond
FT Domain 52..102 /note = Kunitz domain predicted by pfscan
FT Disulfide-bond 52..102 /note = predicted disulfide bond
FT Disulfide-bond 61..85 /note = predicted disulfide bond
FT Disulfide-bond 77..98 /note = predicted disulfide bond
XX
FN WO2003070770-A2.
XX
XX
PD 28-AUG-2003.
XX
PF 18-FEB-2003; 2003WO-EP001629.
XX
XX 21-FEB-2002; 2002US-0358683P.
XX (GENE-) GENEPROT INC.
XX
XX Bougueleret L, Bairoch A, Niknejad A;
XX
XX WPI; 2003-663849/62.
DR
XX
XX New engineered human Kunitz-type protease inhibitor for diagnosing,
PT preventing or treating conditions associated with excessive proteinase
PT activity, e.g. inflammation, pulmonary injuries, myocardial infarction or
PT hemorrhage.
XX
XX Claim 5; Page 71; 87pp; English.
XX
XX The present invention describes an isolated, purified or recombinant DJ11

CC polypeptide comprising a Kunitz-type protease inhibitor domain or its
CC biologically active portion. The polypeptide comprises at least 98 %
CC identity to residues 77-127 of a 131 amino acid sequence (S1, see
CC ADA19800), or to residues 52-102 of a 106 amino acid sequence (S2, see
CC ADA19801). DJ11 has antiinflammatory, antiallergic, thrombolytic,
CC anticoagulant, cardiant, vasotropic, antibacterial, immunosuppressive,
CC antirheumatic, antiarthritic, nephrotropic, antiporiatic and vulnary
CC activities, and can be used as a protease inhibitor and in gene therapy.
CC diagnosing, preventing or treating conditions associated with excessive
CC proteinase activity, such as acute pancreatitis, pulmonary injury,
CC allergy-induced protease release, deep vein thrombosis, myocardial
CC infarction, shock (including septic shock), hyperfibrinolytic
CC haemorrhage, and especially, inflammatory disorders (e.g. emphysema,
CC idiopathic pulmonary fibrosis, rheumatoid arthritis, glomerulonephritis,
CC chronic inflammatory bowel disease or psoriasis). The DJ11 proteins may
CC be used in preserving platelet function, organ preservation or in wound
CC healing. The polynucleotide sequence encoding DJ11 may be used as
CC hybridisation probes, in chromosome and gene mapping, in the generation
CC of antisense RNA and DNA, and as targets for pharmaceutical intervention.
CC The present sequence represents the mature form of an engineered human
CC DJ11 protein from the present invention.
XX
SQ Sequence 106 AA;
XX
Query Match 80.9%; Score 106; DB 7; Length 106;
Best Local Similarity 100.0%; Pred. No. 2.6e-104;
Matches 106; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 26 EGILGKCPKIKVCEVEEIDQCTKPRDCPENMKCCPFSCGKCLDFRKDCSMPQAGP 85
DB 1 EGILGKCPKIKVCEVEEIDQCTKPRDCPENMKCCPFSCGKCLDFRKDCSMPQAGP 60
QY 86 CLASIPHHWYNNKTKICSEFIYGGCGQNNNFQTEAICLVTCCKYH 131
DB 61 CLASIPHHWYNNKTKICSEFIYGGCGQNNNFQTEAICLVTCCKYH 106

RESULT 4
ABP69809
ID ABP69809 standard; protein; 86 AA.
XX
AC ABP69809;
XX
DT 20-JAN-2003 (first entry)
XX
XX Human polypeptide SEQ ID NO 1856.
KW Human; genome mapping; gene therapy; food supplement; virus; fungus;
KW cell-proliferative disorder; neurodegenerative disease; bacterial;
KW Parkinson's disease; Alzheimer's disease; autoimmune disease;
KW multiple sclerosis; diabetes; genetic disorder; wound; burn; infection;
KW arthritis; cytostatic; immunomodulator; nootropic; neuroprotective;
KW antiparkinsonian; antidiabetic; immunosuppressive; dermatological;
KW haemostatic; vulnary; fungicide; antibacterial; virucide; protozoacide;
KW antiarthritic.
XX
OS Homo sapiens.
XX
FN WO200270539-A2.
XX
PD 12-SEP-2002.
XX
XX 05-MAR-2002; 2002WO-US005095.
XX
XX 05-MAR-2001; 2001US-00799451.
XX (HYGE-) HYSEQ INC.
XX
XX Tang YT, Zhou P, Goodrich RW, Asundi V, Zhang J, Zhao QA, Ren F;
XX Xue AJ, Yang Y, Ma Y, Yamazaki V, Chen R, Wang Z, Ghosh M;
XX Wehrman T, Wang J, Wang D, Drmanac RT;
XX

XX DJ11; Kunitz-type protease inhibitor domain; antiinflammatory;
KW anti-allergic; thrombolytic; anticoagulant; cardiant; vasotropic;
KW antibacterial; immunosuppressive; antirheumatic; antiarthritic;
KW nephrotropic; antipruritic; vulnery; protease inhibitor; gene therapy;
KW acute pancreatitis; pulmonary injury; allergy-induced protease release;
KW deep vein thrombosis; myocardial infarction; shock; septic shock;
KW hyperfibrinolytic haemorrhage; inflammatory disorder; emphysema;
KW idiopathic pulmonary fibrosis; rheumatoid arthritis; glomerulonephritis;
KW chronic inflammatory bowel disease; psoriasis.
XX Synthetic.
OS Homo sapiens.
XX WO2003070770-A2.
XX 28-AUG-2003.
XX 18-FEB-2003; 2003WO-EP001629.
XX 21-FEB-2002; 2002US-0358683P.
XX (GENE-) GENEPROT INC.
XX Bougueleret L, Bairoch A, Niknejad A;
PI WPI; 2003-663849/62.
XX DR
XX New engineered human Kunitz-type protease inhibitor for diagnosing,
PT preventing or treating conditions associated with excessive proteinase
PT activity, e.g. inflammation, pulmonary injuries, myocardial infarction or
PT hemorrhage.
XX Disclosure; Page 82; 87pp; English.
XX The present invention describes an isolated, purified or recombinant DJ11
CC polypeptide comprising a Kunitz-type protease inhibitor domain or its
CC biologically active portion. The polypeptide comprises at least 98 %
CC identity to residues 77-127 of a 131 amino acid sequence (S1, see
CC ADA19800), or to residues 52-102 of a 106 amino acid sequence (S2, see
CC ADA19801). DJ11 has antiinflammatory, antiallergic, thrombolytic,
CC anticoagulant, cardiant, vasotropic, antibacterial, immunosuppressive,
CC antirheumatic, antiarthritic, nephrotropic, antipruritic and vulnery
CC activities, and can be used as a protease inhibitor and in gene therapy.
CC Composition and methods from the present invention can be used in
CC diagnosing, preventing or treating conditions associated with excessive
CC proteinase activity, such as acute pancreatitis, pulmonary injury,
CC allergy-induced protease release, deep vein thrombosis, myocardial
CC infarction, shock (including septic shock), hyperfibrinolytic
CC haemorrhage, and especially, inflammatory disorders (e.g. emphysema,
CC idiopathic pulmonary fibrosis, rheumatoid arthritis, glomerulonephritis,
CC chronic inflammatory bowel disease or psoriasis). The DJ11 proteins may
CC be used in preserving platelet function, organ preservation or in wound
CC healing. The polynucleotide sequence encoding DJ11 may be used as
CC hybridisation probes, in chromosome and gene mapping, in the generation
CC of antisense RNA and DNA, and as targets for pharmaceutical intervention.
CC The present sequence represents a partial engineered human DJ11 protein
CC amino acid sequence from the present invention.
XX Sequence 98 AA;
SQ
Query Match 48.9%; Score 64; DB 7; Length 98;
Best Local Similarity 100.0%; Pred. No. 1e-59;
Matches 64; Conservative 0; Mismatches 0; Gaps 0;
Indels 0;
QY 1 MGLSGLLPILVFPILLGDIQBPCHAGILGKPCPKIKVCEVEEIDQCTKPCPENMKC 60
DB 1 MGLSGLLPILVFPILLGDIQBPCHAGILGKPCPKIKVCEVEEIDQCTKPCPENMKC 60
QY 61 CPFS 64
DB 61 CPFS 64

RESULT 7
ABBI2236
ID ABB12236 standard; peptide; 101 AA.
XX
AC ABB12236;
XX
DT 11-JAN-2002 (first entry)
DE Human eppin-1 homologue, SEQ ID NO:2606.
XX Human; cytokine; cell proliferation; cell differentiation; growth factor;
KW haematopoiesis regulation; tissue growth; immunomodulator; activin;
KW inhibin; chemotaxis; chemokinesis; thrombolysis; oncogenesis;
KW proliferation; metastasis; cancer; tumour; haematopoietic disorder;
KW myeloid cell disorder; lymphoid cell disorder; asthma; arthritis;
KW chronic inflammatory condition; proliferative retinopathy;
KW atherosclerosis; coronary heart disease; arterial ischaemia;
KW bone disorder; osteoporosis; vascular growth disorder;
KW tissue regeneration; wound healing; infection; immune disorder;
KW cell culture; drug screening; gene therapy; antiinflammatory;
KW antiasthmatic; antiarthritic; haemostatic; antiarteriosclerotic;
KW cytostatic; osteopathic; vasotropic; cardiant; virucide; antibacterial;
KW antifungal; vulnery; antiulcer.
XX Homo sapiens.
XX WO200157188-A2.
XX 09-AUG-2001.
XX 05-FEB-2001; 2001WO-US003800.
XX 03-FEB-2000; 2000US-00496914.
XX 27-APR-2000; 2000US-00560875.
XX (HVSE-) HVSEQ INC.
XX Tang YT, Liu C, Drmanac RT;
PI WPI; 2001-457740/49.
DR N-PSDB; ABA09480.
DR Human proteins and DNA encoding sequences useful for preventing, treating
PT and ameliorating a medical condition in a mammalian subject e.g. arthritis
PT and cancer.
XX Claim 20; Page 318; 1963pp; English.
XX Sequences ABB10981-ABBI2330 represent 1350 novel human polypeptides, and
CC sequences ABA08225-ABA09574 represent nucleic acids encoding them. The
CC invention also relates to vectors and recombinant host cells comprising a
CC nucleotide of the invention, methods of producing the novel polypeptides,
CC antibodies against the polypeptides, methods of detecting the nucleotides
CC or polypeptides in a sample, and methods of identifying compounds which
CC bind to polypeptides of the invention. Although novel, many of the
CC polypeptides of the invention have homology to known proteins, and hence
CC giving an insight into their probable biological activities, and hence
CC potential therapeutic applications. The polypeptides of the invention may
CC have various activities, including cytokine, cell proliferation or cell
CC differentiation activities; stem cell growth factor activity;
CC haematopoiesis regulatory activity; tissue growth activity;
CC immunomodulatory activity; activin- or inhibin-related activities;
CC chemotactic or chemokinetic activities; haemostatic, thrombotic or
CC thrombolytic activities; receptor or ligand activities; or may be
CC involved in oncogenesis, cancer cell proliferation or metastasis.
CC Depending on their biological activities, polypeptides and nucleotides of
CC the invention are useful for preventing, treating or ameliorating medical
CC conditions, e.g., by protein or gene therapy. Such conditions include
CC cancers, haematopoietic disorders (e.g., myeloid or lymphoid cell
CC disorders), chronic inflammatory conditions (e.g., asthma or arthritis),
CC proliferative retinopathy, atherosclerosis, coronary heart disease,
CC arterial ischaemia, bone disorders (e.g., osteoporosis), and abnormal

CC vascular growth. Polypeptides involved with tissue regeneration and
 CC repair (or nucleic acids encoding them) may be used to promote wound
 CC healing (e.g., of burns, incisions and ulcers), while those with
 CC immunomodulatory activities may be used in the treatment of viral,
 CC bacterial and fungal infections in addition to immune disorders.
 CC Polypeptides with growth factor activity may be used in cell cultures to
 CC promote cell growth. For example, such polypeptides may be used to
 CC manipulate stem cells in culture to give rise to neuroepithelial cells
 CC that can be used to augment or replace cells damaged by illness,
 CC autoimmune disease or accidental damage. The polypeptides and nucleotides
 CC may also be used in the diagnosis of the above conditions, and in drug
 CC screening techniques. The present sequence represents a novel human
 CC polypeptide of the invention
 XX
 XX Sequence 101 AA;

Query Match 48.9%; Score 64; DB 4; Length 101;
 Best Local Similarity 100.0%; Pred. No. 1.1e-59;
 Matches 64; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 MGLSGLLPILVFPFILLGDIQEPGHAEGLGKPCPKIKVECEVEIDQCTKPRDCPENMKC 60
 Db 16 MGLSGLLPILVFPFILLGDIQEPGHAEGLGKPCPKIKVECEVEIDQCTKPRDCPENMKC 75
 Qy 61 CPFS 64
 Db 76 CPFS 79

RESULT 8
 ADA19814
 ID ADA19814 standard; protein; 131 AA.
 XX
 AC ADA19814;
 XX
 XX 20-NOV-2003 (first entry)
 XX
 XX Human DJ11 protein SEQ ID NO:15.

XX DJ11; Kunitz-type protease inhibitor domain; antiinflammatory;
 KW anti-allergic; thrombolytic; anticoagulant; cardiant; vasotropic;
 KW antibacterial; immunosuppressive; antirheumatic; antiarthritic;
 KW nephrotropic; antipsoriatic; vulnary; protease inhibitor; gene therapy;
 KW acute pancreatitis; pulmonary injury; allergy-induced protease release;
 KW deep vein thrombosis; myocardial infarction; shock; septic shock;
 KW hyperfibrinolytic haemorrhage; inflammatory disorder; emphysema;
 KW idiopathic pulmonary fibrosis; rheumatoid arthritis; glomerulonephritis;
 KW chronic inflammatory bowel disease; psoriasis.

XX Homo sapiens.
 XX WO2003070770-A2.
 XX
 XX 28-AUG-2003.
 XX
 XX 18-FEB-2003; 2003WO-EP001629.
 XX
 XX 21-FEB-2002; 2002US-0358683P.
 XX (GENE-) GENEPROT INC.

XX Bougueleret L, Bairoch A, Niknejad A;
 XX WPI; 2003-663849/62.
 XX
 XX New engineered human Kunitz-type protease inhibitor for diagnosing,
 PT preventing or treating conditions associated with excessive proteinase
 PT activity, e.g. inflammation, pulmonary injuries, myocardial infarction or
 PT hemorrhage.

XX Disclosure; Fig 1; 87pp; English.
 XX
 XX The present invention describes an isolated, purified or recombinant DJ11

CC polypeptide comprising a Kunitz-type protease inhibitor domain or its
 CC biologically active portion. The polypeptide comprises at least 98 %
 CC identity to residues 77-127 of a 131 amino acid sequence (S1, see
 CC ADA19800), or to residues 52-102 of a 106 amino acid sequence (S2, see
 CC ADA19801). DJ11 has antiinflammatory, anti-allergic, thrombolytic,
 CC anticoagulant, cardiant, vasotropic, antibacterial, immunosuppressive,
 CC antirheumatic, antiarthritic, nephrotropic, antipsoriatic and vulnary
 CC activities, and can be used as a protease inhibitor and in gene therapy.
 CC Composition and methods from the present invention can be used in
 CC diagnosing, preventing or treating conditions associated with excessive
 CC proteinase activity, such as acute pancreatitis, pulmonary injury,
 CC allergy-induced protease release, deep vein thrombosis, myocardial
 CC infarction, shock (including septic shock), hyperfibrinolytic
 CC haemorrhage, and especially, inflammatory disorders (e.g. emphysema,
 CC idiopathic pulmonary fibrosis, rheumatoid arthritis, glomerulonephritis,
 CC chronic inflammatory bowel disease or psoriasis). The DJ11 proteins may
 CC be used in preserving platelet function, organ preservation or in wound
 CC healing. The polynucleotide sequence encoding DJ11 may be used as
 CC hybridisation probes, in chromosome and gene mapping, in the generation
 CC of antisense RNA and DNA, and as targets for pharmaceutical intervention.
 CC The present sequence represents a human DJ11 protein given in comparison
 CC with DJ11 proteins in the exemplification of the present invention.
 XX
 XX Sequence 131 AA;

Query Match 48.9%; Score 64; DB 7; Length 131;
 Best Local Similarity 100.0%; Pred. No. 1.3e-59;
 Matches 64; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MGLSGLLPILVFPFILLGDIQEPGHAEGLGKPCPKIKVECEVEIDQCTKPRDCPENMKC 60
 Db 1 MGLSGLLPILVFPFILLGDIQEPGHAEGLGKPCPKIKVECEVEIDQCTKPRDCPENMKC 60
 Qy 61 CPFS 64
 Db 61 CPFS 64

RESULT 9
 ADA19804
 ID ADA19804 standard; protein; 43 AA.
 XX
 AC ADA19804;
 XX
 XX 20-NOV-2003 (first entry)
 XX
 XX Engineered human DJ11 partial amino acid sequence SEQ ID NO:5.

XX DJ11; Kunitz-type protease inhibitor domain; antiinflammatory;
 KW anti-allergic; thrombolytic; anticoagulant; cardiant; vasotropic;
 KW antibacterial; immunosuppressive; antirheumatic; antiarthritic;
 KW nephrotropic; antipsoriatic; vulnary; protease inhibitor; gene therapy;
 KW acute pancreatitis; pulmonary injury; allergy-induced protease release;
 KW deep vein thrombosis; myocardial infarction; shock; septic shock;
 KW hyperfibrinolytic haemorrhage; inflammatory disorder; emphysema;
 KW idiopathic pulmonary fibrosis; rheumatoid arthritis; glomerulonephritis;
 KW chronic inflammatory bowel disease; psoriasis.

XX Synthetic.
 XX Homo sapiens.
 XX WO2003070770-A2.
 XX
 XX 28-AUG-2003.
 XX
 XX 18-FEB-2003; 2003WO-EP001629.
 XX
 XX 21-FEB-2002; 2002US-0358683P.
 XX (GENE-) GENEPROT INC.
 XX Bougueleret L, Bairoch A, Niknejad A;
 XX

DR WPI; 2003-663849/62.
XX New engineered human Kunitz-type protease inhibitor for diagnosing,
PT preventing or treating conditions associated with excessive proteinase
PT activity, e.g. inflammation, pulmonary injuries, myocardial infarction or
PT hemorrhage.
XX
PS Disclosure; Page 79; 87pp; English.
XX
XX The present invention describes an isolated, purified or recombinant DJ11
CC polypeptide comprising a Kunitz-type protease inhibitor domain or its
CC polypeptidally active portion. The polypeptide comprises at least 98 %
CC identity to residues 77-127 of a 131 amino acid sequence (S1, see
CC ADA19800), or to residues 52-102 of a 106 amino acid sequence (S2, see
CC ADA19801). DJ11 has antiinflammatory, anti-allergic, thrombolytic,
CC anticoagulant, cardiant, vasotropic, antibacterial, immunosuppressive,
CC antirheumatic, antiarthritic, nephrotropic, antipariatic and vulnary
CC activities, and can be used as a protease inhibitor and in gene therapy.
CC Composition and methods from the present invention can be used in
CC diagnosing, preventing or treating conditions associated with excessive
CC proteinase activity, such as acute pancreatitis, pulmonary injury,
CC allergy-induced protease release, deep vein thrombosis, myocardial
CC infarction, shock (including septic shock), hyperfibrinolytic
CC haemorrhage, and especially, inflammatory disorders (e.g. emphysema,
CC idiopathic pulmonary fibrosis, rheumatoid arthritis, glomerulonephritis,
CC chronic inflammatory bowel disease or psoriasis). The DJ11 proteins may
CC be used in preserving platelet function, organ preservation or in wound
CC healing. The polynucleotide sequence encoding DJ11 may be used as
CC hybridisation probes, in chromosome and gene mapping, in the generation
CC of antisense RNA and DNA, and as targets for pharmaceutical intervention.
CC The present sequence represents a partial engineered human DJ11 protein
CC amino acid sequence from the present invention.
XX
SQ Sequence 43 AA;
Query Match 25.2%; Score 33; DB 7; Length 43;
Best Local Similarity 100.0%; Pred. No. 4.6e-27;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 32 PCPKIKVEVEEIDQCTKPRDCPENMKCCPFS 64
DB 1 PCPKIKVEVEEIDQCTKPRDCPENMKCCPFS 33
RESULT 10
ADM85103
ID ADM85103 standard; protein; 179 AA.
XX
XX ADM85103;
XX
XX 18-NOV-2004 (first entry)
XX
XX Human diagnostic and therapeutic pproteins SEQ ID NO:5352.
XX
XX gene therapy; human diagnostic and therapeutic polynucleotide; dithp.
XX
XX Homo sapiens.
XX
XX WO2004023973-A2.
XX
XX 25-MAR-2004.
XX
XX 12-SEP-2003; 2003WO-05028227.
XX
XX 12-SEP-2002; 2002US-0410259P.
XX
XX 12-SEP-2002; 2002US-0410260P.
XX
XX (INCY-) INCYTE CORP.
XX
XX Schmidt JP, Wright RJ, Bruns CM, Marjanovic MM, Shen F;
PI Harthshorne TA, Suchorolski MT, Altus CM, Pitts SJ, Elder LV;
PI Mooney EM, Deleage AM, Panesar IS, Banville SC, Reddy TP;
PI Stevens KA, Blanchard JL, Panzer SR, Wang X, Au AP, Gerstin EH;

PI Peralta CH, Anderson SB, Rioux P, Shen EJ, Wu MC, Stuve LL;
PI Lagace RE, Spiro FA, Stewart EA, Wingrove J, Vitt UA, Kirtson ES;
PI Xu Y, Kwong M, Policky JL, Hurwitz BL, Ma Y, Jackson JL, Gietzen D;
PI Patury S, Shi X, Suarez CJ;
XX
XX WPI; 2004-329368/30.
XX
XX N-PSDB; ACN43755.
XX
XX New diagnostic and therapeutic polynucleotides and polypeptides, useful
PT in diagnosing a condition, disease or disorder associated with human
PT molecules, e.g. autoimmune or inflammatory disorders, in gene therapy or
PT in gene mapping.
XX
XX Claim 27; Page; 190pp; English.
XX
XX The invention relates to novel diagnostic and therapeutic polynucleotides
CC selected from one of the 2722 sequences defined in the specification. A
CC polynucleotide of the invention may have a use in gene therapy. The human
CC polynucleotide and therapeutic polynucleotides (dithp) or polypeptides may be
CC used to diagnose a particular condition, disease or disorder associated
CC with human molecules, e.g. cell proliferative disorders,
CC autoimmune/inflammatory disorder, developmental disorder, endocrine
CC disorder, neurological disorders, gastrointestinal disorders, or
CC infections caused by virus, bacteria, fungi or parasite. The dithp
CC molecules may also be used in genetic mapping, in identifying individuals
CC from minute biological samples, in detecting single nucleotide
CC polymorphisms, as molecular weight markers, and for somatic or germline
CC gene therapy. The present sequence represents a dithp protein of the
CC invention. Note: The sequence data for this patent is not represented in
CC the printed specification, but was obtained in electronic format directly
CC from WIPO at www.wipo.int/pct/en/sequences/listing.htm
XX
XX Sequence 179 AA;
Query Match 25.2%; Score 33; DB 8; Length 179;
Best Local Similarity 100.0%; Pred. No. 1.5e-26;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 32 PCPKIKVEVEEIDQCTKPRDCPENMKCCPFS 64
DB 132 PCPKIKVEVEEIDQCTKPRDCPENMKCCPFS 164
RESULT 11
ADA19803
ID ADA19803 standard; peptide; 30 AA.
XX
XX ADA19803;
XX
XX 20-NOV-2003 (first entry)
XX
XX Engineered human DJ11 partial amino acid sequence SEQ ID NO:4.
XX
XX DJ11; Kunitz-type protease inhibitor domain; antiinflammatory;
XX antiallergic; thrombolytic; anticoagulant; cardiant; vasotropic;
XX antibacterial; immunosuppressive; antirheumatic; antipariatic;
XX nephrotropic; antipariatic; vulnary; allergy-induced protease release;
XX acute pancreatitis; pulmonary injury; allergic-induced protease release;
XX deep vein thrombosis; myocardial infarction; shock; septic shock;
XX hyperfibrinolytic haemorrhage; inflammatory disorder; emphysema;
XX idiopathic pulmonary fibrosis; rheumatoid arthritis; glomerulonephritis;
XX chronic inflammatory bowel disease; psoriasis.
XX
XX Synthetic.
XX
XX Homo sapiens.
XX
XX WO2003070770-A2.
XX
XX 28-AUG-2003.
XX
XX 18-FEB-2003; 2003WO-EP001629.
XX
XX 21-FEB-2002; 2002US-0358683P.

XX PA (GENE-) GENEPROT INC.
 XX PI Bougueleret L, Bairoch A, Niknejad A;
 XX DR WPI; 2003-663849/62.
 XX XX
 XX PT New engineered human Kunitz-type protease inhibitor for diagnosing,
 PT preventing or treating conditions associated with excessive proteinase
 PT activity, e.g. inflammation, pulmonary injuries, myocardial infarction or
 PT hemorrhage.
 XX PT
 XX PS Disclosure; Page 79; 87pp; English.
 XX CC The present invention describes an isolated, purified or recombinant DJ11
 CC polypeptide comprising a Kunitz-type protease inhibitor domain or its
 CC biologically active portion. The polypeptide comprises at least 98 %
 CC identity to residues 77-127 of a 131 amino acid sequence (S1, see
 CC ADA19800), or to residues 52-102 of a 106 amino acid sequence (S2, see
 CC ADA19801). DJ11 has antiinflammatory, antiallergic, thrombolytic,
 CC anticoagulant, cardiant, vasotropic, antibacterial, immunosuppressive,
 CC antirheumatic, antiarthritic, nephrotropic, antipsoriatic and vulnary
 CC activities, and can be used as a protease inhibitor and in gene therapy.
 CC Composition and methods from the present invention can be used in
 CC diagnosing, preventing or treating conditions associated with excessive
 CC proteinase activity, such as acute pancreatitis, pulmonary injury,
 CC allergy-induced protease release, deep vein thrombosis, myocardial
 CC infarction, shock (including septic shock), hyperfibrinolytic
 CC haemorrhage, and especially, inflammatory disorders (e.g. emphysema,
 CC idiopathic pulmonary fibrosis, rheumatoid arthritis, glomerulonephritis,
 CC chronic inflammatory bowel disease or psoriasis). The DJ11 proteins may
 CC be used in preserving platelet function, organ preservation or in wound
 CC healing. The polynucleotide sequence encoding DJ11 may be used as
 CC hybridisation probes, in chromosome and gene mapping, in the generation
 CC of antisense RNA and DNA, and as targets for pharmaceutical intervention.
 CC The present sequence represents a partial engineered human DJ11 protein
 CC amino acid sequence from the present invention.
 XX CC
 XX SQ Sequence 30 AA;
 Query Match 22.9%; Score 30; DB 7; Length 30;
 Best Local Similarity 100.0%; Pred. No. 5.2e-24;
 Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 MGLSGLPILVPFILLGDIQPGHAEGLG 30
 Db 1 MGLSGLPILVPFILLGDIQPGHAEGLG 30
 RESULT 12
 ADA19805
 ID ADA19805 standard; peptide; 24 AA.
 XX AC ADA19805;
 XX XX
 XX DT 20-NOV-2003 (first entry)
 XX DE Engineered human DJ11 partial amino acid sequence SEQ ID NO:6.
 XX KW DJ11; Kunitz-type protease inhibitor domain; antiinflammatory;
 KW antiallergic; thrombolytic; anticoagulant; cardiant; vasotropic;
 KW antibacterial; immunosuppressive; antirheumatic; antiarthritic;
 KW nephrotropic; antipsoriatic; vulnary; protease inhibitor; gene therapy;
 KW acute pancreatitis; pulmonary injury; allergy-induced protease release;
 KW deep vein thrombosis; myocardial infarction; shock; septic shock;
 KW hyperfibrinolytic haemorrhage; inflammatory disorder; emphysema;
 KW idiopathic pulmonary fibrosis; rheumatoid arthritis; glomerulonephritis;
 KW chronic inflammatory bowel disease; psoriasis.
 XX OS Synthetic.
 OS Homo sapiens.
 XX XX
 XX PN WO2003070770-A2.

XX PD 28-AUG-2003.
 XX PF 18-FEB-2003; 2003WO-EP001629.
 XX PR 21-FEB-2002; 2002US-0358683P.
 XX XX
 XX PA (GENE-) GENEPROT INC.
 XX PI Bougueleret L, Bairoch A, Niknejad A;
 XX DR WPI; 2003-663849/62.
 XX XX
 XX PT New engineered human Kunitz-type protease inhibitor for diagnosing,
 PT preventing or treating conditions associated with excessive proteinase
 PT activity, e.g. inflammation, pulmonary injuries, myocardial infarction or
 PT hemorrhage.
 XX PT
 XX PS Disclosure; Page 79-80; 87pp; English.
 XX CC The present invention describes an isolated, purified or recombinant DJ11
 CC polypeptide comprising a Kunitz-type protease inhibitor domain or its
 CC biologically active portion. The polypeptide comprises at least 98 %
 CC identity to residues 77-127 of a 131 amino acid sequence (S1, see
 CC ADA19800), or to residues 52-102 of a 106 amino acid sequence (S2, see
 CC ADA19801). DJ11 has antiinflammatory, antiallergic, thrombolytic,
 CC anticoagulant, cardiant, vasotropic, antibacterial, immunosuppressive,
 CC antirheumatic, antiarthritic, nephrotropic, antipsoriatic and vulnary
 CC activities, and can be used as a protease inhibitor and in gene therapy.
 CC Composition and methods from the present invention can be used in
 CC diagnosing, preventing or treating conditions associated with excessive
 CC proteinase activity, such as acute pancreatitis, pulmonary injury,
 CC allergy-induced protease release, deep vein thrombosis, myocardial
 CC infarction, shock (including septic shock), hyperfibrinolytic
 CC haemorrhage, and especially, inflammatory disorders (e.g. emphysema,
 CC idiopathic pulmonary fibrosis, rheumatoid arthritis, glomerulonephritis,
 CC chronic inflammatory bowel disease or psoriasis). The DJ11 proteins may
 CC be used in preserving platelet function, organ preservation or in wound
 CC healing. The polynucleotide sequence encoding DJ11 may be used as
 CC hybridisation probes, in chromosome and gene mapping, in the generation
 CC of antisense RNA and DNA, and as targets for pharmaceutical intervention.
 CC The present sequence represents a partial engineered human DJ11 protein
 CC amino acid sequence from the present invention.
 XX CC
 XX SQ Sequence 24 AA;
 Query Match 18.3%; Score 24; DB 7; Length 24;
 Best Local Similarity 100.0%; Pred. No. 1e-17;
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 75 DICSMPOEAGPCLASTPHWYNNK 98
 Db 1 DICSMPOEAGPCLASTPHWYNNK 24
 RESULT 13
 ADA19806
 ID ADA19806 standard; peptide; 33 AA.
 XX AC ADA19806;
 XX XX
 XX DT 20-NOV-2003 (first entry)
 XX DE Engineered human DJ11 partial amino acid sequence SEQ ID NO:7.
 XX KW DJ11; Kunitz-type protease inhibitor domain; antiinflammatory;
 KW antiallergic; thrombolytic; anticoagulant; cardiant; vasotropic;
 KW antibacterial; immunosuppressive; antirheumatic; antiarthritic;
 KW nephrotropic; antipsoriatic; vulnary; protease inhibitor; gene therapy;
 KW acute pancreatitis; pulmonary injury; allergy-induced protease release;
 KW deep vein thrombosis; myocardial infarction; shock; septic shock;
 KW hyperfibrinolytic haemorrhage; inflammatory disorder; emphysema;
 KW idiopathic pulmonary fibrosis; rheumatoid arthritis; glomerulonephritis;

KW chronic inflammatory bowel disease; psoriasis.
 XX Synthetic.
 OS Homo sapiens.
 XX WO2003070770-A2.
 XX 28-AUG-2003.
 XX 18-FEB-2003; 2003WO-EP001629.
 XX 21-FEB-2002; 2002US-0358683P.
 XX (GENE-) GENEPROT INC.
 XX Bougueleret L, Bairoch A, Niknejad A;
 XX WPI; 2003-663849/62.
 XX New engineered human Kunitz-type protease inhibitor for diagnosing,
 XX preventing or treating conditions associated with excessive proteinase
 XX activity, e.g. inflammation, pulmonary injuries, myocardial infarction or
 XX hemorrhage.
 XX Disclosure; Page 80; 87pp; English.
 XX The present invention describes an isolated, purified or recombinant DJ11
 XX polypeptide comprising a Kunitz-type protease inhibitor domain or its
 XX biologically active portion. The polypeptide comprises at least 98 %
 XX identity to residues 77-127 of a 131 amino acid sequence (S1, see
 XX ADA19800), or to residues 52-102 of a 106 amino acid sequence (S2, see
 XX ADA19801). DJ11 has antiinflammatory, antiallergic, thrombolytic,
 XX anticoagulant, cardiant, vasotropic, antibacterial, immunosuppressive,
 XX antirheumatic, antiarthritic, nephrotropic, antiporiatic and vulnary
 XX activities, and can be used as a protease inhibitor and in gene therapy.
 XX Composition and methods from the present invention can be used in
 XX diagnosing, preventing or treating conditions associated with excessive
 XX proteinase activity, such as acute pancreatitis, pulmonary injury,
 XX allergy-induced protease release, deep vein thrombosis, myocardial
 XX infarction, shock (including septic shock), hyperfibrinolytic
 XX haemorrhage, and especially, inflammatory disorders (e.g. emphysema,
 XX idiopathic pulmonary fibrosis, rheumatoid arthritis, glomerulonephritis,
 XX chronic inflammatory bowel disease or psoriasis). The DJ11 proteins may
 XX be used in preserving platelet function, organ preservation or in wound
 XX healing. The polynucleotide sequence encoding DJ11 may be used as
 XX hybridisation probes, in chromosome and gene mapping, in the generation
 XX of antisense RNA and DNA, and as targets for pharmaceutical intervention.
 XX The present sequence represents a partial engineered human DJ11 protein
 XX amino acid sequence from the present invention.
 XX Sequence 33 AA;
 XX Query Match 16.0%; Score 21; DB 7; Length 33;
 XX Best Local Similarity 100.0%; Pred. No. 2.1e-14;
 XX Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 111 QGNNNNFQTEAICLVCKKYH 131
 DB 13 QGNNNNFQTEAICLVCKKYH 33
 RESULT 14
 ADA19809
 ID ADA19809 standard; peptide; 33 AA.
 XX ADA19809;
 XX 20-NOV-2003 (first entry)
 XX Engineered human DJ11 partial amino acid sequence SEQ ID NO:10.
 DE DJ11; Kunitz-type protease inhibitor domain; antiinflammatory;
 KW antiallergic; thrombolytic; anticoagulant; cardiant; vasotropic;
 XX

KW antibacterial; immunosuppressive; antirheumatic; antiarthritic;
 KW nephrotropic; antiporiatic; vulnary; protease inhibitor; gene therapy;
 KW acute pancreatitis; pulmonary injury; allergy-induced protease release;
 KW deep vein thrombosis; myocardial infarction; shock; septic shock;
 KW hyperfibrinolytic haemorrhage; inflammatory disorder; emphysema;
 KW idiopathic pulmonary fibrosis; rheumatoid arthritis; glomerulonephritis;
 KW chronic inflammatory bowel disease; psoriasis.
 XX Synthetic.
 OS Homo sapiens.
 XX WO2003070770-A2.
 XX 28-AUG-2003.
 XX 18-FEB-2003; 2003WO-EP001629.
 XX 21-FEB-2002; 2002US-0358683P.
 XX (GENE-) GENEPROT INC.
 XX Bougueleret L, Bairoch A, Niknejad A;
 XX WPI; 2003-663849/62.
 XX New engineered human Kunitz-type protease inhibitor for diagnosing,
 XX preventing or treating conditions associated with excessive proteinase
 XX activity, e.g. inflammation, pulmonary injuries, myocardial infarction or
 XX hemorrhage.
 XX Disclosure; Page 82-83; 87pp; English.
 XX The present invention describes an isolated, purified or recombinant DJ11
 XX polypeptide comprising a Kunitz-type protease inhibitor domain or its
 XX biologically active portion. The polypeptide comprises at least 98 %
 XX identity to residues 77-127 of a 131 amino acid sequence (S1, see
 XX ADA19800), or to residues 52-102 of a 106 amino acid sequence (S2, see
 XX ADA19801). DJ11 has antiinflammatory, antiallergic, thrombolytic,
 XX anticoagulant, cardiant, vasotropic, antibacterial, immunosuppressive,
 XX antirheumatic, antiarthritic, nephrotropic, antiporiatic and vulnary
 XX activities, and can be used as a protease inhibitor and in gene therapy.
 XX Composition and methods from the present invention can be used in
 XX diagnosing, preventing or treating conditions associated with excessive
 XX proteinase activity, such as acute pancreatitis, pulmonary injury,
 XX allergy-induced protease release, deep vein thrombosis, myocardial
 XX infarction, shock (including septic shock), hyperfibrinolytic
 XX haemorrhage, and especially, inflammatory disorders (e.g. emphysema,
 XX idiopathic pulmonary fibrosis, rheumatoid arthritis, glomerulonephritis,
 XX chronic inflammatory bowel disease or psoriasis). The DJ11 proteins may
 XX be used in preserving platelet function, organ preservation or in wound
 XX healing. The polynucleotide sequence encoding DJ11 may be used as
 XX hybridisation probes, in chromosome and gene mapping, in the generation
 XX of antisense RNA and DNA, and as targets for pharmaceutical intervention.
 XX The present sequence represents a partial engineered human DJ11 protein
 XX amino acid sequence from the present invention.
 XX Sequence 33 AA;
 XX Query Match 16.0%; Score 21; DB 7; Length 33;
 XX Best Local Similarity 100.0%; Pred. No. 2.1e-14;
 XX Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 111 QGNNNNFQTEAICLVCKKYH 131
 DB 13 QGNNNNFQTEAICLVCKKYH 33
 RESULT 15
 ADA19813
 ID ADA19813 standard; protein; 134 AA.
 XX ADA19813;
 XX

DT 20-NOV-2003 (first entry)
 DE Mouse EPPIN protein SEQ ID NO:14.
 XX
 KW DJ11; Kunitz-type protease inhibitor domain; antiinflammatory;
 KW anti-allergic; thrombolytic; anticoagulant; cardiant; vasotropic;
 KW antibacterial; immunosuppressive; antirheumatic; antiarthritic;
 KW nephrotropic; antiporiatic; vulnary; protease inhibitor; gene therapy;
 KW acute pancreatitis; pulmonary injury; allergy-induced protease release;
 KW deep vein thrombosis; myocardial infarction; shock; septic shock;
 KW hyperfibrinolytic haemorrhage; inflammatory disorder; emphysema;
 KW idiopathic pulmonary fibrosis; rheumatoid arthritis; glomerulonephritis;
 KW chronic inflammatory bowel disease; psoriasis; EPPIN.
 XX
 OS Mus musculus.
 XX
 XX WO2003070770-A2.
 XX
 XX 28-AUG-2003.
 XX
 XX 18-FEB-2003; 2003WO-EP001629.
 XX
 XX 21-FEB-2002; 2002US-0358683P.
 XX
 XX (GENE-) GENEPROT INC.
 XX
 XX Bougueleret L, Bairoch A, Niknejad A;
 XX
 XX WPI; 2003-663849/62.
 XX
 XX New engineered human Kunitz-type protease inhibitor for diagnosing,
 XX preventing or treating conditions associated with excessive proteinase
 XX activity, e.g. inflammation, pulmonary injuries, myocardial infarction or
 XX hemorrhage.
 XX
 XX Disclosure; Fig 1; 87pp; English.
 XX
 XX The present invention describes an isolated, purified or recombinant DJ11
 XX polypeptide comprising a Kunitz-type protease inhibitor domain or its
 XX biologically active portion. The polypeptide comprises at least 98 %
 XX identity to residues 77-127 of a 131 amino acid sequence (S1, see
 XX ADA19800), or to residues 52-102 of a 106 amino acid sequence (S2, see
 XX ADA19801). DJ11 has antiinflammatory, anti-allergic, thrombolytic,
 XX anticoagulant, cardiant, vasotropic, antibacterial, immunosuppressive,
 XX antirheumatic, antiarthritic, nephrotropic, antiporiatic and vulnary
 XX activities, and can be used as a protease inhibitor and in gene therapy.
 XX Composition and methods from the present invention can be used in
 XX diagnosing, preventing or treating conditions associated with excessive
 XX proteinase activity, such as acute pancreatitis, pulmonary injury,
 XX allergy-induced protease release, deep vein thrombosis, myocardial
 XX infarction, shock (including septic shock) hyperfibrinolytic
 XX haemorrhage, and especially, inflammatory disorders (e.g. emphysema,
 XX idiopathic pulmonary fibrosis, rheumatoid arthritis, glomerulonephritis,
 XX chronic inflammatory bowel disease or psoriasis). The DJ11 proteins may
 XX be used in preserving platelet function, organ preservation or in wound
 XX healing. The polynucleotide sequence encoding DJ11 may be used as
 XX hybridisation probes, in chromosome and gene mapping, in the generation
 XX of antisense RNA and DNA, and as targets for pharmaceutical intervention.
 XX The present sequence represents a mouse EPPIN protein given in comparison
 XX with DJ11 proteins in the exemplification of the present invention.
 XX
 XX Sequence 134 AA;
 XX
 XX Query Match 10.7%; Score 14; DB 7; Length 134;
 XX Best Local Similarity 100.0%; Pred. No. 1.9e-06;
 XX Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 XX
 XX QY 105 FYGGCGGNNNNFQ 118
 XX |
 XX 105 FYGGCGGNNNNFQ 118
 XX
 XX RESULT 16
 XX
 XX Query Match 10.7%; Score 12; DB 4; Length 43;
 XX Best Local Similarity 100.0%; Pred. No. 9.6e-05;
 XX Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 XX
 XX QY 107 YGGCGGNNNNFQ 118
 XX |
 XX 21 YGGCGGNNNNFQ 32
 XX
 XX RESULT 17
 XX AAW75257
 XX ID AAW75257 standard; protein; 51 AA.
 XX
 XX AC AAW75257;
 XX
 XX DT 29-JAN-1999 (first entry)
 XX
 XX DE Fragment of human secreted protein encoded by gene 24.

AAE13096
 ID AAE13096 standard; peptide; 43 AA.
 XX
 XX AAE13096;
 XX
 XX 28-JAN-2002 (first entry)
 XX
 XX Human serine proteinase inhibitor BTL.009 peptide fragment #2.
 XX
 XX Human, BTL.009 protein; serine proteinase inhibitor; cytostatic;
 XX nephrotropic; idiopathic pulmonary fibrosis; cystic fibrosis; emphysema;
 XX rheumatoid arthritis; adult respiratory distress syndrome; angioplasty;
 XX blood coagulation; glomerulonephritis; prophylactic; platelet activation;
 XX neutrophil; monocyte; granulocyte; organ failure; inflammatory disease;
 XX elastase inhibitor; chymotrypsin inhibitor; lung injury; vascular injury;
 XX therapeutic.
 XX
 XX Homo sapiens.
 XX
 XX US6294648-B1.
 XX
 XX 25-SEP-2001.
 XX
 XX 20-JUL-1999; 99US-00358569.
 XX
 XX 20-JUL-1999; 99US-00358569.
 XX
 XX (FARB) BAYER CORP.
 XX
 XX Delaria K, Roczniaak S, Davies C;
 XX
 XX WPI; 2001-662224/76.
 XX
 XX New isolated protein for inhibiting human serine proteinase activity in the
 XX treatment of e.g. emphysema and adult respiratory distress syndrome.
 XX
 XX Disclosure; Col 5-6; 16pp; English.
 XX
 XX The invention relates to human BTL.009 protein, a serine proteinase
 XX inhibitor of the Kunitz family that exhibits greater potency towards
 XX neutral serine proteinases. BTL.009 protein is found to inhibit leukocyte
 XX elastase, chymotrypsin-like protease and trypsin-like protease. BTL.009
 XX protein is useful for treating emphysema, idiopathic pulmonary fibrosis,
 XX adult respiratory distress syndrome, cystic fibrosis, rheumatoid
 XX arthritis, organ failure, glomerulonephritis, other inflammatory diseases
 XX and diseases involving lung and vascular injury. BTL.009 is also useful
 XX for preventing neutrophil and monocyte activation and formation of active
 XX oxygen species during the oxidative burst of stimulated granulocytes.
 XX BTL.009 is useful for reducing platelet activation and blood coagulation
 XX and for the prophylactic or therapeutic treatment of patients undergoing
 XX angioplasty. The present sequence is human serine proteinase inhibitor
 XX BTL.009 peptide fragment related to the invention
 XX
 XX Sequence 43 AA;
 XX
 XX Query Match 9.2%; Score 12; DB 4; Length 43;
 XX Best Local Similarity 100.0%; Pred. No. 9.6e-05;
 XX Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 XX
 XX QY 107 YGGCGGNNNNFQ 118
 XX |
 XX 21 YGGCGGNNNNFQ 32
 XX
 XX RESULT 17
 XX AAW75257
 XX ID AAW75257 standard; protein; 51 AA.
 XX
 XX AC AAW75257;
 XX
 XX DT 29-JAN-1999 (first entry)
 XX
 XX DE Fragment of human secreted protein encoded by gene 24.

XX Human; secreted protein; fusion protein; gene therapy; protein therapy;
 KW diagnosis; tissue; cancer; tumour; neurodegenerative disorder; leukaemia;
 KW developmental abnormality; foetal deficiency; blood; allergy; renal;
 KW immune system; asthma; lymphocytic disease; brain; hepatic; lymphoma;
 KW inflammation; ischaemic shock; Alzheimer's disease; restenosis; AIDS;
 KW cognitive disorder; schizophrenia; prostate; obesity; osteoclast; thymus;
 KW osteoporosis; arthritis; testis; lung; thyroiditis; thyroid; digestion;
 KW endocrine; metabolism; regulation; malabsorption; gastritis; neoplasm.
 XX Homo sapiens.
 XX WO9840483-A2.
 XX 17-SEP-1998.
 XX 12-MAR-1998; 98WO-US004858.
 XX 14-MAR-1997; 97US-0040710P.
 PR 14-MAR-1997; 97US-0040762P.
 PR 30-MAY-1997; 97US-0048100P.
 PR 30-MAY-1997; 97US-0048189P.
 PR 30-MAY-1997; 97US-0048357P.
 PR 30-MAY-1997; 97US-0050934P.
 PR 06-JUN-1997; 97US-0048970P.
 PR 05-SEP-1997; 97US-0057765P.
 PR 19-DEC-1997; 97US-0068368P.
 XX (HUMA-) HUMAN GENOME SCI INC.
 XX Ruben SM, Rosen CA, Li Y, Zeng Z, Kyaw H, Fischer CL, Li H;
 PI Soppet DR, Gentz RL, Wei YF, Moore PA, Young PE, Greene JM;
 PI Ferrie AM;
 XX WPI; 1998-520811/44.
 DR N-PSDB; AAV34309.
 XX Isolated human poly:nucleotide(s) encoding secretory peptide(s) - used to
 PT develop products for the diagnosis and treatment of e.g. inflammation,
 PT cancers, CNS disorders or immune system disorders.
 XX Disclosure; Page 24; 201pp; English.
 CC This sequence represents a fragment of a secreted human protein encoded
 CC by the nucleic acid molecule designated Gene 24 (AAV34309). The gene can
 CC be used to generate fusion proteins by linking to the gene to a human
 CC immunoglobulin Fc portion (e.g. AAV34277) for increasing the stability of
 CC the fused protein as compared to the human protein only. The invention
 CC relates to 28 novel genes and their fragments (nucleic acid sequences:
 CC AAV34286-V34325; amino acid sequences AAV75196-W75235) which are useful
 CC for preventing, treating or ameliorating medical conditions e.g. by
 CC protein or gene therapy. Also, pathological conditions can be diagnosed
 CC by determining the amount of the new polypeptides in a sample or by
 CC determining the presence of mutations in the new polynucleotides.
 CC Specific uses are described for each of the 28 polynucleotides, based on
 CC which tissues they are most highly expressed in (see AAV34286 for
 CC described uses)
 XX Sequence 51 AA;
 SQ Query Match 9.2%; Score 12; DB 2; Length 51;
 Best Local Similarity 100.0%; Pred. No. 0.00011;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 107 YGCGCGNNNFQ 118
 DB 31 YGCGCGNNNFQ 42
 RESULT 18
 AAE27025
 ID AAE27025 standard; protein; 51 AA.
 XX

AC AAE27025;
 XX 13-DEC-2002 (first entry)
 DT Human gene 24 encoded secreted protein variant, SEQ ID NO:118.
 DE Human; immunodeficiency; X-linked agammaglobulinemia; septic shock;
 XX autoimmune disorder; rheumatoid arthritis; multiple sclerosis; cancer;
 KW Grave's disease; diabetes mellitus; haematopoietic disorder; stroke;
 KW respiratory disorder; asthma; allergy; gastrointestinal disorder;
 KW inflammatory bowel disease; neurodegenerative disorder; hepatitis;
 KW Parkinson's disease; Alzheimer's disease; cardiovascular disorder;
 KW atherosclerosis; myocarditis; renal disorder; fungicide; virucide;
 KW hyperproliferative disorder; acute glomerulonephritis; tonsillitis;
 KW respiratory disorder; rhinitis; sinusitis; neurological disease;
 KW endocrine disorder; Addison's disease; reproductive system disorder;
 KW endometriosis; vasotropic; vulnary; cytostatic; nootropic; cardiant;
 KW anti-HIV; tranquilliser; gout; antiparasitic.
 XX Homo sapiens.
 OS US2002077287-A1.
 PN 20-JUN-2002.
 XX 11-MAY-2001; 2001US-00852659.
 PF 11-SEP-1998; 98US-00152060.
 XX (RUBE/) RUBEN S M.
 PA (ROSE/) ROSEN C A.
 PA (LIYY/) LI Y.
 PA (ZENG/) ZENG Z.
 PA (KYAW/) KYAW H.
 PA (FISC/) FISCHER C L.
 PA (LIHH/) LI H.
 PA (SOPP/) SOPPET D R.
 PA (GENTZ/) GENTZ R L.
 PA (WEIY/) WEI Y.
 PA (MOOR/) MOORE P A.
 PA (YOUN/) YOUNG P E.
 PA (GREE/) GREENE J M.
 PA (FERR/) FERRIE A M.
 XX Ruben SM, Rosen CA, Li Y, Zeng Z, Kyaw H, Fischer CL, Li H;
 PI Soppet DR, Gentz RL, Wei Y, Moore PA, Young PE, Greene JM;
 PI Ferrie AM;
 XX WPI; 2002-598780/64.
 DR Novel human secreted polypeptides and polynucleotides for diagnosing,
 PT preventing, treating immune, hyperproliferative, cardiovascular,
 PT neurological, reproductive disorders and identifying modulators of
 PT therapeutic use.
 XX Disclosure; Page 16; 209pp; English.
 PS AAD44636-AAD44676 represent cDNAs corresponding to 28 human secreted
 CC protein genes, and AAE26959-AAE26999 represent the proteins they encode.
 CC AAE27000-AAE27025 represent human secreted protein fragments or their
 CC variants. The secreted proteins and genes are useful for preventing,
 CC treating or ameliorating medical conditions, e.g., by protein or gene
 CC therapy. Specific uses are described for each of the 28 genes, based on
 CC the tissues in which they are most highly expressed and include
 CC developing products for the diagnosis or treatment of immunodeficiencies,
 CC e.g., X-linked agammaglobulinemia, B cell immunodeficiencies, severe
 CC combined immunodeficiencies, autoimmune disorders e.g., systemic lupus
 CC erythematosus, rheumatoid arthritis, multiple sclerosis, autoimmune
 CC thyroiditis, autoimmune haemolytic anaemia, Goodpasture's syndrome,
 CC Grave's disease, diabetes mellitus, dermatitis, inflammatory conditions
 CC including septic shock, sepsis, reperfusion injury, inflammatory bowel
 CC disease, Crohn's disease, haematopoietic disorders, respiratory disorders
 CC e.g., asthma and allergy, gastrointestinal disorders e.g., inflammatory

CC bowel disease), cancers e.g., gastric, ovarian, lung, liver, bladder and
CC breast), central nervous system (CNS) disorders e.g., ischaemic brain
CC injury and/or stroke, neurodegenerative disorders e.g., Parkinson's
CC disease and Alzheimer's disease, AIDS-related dementia and prion disease,
CC cardiovascular disorders e.g., myocarditis, arrhythmias, atherosclerosis,
CC inflammatory disorders e.g., hepatitis, gout, trauma, pancreatitis,
CC sarcoidosis and allogeneic transplant rejection, blood-related disorder
CC (thrombosis, arterial thrombosis, atherosclerosis), hyperproliferative
CC disorders, respiratory disorders e.g. rhinitis, sinusitis, tonsillitis,
CC lung cancer, allergic disorders, pneumonitis, renal disorders. e.g. acute
CC glomerulonephritis, neurological diseases, liver disorders, endocrine
CC disorders e.g., hyperthyroidism, Addison's disease, hyperpituitarism,
CC infectious diseases and reproductive system disorders e.g. endometriosis.
CC The present sequence represents a human secreted protein variant of the
CC invention
XX
SQ Sequence 51 AA;
Query Match 9.2%; Score 12; DB 5; Length 51;
Best Local Similarity 100.0%; Pred. No. 0.00011; Mismatches 0; Gaps 0;
Matches 12; Conservative 0; Indels 0; Gaps 0;
Qy 107 YGCGCGNNNNFQ 118
Db 31 YGCGCGNNNNFQ 42
RESULT 19
AAE27163 Human gene 24 encoded secreted protein fragment kunitz-type domain.
ID AAE27163 standard; protein; 51 AA.
AC AAE27163;
XX
DT 13-DEC-2002 (first entry)
XX
DE Human gene 24 encoded secreted protein fragment kunitz-type domain.
XX
KW Human; secreted protein; autoimmune disease; hyperproliferative disorder;
KW rheumatoid arthritis; neoplasm; cerebrovascular disorder; angiogenesis;
KW cerebral ischaemia; cardiovascular disorder; nervous system disorder;
KW cardiac arrest; Alzheimer's disease; ocular disorder; wound healing;
KW infection; corneal infection; skin aging; food additive; preservative;
KW tissue regeneration; immunosuppressive; antiproliferative; cytostatic;
KW cardiant; vasotropic; cerebroprotective; nootropic; neuroprotective;
KW antibacterial; virucide; fungicide; ophthalmological; gene therapy;
KW vulnerary.
XX
OS Homo sapiens.
XX
PN US2002076756-A1.
XX
PD 20-JUN-2002.
XX
PF 11-MAY-2001; 2001US-00853161.
XX
PR 02-FEB-2001; 2001US-0265583P.
XX
PA (RUBE/) RUBEN S M.
PA (ROSE/) ROSEN C A.
PA (LIYY/) LI Y.
PA (ZENG/) ZENG Z.
PA (KYAW/) KYAW H.
PA (FISC/) FISCHER C L.
PA (LIHH/) LI H.
PA (SOPP/) SOPPET D R.
PA (GENT/) GENTZ R L.
PA (WEIY/) WEI Y.
PA (MOOR/) MOORE P A.
PA (YOUN/) YOUNG P E.
PA (GREE/) GREENE J M.
PA (FERR/) FERRIE A M.
XX
PI Ruben SM, Rosen CA, Li Y, Zeng Z, Kyaw H, Fischer CL, Li H;

PI Soppet DR, Gentz RL, Wei Y, Moore PA, Young PE, Greene JM;
PI Ferrie AM;
XX
XX WPI; 2002-574454/61.
XX
XX New nucleic acid molecules encoding 28 human secreted proteins, useful
XX for diagnosing, preventing, treating or ameliorating medical conditions
XX PT and as food additives or preservatives.
XX
XX Disclosure; Page 16; 209pp; English.
XX
XX AAD4854-AAD4984 represent cDNAs corresponding to 28 human secreted
XX protein genes, and AAE27097-AAE27137 represent the proteins they encode.
XX AAE27138-AAE27164 represent human secreted protein fragments. The genes
XX and their corresponding secreted proteins are useful for preventing,
XX treating or ameliorating medical conditions, e.g., by protein or gene
XX therapy. Secreted protein sequences of the invention are useful for the
XX diagnosis or treatment of disorders such as autoimmune diseases (e.g.
XX rheumatoid arthritis), hyperproliferative disorders (e.g. neoplasms of
XX the breast or liver), cerebrovascular disorders (e.g. cerebral ischaemia,
XX angiogenesis), cardiovascular disorders (e.g. cardiac arrest), nervous
XX system disorders (e.g. Alzheimer's disease), infections caused by fungi,
XX bacteria and viruses and ocular disorders (e.g. corneal infection). The
XX polypeptides can also be used to aid wound healing and epithelial cell
XX proliferation, to prevent skin aging due to sunburn, to maintain organs
XX before transplantation, for supporting cell culture of primary tissues,
XX to regenerate tissues and in chemotaxis. They can also be used as food
XX additives or preservative to increase or decrease storage capabilities,
XX fat content, lipid, protein, carbohydrate, vitamins, minerals, cofactors
XX and other nutritional components. The present sequence represents a human
XX secreted protein fragment kunitz-type domain referred to in the
XX disclosure of the invention
XX
SQ Sequence 51 AA;
Query Match 9.2%; Score 12; DB 5; Length 51;
Best Local Similarity 100.0%; Pred. No. 0.00011; Mismatches 0; Gaps 0;
Matches 12; Conservative 0; Indels 0; Gaps 0;
Qy 107 YGCGCGNNNNFQ 118
Db 31 YGCGCGNNNNFQ 42
RESULT 20
ADG98845
ID ADG98845 standard; protein; 51 AA.
XX
XX AC ADG98845;
XX
XX 11-MAR-2004 (first entry)
XX
XX Human secreted protein gene 24 protein #3.
XX
XX Secreted protein; gene therapy; neural disorder; immune system disorders;
XX muscular disorder; reproductive disorder; gastrointestinal disorder;
XX pulmonary disorder; cardiovascular disorder; renal disorder;
XX proliferative disorder; cancer; systemic lupus erythematosus;
XX rheumatoid arthritis; multiple sclerosis; thyroiditis; anaemia;
XX Grave's disease; diabetes; hepatitis; asthma; allergy; nephritis;
XX Parkinson's disease; Alzheimer's disease; atherosclerosis;
XX myocardial infarction; AIDS; infection; human.
XX
XX Homo sapiens.
XX
XX US2003225009-A1.
XX
XX 04-DEC-2003.
XX
XX 30-JAN-2002; 2002US-00058993.
XX
XX 14-MAR-1997; 97US-0040710P.
XX
XX 14-MAR-1997; 97US-0040762P.
XX

PR 30-MAY-1997; 97US-0048100P.
PR 30-MAY-1997; 97US-0048189P.
PR 30-MAY-1997; 97US-0048357P.
PR 30-MAY-1997; 97US-0050934P.
PR 06-JUN-1997; 97US-0048970P.
PR 05-SEP-1997; 97US-0057765P.
PR 19-DEC-1997; 97US-0069368P.
PR 12-MAR-1998; 98WO-US004858.
PR 11-SEP-1998; 98US-00152060.
PR 02-FEB-2001; 2001US-0265583P.
PR 11-MAY-2001; 2001US-00852659.
PR 11-MAY-2001; 2001US-00852797.
PR 11-MAY-2001; 2001US-00853161.
XX
PA (ROSE/) ROSEN C A.
PA (RUBE/) RUBEN S M.
PA (LIYY/) LI Y.
PA (ZENG/) ZENG Z.
PA (KYAW/) KYAW H.
PA (FISC/) FISCHER C L.
PA (LIHH/) LI H.
PA (SOPP/) SOPPET D R.
PA (GENT/) GENTZ R L.
PA (WEIY/) WEI Y.
PA (MOOR/) MOORE P A.
PA (YOUN/) YOUNG P E.
PA (GREE/) GREENE J M.
PA (FERR/) FERRIE A M.
PA (HAST/) HASTINGS G A.
XX
PI Rosen CA, Ruben SM, Li Y, Zeng Z, Kyaw H, Fischer CL, Li H;
PI Soppet DR, Gentz RL, Wei Y, Moore PA, Young PE, Greene JM;
PI Ferrie AM, Hastings GA;
XX
DR WPI; 2004-042167/04.
XX
PT New polypeptides and nucleic acid molecules for diagnosing, preventing or
PT treating diseases associated with aberrant expression or activity of the
PT polypeptide, e.g. cancer, asthma, AIDS, Parkinson's disease or diabetes.
XX
PS Disclosure; SEQ ID NO 118; 320pp; English.
XX
CC The invention relates to an isolated nucleic acid molecule encoding a
CC secreted protein that is at least 95% identical to a polynucleotide
CC fragment of any of the nucleotide sequences listed in table 1A of the
CC specification, which is hybridisable to the nucleotide sequences, a
CC polynucleotide encoding a polypeptide (or a polypeptide fragment, domain
CC or epitope of any of the amino acid sequences) listed in table 1A of the
CC specification, a polynucleotide which is an (allelic) variant of the
CC nucleotide sequences listed in the specification, a polynucleotide which
CC encodes a species homologue of the above amino acid sequences, a
CC polynucleotide capable of hybridising under stringent conditions to any
CC of the above polynucleotides, where the polynucleotide does not hybridise
CC under stringent conditions to a nucleic acid molecule having a nucleotide
CC sequence of only A or T residues. Also included are a recombinant vector
CC comprising the above nucleic acid molecule, making a recombinant host
CC cell comprising the above nucleic acid molecule, an isolated polypeptide
CC comprising a sequence that is at least 95% identical to the polypeptide
CC (or its fragment, domain, epitope, secreted form, (allelic) variant or
CC homologue) encoded by the above nucleic acid molecule, an isolated
CC antibody that binds specifically to the above polypeptide, a recombinant
CC host cell produced by the above method and that expresses the above
CC polypeptide, making an isolated polypeptide, preventing, treating or
CC ameliorating a medical condition, diagnosing a pathological condition or
CC a susceptibility to a pathological condition in a subject, identifying a
CC binding partner to the above polypeptide, the gene corresponding to the
CC cDNA sequence given in the specification, and identifying an activity in
CC a biological assay. The nucleic acid molecule and polypeptide are useful
CC in diagnosing, preventing, prognosing or treating diseases or disorders
CC associated with aberrant expression and/or activity of the above
CC polypeptide, such as neural disorders, immune system disorders, muscular
CC disorders, reproductive disorders, gastrointestinal disorders, pulmonary
CC disorders, cardiovascular disorders, renal disorders, proliferative

CC disorders and/or cancers. In particular, these diseases are systemic
CC lupus erythematosus, rheumatoid arthritis, multiple sclerosis,
CC thyroiditis, anaemia, Grave's disease, diabetes, hepatitis, asthma,
CC allergies, nephritis, Parkinson's disease, Alzheimer's disease,
CC atherosclerosis, myocardial infarction, AIDS and infections. The methods
CC may be used for identifying agonists and antagonists of the
CC polynucleotide and polypeptide. The present sequence is a protein from
CC one of the 28 disclosed secreted protein genes, it is not clear whether
CC this is an alternative expressed protein or a fragment of one of the
CC claimed proteins.

XX Sequence 51 AA;

Query Match 9.2%; Score 12; DB 8; Length 51;
Best Local Similarity 100.0%; Pred. No. 0.00011;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 107 YGGCGGNNNFQ 118
|||
DB 31 YGGCGGNNNFQ 42

RESULT 21

AAE13084
ID AAE13084 standard; peptide; 58 AA.

XX
AC AAE13084;

XX
DT 28-JAN-2002 (first entry)

XX
DE Human serine proteinase inhibitor BTL.009 peptide.

XX
DE Human; BTL.009 protein; serine proteinase inhibitor; cytostatic;
KW nephrotropic; idiopathic pulmonary fibrosis; cystic fibrosis; emphysema;
KW rheumatoid arthritis; adult respiratory distress syndrome; angioedema;
KW blood coagulation; glomerulonephritis; prophylactic; platelet activation;
KW neutrophil; monocyte; granulocyte; organ failure; inflammatory disease;
KW elastase inhibitor; chymotrypsin inhibitor; lung injury; vascular injury;
KW therapeutic.

XX
OS Homo sapiens.

XX
PN US6294648-B1.

XX
PD 25-SEP-2001.

XX
PF 20-JUL-1999; 99US-00358569.

XX
PR 20-JUL-1999; 99US-00358569.

XX
PA (FARB) BAYER CORP.

XX
PI Delaria K, Roczniak S, Davies C;

XX
WPI; 2001-662224/76.

XX
PT New isolated protein for inhibiting human serine protease activity in the
PT treatment of e.g. emphysema and adult respiratory distress syndrome.

XX
PS Claim 1; Col 15-16; 16pp; English.

XX
CC The invention relates to human BTL.009 protein, a serine proteinase
CC inhibitor of the Kunitz family that exhibits greater potency towards
CC neutral serine proteinases. BTL.009 protein is found to inhibit leukocyte
CC elastase, chymotrypsin-like protease and trypsin-like protease. BTL.009
CC protein is useful for treating emphysema, idiopathic pulmonary fibrosis,
CC adult respiratory distress syndrome, cystic fibrosis, rheumatoid
CC arthritis, organ failure, glomerulonephritis, other inflammatory diseases
CC and diseases involving lung and vascular injury. BTL.009 is also useful
CC for preventing neutrophil and monocyte activation and formation of active
CC oxygen species during the oxidative burst of stimulated granulocytes.
CC BTL.009 is useful for reducing platelet activation and blood coagulation
CC and for the prophylactic or therapeutic treatment of patients undergoing

CC angioplasty. The present sequence is human serine proteinase inhibitor
CC BTL.009 peptide corresponding to Kunitz domain used in the
CC exemplification of the invention. Note: The present sequence shown in
CC column 14 and sequence listing of the specification lacks 3 amino acid
CC residues at the C-terminal end
XX
SQ Sequence 58 AA;

Query Match 9.2%; Score 12; DB 4; Length 58;
Best Local Similarity 100.0%; Pred. No. 0.00012;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 107 YGGCQGNNNFQ 118
| | | | | | | | | |
Db 35 YGGCQGNNNFQ 46

RESULT 22
AAB60630
ID AAB60630 standard; protein; 58 AA.
XX
AC AAB60630;
XX
DT 27-APR-2001 (first entry)
XX
DE Kunitz domain, SEQ ID NO:8, used to identify BTL.010 protein.
XX
KW Human BTL.010; neutral serine proteinase inhibitor; elastase inhibitor;
KW proteinase-3 inhibitor; Kunitz domain; emphysema;
KW idiopathic pulmonary fibrosis; adult respiratory distress syndrome;
KW cystic fibrosis; rheumatoid arthritis; organ failure; glomerulonephritis;
KW platelet activation; blood coagulation; neutrophil activation;
KW monocyte activation; angioplasty; inflammatory disease; lung injury;
KW vascular injury; nephrotropic; antirheumatic; antiarthritic.
XX
OS Unidentified.
XX
XX US6180607-B1.
XX
XX 30-JAN-2001.
XX
XX 05-AUG-1999; 99US-00369494.
XX
XX 05-AUG-1999; 99US-00369494.
XX
XX (DAVI//) DAVIES C.
XX (CHEN//) CHEN D.
XX (ROCZ//) ROCZNIAK S.
XX
XX Davies C, Chen D, Roczniaak S;
XX WPI; 2001-190860/19.
XX
XX Novel serine proteinase inhibitor of the Kunitz family, BTL.010 useful
XX for treating emphysema, cystic fibrosis, adult respiratory distress
XX syndrome, rheumatoid arthritis, organ failure and glomerulonephritis.
XX
XX Disclosure; Col 6; 17pp; English.
XX
XX The invention relates to a novel human serine proteinase inhibitor of the
XX Kunitz family, BTL.010 (fragments given in AAB60623, AAB60631 and
XX AAB60634). The BTL.010 protein is thought to preferentially inhibit
XX neutral serine proteinases such as elastase and proteinase-3, relative to
XX trypsin-like and chymotrypsin-like proteinases. A substantial proportion of
XX the BTL.010 protein Kunitz domain (AAB60631) was identified via homology
XX searching in the GenBank high throughput genomic (HTG) DNA sequence
XX database using the Kunitz domain sequences AAB60630, and was confirmed as
XX being novel using the Kunitz domain sequences AAB60632, and AAB60633.
XX This sequence information was extended to provide a larger region of
XX BTL.010 protein sequence data (AAB60634) by identifying an open reading
XX frame (ORF) which comprised DNA encoding the BTL.010 Kunitz domain
XX fragment in a 399 bp fragment of human genomic DNA (AAFS9750),
XX corresponding to bases 16016-16414 of GenBank accession number AC004846.

CC The entire BTL.010 Kunitz domain sequence (AAB60623) was obtained from
CC the BTL.010 ORF-encoded sequence. The BTL.010 protein, and pharmaceutical
CC compositions comprising it, may be used for inhibiting protease activity,
CC particularly that of leukocyte elastase, in the prevention, treatment or
CC amelioration of medical conditions such as emphysema, idiopathic
CC pulmonary fibrosis, adult respiratory distress syndrome, cystic fibrosis,
CC rheumatoid arthritis, organ failure or glomerulonephritis. BTL.010
CC compositions of the invention modulate at least one physiological
CC condition such as platelet activation, blood coagulation, neutrophil
CC activation, or monocyte activation. BTL.010 is also useful for the
CC prophylactic or therapeutic treatment of patients undergoing angioplasty,
CC and for the treatment of inflammatory diseases and diseases involving
CC lung and vascular injury. The present sequence represents a Kunitz domain
CC sequence used to identify the BTL.010 protein
XX
SQ Sequence 58 AA;

Query Match 9.2%; Score 12; DB 4; Length 58;
Best Local Similarity 100.0%; Pred. No. 0.00012;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 107 YGGCQGNNNFQ 118
| | | | | | | | | |
Db 35 YGGCQGNNNFQ 46

RESULT 23
ADF41997
ID ADF41997 standard; protein; 58 AA.
XX
AC ADF41997;
XX
DT 12-FEB-2004 (first entry)
XX
DE Human CAB37 Kunitz domain peptide.
XX
XX albumin fusion; Kunitz domain; cytostatic; haemostatic;
XX hereditary angioedema; cancer; bleeding; gene therapy; human; CAB37.
XX
XX Homo sapiens.
XX
XX WO2003066824-A2.
XX
XX 14-AUG-2003.
XX
XX 07-FEB-2003; 2003WO-US003616.
XX
XX 07-FEB-2002; 2002US-0355547P.
XX
XX (AVET) AVENTIS BEHRING GMBH.
XX (AVET) AVENTIS BEHRING LLC.
XX (DELZ) DELTA BIOTECHNOLOGY LTD.
XX (DYAX-) DYAX CORP.
XX
XX Hauser H, Weimer T, Romberg V, Kee SM, Sleep D, Ladner RC;
XX Ley AC;
XX WPI; 2003-731497/69.
XX
XX Albumin fusion protein comprising a Kunitz domain peptide and an albumin,
XX useful for preparing a composition for treating a patient with hereditary
XX angioedema or angioedema-related disease, cancer or bleeding disorder.
XX
XX Disclosure; Page 20; 110pp; English.
XX
XX The invention relates to a novel albumin fusion protein comprising a
XX Kunitz domain peptide or its fragment or variant and an albumin or its
XX fragment or variant. The fusion protein of the invention demonstrates
XX cytostatic and haemostatic activities and may be useful for preparing a
XX composition for treating a patient with hereditary angioedema, an
XX angioedema-related disease, cancer, a cancer-related disease or a
XX bleeding disorder, as well as during gene therapy procedures. The current
XX sequence is that of the human Kunitz domain peptide of the invention.

```
XX SQ Sequence 58 AA;
Query Match 9.2%; Score 12; DB 7; Length 58;
Best Local Similarity 100.0%; Pred. No. 0.00012;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 107 YGGCQGNNNFQ 118
DB 35 YGGCQGNNNFQ 46
|||||

RESULT 24
ADL16838
ID ADL16838 standard; peptide; 58 AA.
XX AC ADL16838;
XX DT 06-MAY-2004 (first entry)
XX DE Human Kunitz domain (KD) peptide.
XX KW BTL.010 protein; serine proteinase inhibitor; Kunitz domain; emphysema;
XX KW idiopathic pulmonary fibrosis; adult respiratory distress syndrome;
XX KW cystic fibrosis; rheumatoid arthritis; organ failure; glomerulonephritis;
XX KW inflammatory disease; oxidative burst; platelet activation;
XX KW blood coagulation; gene therapy; human; KD.
XX OS Homo sapiens.
XX PN US6689582-B1.
XX PD 10-FEB-2004.
XX PF 12-MAY-2000; 2000US-00569670.
XX PR 05-AUG-1999; 99US-00369494.
XX PA (FARB ) BAYER PHARM CORP.
XX PI Davies C, Chen D, Roczniak S;
XX WPI; 2004-141424/14.
XX DR New isolated polynucleotide encoding BTL.010 serine proteinase, useful
XX PT for treating e.g. emphysema, idiopathic pulmonary fibrosis, adult
XX PT respiratory distress syndrome, cystic fibrosis, rheumatoid arthritis or
XX PT glomerulonephritis.
XX PS Disclosure; SEQ ID NO 8; 17pp; English.
XX CC The invention relates to BTL.010, a human serine proteinase inhibitor of
XX CC the Kunitz family and its corresponding nucleic acid sequence. The
XX CC sequences of the invention are useful for treating diseases, e.g.
XX CC emphysema, idiopathic pulmonary fibrosis, adult respiratory distress
XX CC syndrome, cystic fibrosis, rheumatoid arthritis, organ failure,
XX CC glomerulonephritis or inflammatory diseases. The BTL.010 protein is also
XX CC useful for preventing neutrophil and monocyte activation and formation of
XX CC active oxygen species during the oxidative burst of stimulated
XX CC granulocytes. It is also useful for reducing platelet activation and
XX CC blood coagulation. BTL.010 DNA is useful in gene therapy. The present
XX CC sequence is human Kunitz domain (KD) peptide.
XX SQ Sequence 58 AA;
Query Match 9.2%; Score 12; DB 8; Length 58;
Best Local Similarity 100.0%; Pred. No. 0.00012;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 107 YGGCQGNNNFQ 118
DB 35 YGGCQGNNNFQ 46
|||||

RESULT 24
ADL16838
ID ADL16838 standard; peptide; 58 AA.
XX AC ADL16838;
XX DT 06-MAY-2004 (first entry)
XX DE Human Kunitz domain (KD) peptide.
XX KW BTL.010 protein; serine proteinase inhibitor; Kunitz domain; emphysema;
XX KW idiopathic pulmonary fibrosis; adult respiratory distress syndrome;
XX KW cystic fibrosis; rheumatoid arthritis; organ failure; glomerulonephritis;
XX KW inflammatory disease; oxidative burst; platelet activation;
XX KW blood coagulation; gene therapy; human; KD.
XX OS Homo sapiens.
XX PN US6689582-B1.
XX PD 10-FEB-2004.
XX PF 12-MAY-2000; 2000US-00569670.
XX PR 05-AUG-1999; 99US-00369494.
XX PA (FARB ) BAYER PHARM CORP.
XX PI Davies C, Chen D, Roczniak S;
XX WPI; 2004-141424/14.
XX DR New isolated polynucleotide encoding BTL.010 serine proteinase, useful
XX PT for treating e.g. emphysema, idiopathic pulmonary fibrosis, adult
XX PT respiratory distress syndrome, cystic fibrosis, rheumatoid arthritis or
XX PT glomerulonephritis.
XX PS Disclosure; SEQ ID NO 8; 17pp; English.
XX CC The invention relates to BTL.010, a human serine proteinase inhibitor of
XX CC the Kunitz family and its corresponding nucleic acid sequence. The
XX CC sequences of the invention are useful for treating diseases, e.g.
XX CC emphysema, idiopathic pulmonary fibrosis, adult respiratory distress
XX CC syndrome, cystic fibrosis, rheumatoid arthritis, organ failure,
XX CC glomerulonephritis or inflammatory diseases. The BTL.010 protein is also
XX CC useful for preventing neutrophil and monocyte activation and formation of
XX CC active oxygen species during the oxidative burst of stimulated
XX CC granulocytes. It is also useful for reducing platelet activation and
XX CC blood coagulation. BTL.010 DNA is useful in gene therapy. The present
XX CC sequence is human Kunitz domain (KD) peptide.
XX SQ Sequence 58 AA;
Query Match 9.2%; Score 12; DB 8; Length 58;
Best Local Similarity 100.0%; Pred. No. 0.00012;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 107 YGGCQGNNNFQ 118
DB 35 YGGCQGNNNFQ 46
|||||

RESULT 26
AAE13093
ID AAE13093 standard; peptide; 64 AA.
XX AC AAE13093;
XX DT 28-JAN-2002 (first entry)
XX DE Human serine proteinase inhibitor BTL.009 C-terminal peptide.
XX KW Human; BTL.009 protein; serine proteinase inhibitor; cytostatic;
XX KW nephrotropic; idiopathic pulmonary fibrosis; cystic fibrosis; emphysema;
XX KW rheumatoid arthritis; adult respiratory distress syndrome; angioplasty;
XX KW blood coagulation; glomerulonephritis; prophylactic; platelet activation;
```



```

Query Match      9.2%; Score 12; DB 5; Length 102;
Best Local Similarity 100.0%; Pred. No. 0.0002;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 107 YGGCGGNNNFQ 118
DB 76 YGGCGGNNNFQ 87

RESULT 28
AAE28009
ID AAE28009 standard; protein; 102 AA.
XX
AC AAE28009;
XX
DT 13-DEC-2002 (first entry)
XX
DE Human gene 24 encoded secreted protein fragment #2.
XX
KW Human; secreted protein; autoimmune disease; hyperproliferative disorder;
KW rheumatoid arthritis; neoplasm; cerebrovascular disorder; angiogenesis;
KW cerebral ischaemia; cardiovascular disorder; nervous system disorder;
KW cardiac arrest; Alzheimer's disease; ocular disorder; wound healing;
KW infection; corneal infection; skin aging; food additive; preservative;
KW tissue regeneration; immunosuppressive; antiproliferative; cytostatic;
KW cardiant; vasotropic; cerebroprotective; nootropic; neuroprotective;
KW antibacterial; virucide; fungicide; ophthalmological; gene therapy;
KW vulnery.
XX
OS Homo sapiens.
XX
PN US2002076756-A1.
XX
PD 20-JUN-2002.
XX
PF 11-MAY-2001; 2001US-00853161.
XX
PR 02-FEB-2001; 2001US-0265583P.
XX
PA (RUBEN S M.
PA (ROSE/) ROSEN C A.
PA (LIYY/) LI Y.
PA (ZENG/) ZENG Z.
PA (KYAW/) KYAW H.
PA (FISC/) FISCHER C L.
PA (LIJH/) LI H.
PA (SOPP/) SOPPET D R.
PA (GENTZ/) GENTZ R L.
PA (WEIY/) WEI Y.
PA (MOOR/) MOORE P A.
PA (YOUN/) YOUNG P E.
PA (GREE/) GREENE J M.
PA (FERR/) FERRIE A M.
XX
PI Ruben SM, Rosen CA, Li Y, Zeng Z, Kyaw H, Fischer CL, Li H;
PI Soppet DR, Gentz RL, Wei Y, Moore PA, Young PE, Greene JM;
PI Ferrie AM;
XX
DR WPI; 2002-574454/61.
XX
PT New nucleic acid molecules encoding 28 human secreted proteins, useful
PT for diagnosing, preventing, treating or ameliorating medical conditions
PT and as food additives or preservatives.
XX
XX Disclosure; Page 17; 209pp; English.
XX
AAAD4854-AAD44984 represent cDNAs corresponding to 28 human secreted
CC protein genes, and AAE27097-AAE27137 represent the proteins they encode.
CC AAE27138-AAE27164 represent human secreted protein fragments. The genes
CC and their corresponding secreted proteins are useful for preventing,
CC treating or ameliorating medical conditions, e.g., by protein or gene
CC therapy. Secreted protein sequences of the invention are useful for the
CC diagnosis or treatment of disorders such as autoimmune diseases (e.g.

```

```

CC rheumatoid arthritis), hyperproliferative disorders (e.g. neoplasms of
CC the breast or liver), cerebrovascular disorders (e.g. cerebral ischaemia,
CC angiogenesis), cardiovascular disorders (e.g. cardiac arrest), nervous
CC system disorders (e.g. Alzheimer's disease), infections caused by fungi,
CC bacteria and viruses and ocular disorders (e.g. corneal infection). The
CC polypeptides can also be used to aid wound healing and epithelial cell
CC proliferation, to prevent skin aging due to sunburn, to maintain organs
CC before transplantation, for supporting cell culture of primary tissues,
CC to regenerate tissues and in chemotaxis. They can also be used as food
CC additives or preservative to increase or decrease storage capabilities,
CC fat content, lipid, protein, carbohydrate, vitamins, minerals, cofactors
CC and other nutritional components. The present sequence represents a human
CC secreted protein fragment referred to in the disclosure of the invention
XX
SQ Sequence 102 AA;

Query Match      9.2%; Score 12; DB 5; Length 102;
Best Local Similarity 100.0%; Pred. No. 0.0002;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 107 YGGCGGNNNFQ 118
DB 76 YGGCGGNNNFQ 87

RESULT 29
ABU65039
ID ABU65039 standard; peptide; 102 AA.
XX
AC ABU65039;
XX
DT 15-MAY-2003 (first entry)
XX
DE Human secreted protein gene 24, protein #3.
XX
KW Secreted protein; immunodeficiency; multiple sclerosis;
KW severe combined immunodeficiency; autoimmune disorder; cancer;
KW rheumatoid arthritis; diabetes mellitus; haematopoietic disorder;
KW inflammatory condition; septic shock; inflammatory bowel disease;
KW Crohn's disease; respiratory disorder; asthma; allergy; stroke;
KW gastrointestinal disorder; central nervous system disorder;
KW ischaemic brain injury; neurodegenerative disorder; Parkinson's disease;
KW Alzheimer's disease; cardiovascular disorder; atherosclerosis;
KW blood-related disorder; thrombosis; atherosclerosis; renal disorder;
KW hyperproliferative disorder; acute glomerulonephritis; Addison's disease;
KW endocrine disorder; liver disease; reproductive system disorder;
KW endometriosis; infectious disease; pancreatic disorder; vaccine;
KW wound repair; angiogenesis; lymphatic disorder; hair loss; body weight;
KW body height; hair colour; human.
XX
OS Homo sapiens.
XX
PN US2002172994-A1.
XX
PD 21-NOV-2002.
XX
PF 11-MAY-2001; 2001US-00852797.
XX
PR 14-MAR-1997; 97US-0040710P.
PR 14-MAR-1997; 97US-0040762P.
PR 30-MAY-1997; 97US-0048100P.
PR 30-MAY-1997; 97US-0048189P.
PR 30-MAY-1997; 97US-0048357P.
PR 30-MAY-1997; 97US-0050934P.
PR 06-JUN-1997; 97US-0048970P.
PR 05-SEP-1997; 97US-0057765P.
PR 19-DEC-1997; 97US-0068368P.
PR 12-MAR-1998; 98WO-US004858.
PR 11-SEP-1998; 98US-00152060.
PR 02-FEB-2001; 2001US-0265583P.
XX
XX (RUBEN S M.
PA (ROSE/) ROSEN C A.

```

PA (LIYY/) LI Y.
PA (ZENG/) ZENG Z.
PA (KYAW/) KYAW H.
PA (FISC/) FISCHER C L.
PA (LIHH/) LI H.
PA (SOPP/) SOPPET D R.
PA (GENT/) GENTZ R L.
PA (WEIY/) WEI Y.
PA (MOOR/) MOORE P A.
PA (YOUN/) YOUNG P E.
PA (GREE/) GREENE J M.
PA (FERR/) FERRIE A M.
XX
PI Ruben SM, Rosen CA, Li Y, Zeng Z, Kyaw H, Fischer CL, Li H;
PI Soppet DR, Gentz RL, Wei Y, Moore PA, Young PE, Greene JM;
PI Ferrie AM;
XX
XX WPI; 2003-310989/30.
XX
XX New human secreted polypeptides and polynucleotides for diagnosing,
PT prognosing, preventing and treating immune, hyperproliferative, liver,
PT kidney, reproductive disorders and for identifying modulators of
PT therapeutic use.
XX
XX Disclosure; Page 16; 209pp; English.
XX
CC The invention relates to an isolated polypeptide comprising an amino acid
CC sequence at least 95% identical to sequence of 28 human secreted
CC proteins, their fragment, polypeptide domain, epitope, secreted form,
CC variant, allelic variant, or species homologue, or the encoded sequence
CC included in ATCC 97921 and 97922. Also included are the encoding nucleic
CC acids, recombinant vectors, host cells, antibodies, and genes. The
CC proteins and nucleic acids are useful for diagnosing, preventing,
CC treating, prognosing or ameliorating a medical condition e.g.
CC immunodeficiencies (e.g. X-linked agammaglobulinaemia, B cell
CC immunodeficiencies, severe combined immunodeficiencies), autoimmune
CC disorders (e.g. systemic erythematous, rheumatoid arthritis, multiple
CC sclerosis, autoimmune thyroiditis, autoimmune haemolytic anaemia, multiple
CC Goodpasture's syndrome, Grave's disease, diabetes mellitus, dermatitis),
CC haematopoietic disorders, inflammatory conditions (e.g. septic shock,
CC sepsis, reperfusion injury, inflammatory bowel disease, Crohn's disease),
CC respiratory disorders (e.g. asthma and allergy), gastrointestinal
CC disorders, cancers (e.g. gastric, ovarian, lung, bladder, liver and
CC breast), central nervous system (CNS) disorders (e.g. ischaemic brain
CC injury and/or stroke, traumatic brain injury), neurodegenerative
CC disorders (e.g. Parkinson's disease and Alzheimer's disease, AIDS-related
CC dementia, and prion disease), cardiovascular disorders (e.g.
CC atherosclerosis, myocarditis, cardiovascular disease, and cardiopulmonary
CC bypass complications), inflammation (e.g. hepatitis, gout, trauma,
CC pancreatitis, sarcoidosis, dermatitis, allogenic transplant rejection),
CC blood-related disorders (thrombosis, arterial thrombosis),
CC hyperproliferative disorders, renal disorders (e.g. acute
CC glomerulonephritis), endocrine disorders (e.g. Addison's disease,
CC hyperthyroidism, hyperpituitarism), liver diseases and disorders,
CC reproductive system disorders (e.g. endometriosis), infectious diseases,
CC and pancreatic disorders. Many other diseases and disorders are listed in
CC the specification. They also useful as a vaccine adjuvant. Further they
CC are useful to enhance or inhibit complement mediated cell lysis, for
CC stimulating wound and tissue repair, angiogenesis, and the repair of
CC vascular or lymphatic diseases or disorders. They are also useful to
CC prevent hair loss, to modulate mammalian characteristics such as body
CC height, weight, hair colour, and to increase or decrease storage
CC capabilities, fat content, lipid, protein, carbohydrate, vitamins,
CC minerals, cofactors or other nutritional components. The proteins are
CC also useful for identifying binding partners. The present sequence
CC represents a secreted protein of the invention
XX
XX Sequence 102 AA;

Query Match 9.2%; Score 12; DB 6; Length 102;
Best Local Similarity 100.0%; Pred. No. 0.0002;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 107 YGGCGNNNNFQ 118
Db |||||
76 YGGCGNNNNFQ 87
RESULT 30
ADG89848
ID ADG89848 standard; protein; 102 AA.
XX
AC ADG89848;
XX
DT 11-MAR-2004 (first entry)
XX
DE Human secreted protein gene 24 protein #6.
XX
KW Secreted protein; gene therapy; neural disorder; immune system disorders;
KW muscular disorder; reproductive disorder; gastrointestinal disorder;
KW pulmonary disorder; cardiovascular disorder; renal disorder;
KW proliferative disorder; cancer; systemic lupus erythematosus;
KW rheumatoid arthritis; multiple sclerosis; thyroiditis; anaemia;
KW Grave's disease; diabetes; hepatitis; asthma; allergy; nephritis;
KW Parkinson's disease; Alzheimer's disease; atherosclerosis;
KW myocardial infarction; AIDS; infection; human.
XX
OS Homo sapiens.
XX
PN US2003225009-A1.
XX
PD 04-DEC-2003.
XX
PF 30-JAN-2002; 2002US-00058993.
XX
PR 14-MAR-1997; 97US-0040710P.
PR 14-MAR-1997; 97US-0040762P.
PR 30-MAY-1997; 97US-0048100P.
PR 30-MAY-1997; 97US-0048189P.
PR 30-MAY-1997; 97US-0048357P.
PR 30-MAY-1997; 97US-0050334P.
PR 06-JUN-1997; 97US-0048970P.
PR 05-SEP-1997; 97US-0057765P.
PR 19-DEC-1997; 97US-0068368P.
PR 12-MAR-1998; 98WO-US0004858.
PR 11-SEP-1998; 98US-00152060.
PR 02-FEB-2001; 2001US-0265583P.
PR 11-MAY-2001; 2001US-0085265P.
PR 11-MAY-2001; 2001US-00852797.
PR 11-MAY-2001; 2001US-00853161.
XX
PA (ROSE/) ROSEN C A.
PA (RUBE/) RUBEN S M.
PA (LIYY/) LI Y.
PA (ZENG/) ZENG Z.
PA (KYAW/) KYAW H.
PA (FISC/) FISCHER C L.
PA (LIHH/) LI H.
PA (SOPP/) SOPPET D R.
PA (GENT/) GENTZ R L.
PA (WEIY/) WEI Y.
PA (MOOR/) MOORE P A.
PA (YOUN/) YOUNG P E.
PA (GREE/) GREENE J M.
PA (FERR/) FERRIE A M.
PA (HAST/) HASTINGS G A.
XX
PI Ruben CA, Ruben SM, Li Y, Zeng Z, Kyaw H, Fischer CL, Li H;
PI Soppet DR, Gentz RL, Wei Y, Moore PA, Young PE, Greene JM;
PI Ferrie AM, Hastings GA;
XX
XX WPI; 2004-042167/04.

New polypeptides and nucleic acid molecules for diagnosing, preventing or
treating diseases associated with aberrant expression or activity of the
polypeptide, e.g. cancer, asthma, AIDS, Parkinson's disease or diabetes.

XX Disclosure; SEQ ID NO 121; 320pp; English.

PS The invention relates to an isolated nucleic acid molecule encoding a

XX secreted protein that is at least 95% identical to a polynucleotide

CC fragment of any of the nucleotide sequences listed in table 1A of the

CC specification, which is hybridisable to the nucleotide sequences, a

CC polynucleotide encoding a polypeptide (or a polypeptide fragment, domain

CC or epitope of any of the amino acid sequences) listed in table 1A of the

CC specification, a polynucleotide which is an (allelic) variant of the

CC nucleotide sequences listed in the specification, a polynucleotide which

CC encodes a species homologue of the above amino acid sequences, a

CC polynucleotide capable of hybridising under stringent conditions to any

CC of the above polynucleotides, where the polynucleotide does not hybridise

CC under stringent conditions to a nucleic acid molecule having a nucleotide

CC sequence of only A or T residues. Also included are a recombinant vector

CC comprising the above nucleic acid molecule, making a recombinant host

CC cell comprising the above nucleic acid molecule, an isolated polypeptide

CC comprising a sequence that is at least 95% identical to the polypeptide

CC (or its fragment, domain, epitope, secreted form, (allelic) variant or

CC homologue) encoded by the above nucleic acid molecule, an isolated

CC antibody that binds specifically to the above polypeptide, a recombinant

CC host cell produced by the above method and that expresses the above

CC polypeptide, making an isolated polypeptide, preventing, treating or

CC ameliorating a medical condition, diagnosing a pathological condition or

CC a susceptibility to a pathological condition in a subject, identifying a

CC binding partner to the above polypeptide, the gene corresponding to the

CC cDNA sequence given in the specification, and identifying an activity in

CC a biological assay. The nucleic acid molecule and polypeptide are useful

CC in diagnosing, preventing, prognosing and/or activity of the above

CC associated with aberrant expression and/or activity of the above

CC polypeptide, such as neural disorders, immune system disorders, muscular

CC disorders, reproductive disorders, gastrointestinal disorders, pulmonary

CC disorders, cardiovascular disorders, renal disorders, proliferative

CC disorders and/or cancers. In particular, these diseases are systemic

CC lupus erythematosus, rheumatoid arthritis, multiple sclerosis,

CC thyroiditis, anaemia, Grave's disease, diabetes, hepatitis, asthma,

CC allergies, nephritis, Parkinson's disease, Alzheimer's disease,

CC atherosclerosis, myocardial infarction, AIDS and infections. The methods

CC may be used for identifying agonists and antagonists of the

CC polynucleotide and polypeptide. The present sequence is a protein from

CC one of the 28 disclosed secreted protein genes, it is not clear whether

CC this is an alternative expressed protein or a fragment of one of the

CC claimed proteins.

XX Sequence 102 AA;

SQ

Query Match 9.2%; Score 12; DB 8; Length 102;

Best Local Similarity 100.0%; Pred. No. 0.0002;

Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 107 YGCGCGNNNFQ 118

DB 76 YGCGCGNNNFQ 87

RESULT 31

AAE27094

ID AAE27094 standard; protein; 117 AA.

XX AC

XX AAE27094;

XX 13-DEC-2002 (first entry)

XX Human secreted protein #1.

XX Human; immunodeficiency; X-linked agammaglobulinaemia; septic shock;

KW autoimmune disorder; rheumatoid arthritis; multiple sclerosis; cancer;

KW Grave's disease; diabetes mellitus; haematopoietic disorder; stroke;

KW respiratory disorder; asthma; allergy; gastrointestinal disorder;

KW inflammatory bowel disease; neurodegenerative disorder; hepatitis;

KW Parkinson's disease; Alzheimer's disease; cardiovascular disorder;

KW atherosclerosis; myocarditis; renal disorder; fungicide; virucide;

KW hyperproliferative disorder; acute glomerulonephritis; tonsillitis;

KW respiratory disorder; rhinitis; sinusitis; neurological disease;

KW endocrine disorder; Addison's disease; reproductive system disorder;

KW endometriosis; vasotropic; vulvular; cytostatic; nontropic; cardiac;

XX anti-HIV; tranquilliser; gout; antiparasitic.

OS Homo sapiens.

XX US2002077287-A1.

PN 20-JUN-2002.

PD 11-MAY-2001; 2001US-00852659.

PF 11-SEP-1998; 98US-00152060.

PR (RUBE/) RUBEN S M.

PA (ROSE/) ROSEN C A.

PA (LIYY/) LI Y.

PA (ZENG/) ZENG Z.

PA (KYAW/) KYAW H.

PA (FISC/) FISCHER C L.

PA (LIHH/) LI H.

PA (SOPP/) SOPPET D R.

PA (GENT/) GENTZ R L.

PA (WEIY/) WEI Y.

PA (MOOR/) MOORE P A.

PA (YOUN/) YOUNG P E.

PA (GREE/) GREENE J M.

PA (FERR/) FERRIE A M.

XX Ruben SM, Rosen CA, Li Y, Zeng Z, Kyaw H, Fischer CL, Li H;

PI Soppet DR, Gentz RL, Wei Y, Moore PA, Young PE, Greene JM;

PI Ferrie AM;

XX WPI; 2002-598780/64.

DR Novel human secreted polypeptides and polynucleotides for diagnosing,

PT preventing, treating immune, hyperproliferative, cardiovascular,

PT neurological, reproductive disorders and identifying modulators of

PT therapeutic use.

XX Disclosure; Page 16; 209pp; English.

PS AAD44636-AAD44676 represent cDNAs corresponding to 28 human secreted

CC protein genes, and AAE26959-AAE26999 represent the proteins they encode.

CC AAE27000-AAE27025 represent human secreted protein fragments or their

CC variants. The secreted proteins and genes are useful for preventing,

CC treating or ameliorating medical conditions, e.g., by protein or gene

CC therapy. Specific uses are described for each of the 28 genes, based on

CC the tissues in which they are most highly expressed and include

CC developing products for the diagnosis or treatment of immunodeficiencies,

CC e.g., X-linked agammaglobulinaemia, B cell immunodeficiencies, severe

CC combined immunodeficiencies, autoimmune disorders e.g., systemic lupus

CC erythematosus, rheumatoid arthritis, multiple sclerosis, autoimmune

CC thyroiditis, autoimmune haemolytic anaemia, Goodpasture's syndrome,

CC Grave's disease, diabetes mellitus, dermatitis, inflammatory bowel

CC including septic shock, sepsis, reperfusion injury, inflammatory disorders

CC disease, Crohn's disease, haematopoietic disorders, respiratory disorders

CC e.g., asthma and allergy, gastrointestinal disorders e.g., inflammatory

CC bowel disease), cancers e.g., gastric, ovarian, lung, liver, bladder and

CC breast), central nervous system (CNS) disorders e.g., ischaemic brain

CC injury and/or stroke, neurodegenerative disorders e.g., Parkinson's

CC disease and Alzheimer's disease, AIDS-related dementia and prion disease,

CC cardiovascular disorders e.g., myocarditis, arrhythmias, atherosclerosis,

CC inflammatory disorders e.g., hepatitis, gout, trauma, pancreatitis,

CC sarcoidosis and allogeneic transplant rejection, blood-related disorder

CC (thrombosis, arterial thrombosis, atherosclerosis), hyperproliferative

CC disorders, respiratory disorders e.g., rhinitis, sinusitis, tonsillitis,

CC lung cancer, allergic disorders, pneumonitis, renal disorders e.g., acute

CC glomerulonephritis, neurological diseases, liver disorders, endocrine

CC disorders e.g., hyperthyroidism, Addison's disease, hyperpituitarism,

CC infectious diseases and reproductive system disorders e.g., endometriosis.

CC The present sequence represents a human secreted protein of the invention
 XX
 SQ Sequence 117 AA;

Query Match 9.2%; Score 12; DB 5; Length 117;
 Best Local Similarity 100.0%; Pred. No. 0.00022;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 107 YGCGCGNNNFQ 118
 |||||
 Db 91 YGCGCGNNNFQ 102

RESULT 32
 AAE27165
 ID AAE27165 standard; protein; 117 AA.

XX
 AC AAE27165;
 XX
 DT 13-DEC-2002 (first entry)
 XX

XX Human gene 24 encoded secreted protein fragment #1.

XX Human; secreted protein; autoimmune disease; hyperproliferative disorder;
 KW rheumatoid arthritis; neoplasm; cerebrovascular disorder; angiogenesis;
 KW cerebral ischaemia; cardiovascular disorder; nervous system disorder;
 KW cardiac arrest; Alzheimer's disease; ocular disorder; wound healing;
 KW infection; corneal infection; skin aging; food additive; preservative;
 KW tissue regeneration; immunosuppressive; antiproliferative; cytostatic;
 KW cardiant; vasotropic; cerebroprotective; nootropic; neuroprotective;
 KW antibacterial; virucide; fungicide; ophthalmological; gene therapy;
 KW
 XX

OS Homo sapiens.

XX US2002076756-A1.

XX 20-JUN-2002.

XX 11-MAY-2001; 2001US-00853161.

XX 02-FEB-2001; 2001US-0265583P.

XX (RUBE/) RUBEN S M.

PA (ROSE/) ROSEN C A.

PA (LIYY/) LI Y.

PA (ZENG/) ZENG Z.

PA (KYAW/) KYAW H.

PA (FISC/) FISCHER C L.

PA (LIHH/) LI H.

PA (SOPP/) SOPPET D R.

PA (GENT/) GENTZ R L.

PA (WEIY/) WEI Y.

PA (MOOR/) MOORE P A.

PA (YOUN/) YOUNG P E.

PA (GREE/) GREENE J M.

PA (FERR/) FERRIE A M.

XX Ruben SM, Rosen CA, Li Y, Zeng Z, Kyaw H, Fischer CL, Li H;

PI Soppet DR, Gentz RL, Wei Y, Moore PA, Young PE, Greene JM;

PI Ferrie AM;

XX WPI; 2002-574454/61.

XX New nucleic acid molecules encoding 28 human secreted proteins, useful
 PT for diagnosing, preventing, treating or ameliorating medical conditions
 PT and as food additives or preservatives.

XX Disclosure; Page 17; 209pp; English.

XX AAD44854-AAD44984 represent cDNAs corresponding to 28 human secreted
 CC protein genes, and AAE27097-AAE27137 represent the proteins they encode.
 CC AAE27138-AAE27164 represent human secreted protein fragments. The genes

CC and their corresponding secreted proteins are useful for preventing,
 CC treating or ameliorating medical conditions, e.g., by protein or gene
 CC therapy. Secreted protein sequences of the invention are useful for the
 CC diagnosis or treatment of disorders such as autoimmune diseases (e.g.
 CC rheumatoid arthritis), hyperproliferative disorders (e.g. neoplasms of
 CC the breast or liver), cerebrovascular disorders (e.g. cerebral ischaemia,
 CC angiogenesis), cardiovascular disorders (e.g. cardiac arrest), nervous
 CC system disorders (e.g. Alzheimer's disease), infections caused by fungi,
 CC bacteria and viruses and ocular disorders (e.g. corneal infection). The
 CC polypeptides can also be used to aid wound healing and epithelial cell
 CC proliferation, to prevent skin aging due to sunburn, to maintain organs
 CC before transplantation, for supporting cell culture of primary tissues,
 CC to regenerate tissues and in chemotaxis. They can also be used as food
 CC additives or preservative to increase or decrease storage capabilities,
 CC fat content, lipid, protein, carbohydrate, vitamins, minerals, cofactors
 CC and other nutritional components. The present sequence represents a human
 CC secreted protein fragment referred to in the disclosure of the invention
 XX
 XX SQ Sequence 117 AA;

Query Match 9.2%; Score 12; DB 5; Length 117;
 Best Local Similarity 100.0%; Pred. No. 0.00022;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 107 YGCGCGNNNFQ 118

Db 91 YGCGCGNNNFQ 102
 |||||

RESULT 33

ABU65038

ID ABU65038 standard; protein; 117 AA.

XX AC ABU65038;

XX 15-MAY-2003 (first entry)

XX Human secreted protein gene 24, protein #4.

XX Secreted protein; immunodeficiency; multiple sclerosis;

KW severe combined immunodeficiency; autoimmune disorder; cancer;

KW rheumatoid arthritis; diabetes mellitus; haematopoietic disorder;

KW inflammatory condition; septic shock; inflammatory bowel disease;

KW Crohn's disease; respiratory disorder; asthma; allergy; stroke;

KW gastrointestinal disorder; central nervous system disorder;

KW ischaemic brain injury; neurodegenerative disorder; Parkinson's disease;

KW Alzheimer's disease; cardiovascular disorder; atherosclerosis;

KW blood-related disorder; thrombosis; atherosclerosis; renal disorder;

KW hyperproliferative disorder; acute glomerulonephritis; Addison's disease;

KW endocrine disorder; liver disease; reproductive system disorder;

KW endometriosis; infectious disease; pancreatic disorder; vaccine;

KW wound repair; angiogenesis; lymphatic disorder; hair loss; body weight;

KW body height; hair colour; human.

XX Homo sapiens.

OS US2002172994-A1.

XX 21-NOV-2002.

XX 11-MAY-2001; 2001US-00852797.

XX 14-MAR-1997; 97US-0040710P.

PR 14-MAR-1997; 97US-0040762P.

PR 30-MAY-1997; 97US-0048100P.

PR 30-MAY-1997; 97US-0048189P.

PR 30-MAY-1997; 97US-0048357P.

PR 30-MAY-1997; 97US-0050934P.

PR 06-JUN-1997; 97US-0048970P.

PR 05-SEP-1997; 97US-0057765P.

PR 19-DEC-1997; 97US-0068368P.

PR 12-MAR-1998; 98WO-US0004858.

PR 11-SEP-1998; 98US-00152060.

XX Human; immunodeficiency; X-linked agammaglobulinaemia; septic shock;
 KW autoimmune disorder; rheumatoid arthritis; multiple sclerosis; cancer;
 KW Grave's disease; diabetes mellitus; haematopoietic disorder; stroke;
 KW respiratory disorder; asthma; allergy; gastrointestinal disorder;
 KW inflammatory bowel disease; neurodegenerative disorder; hepatitis;
 KW Parkinson's disease; Alzheimer's disease; cardiovascular disorder;
 KW atherosclerosis; myocarditis; renal disorder; fungicide; virucide;
 KW hyperproliferative disorder; acute glomerulonephritis; tonsillitis;
 KW respiratory disorder; rhinitis; sinusitis; neurological disease;
 KW endocrine disorder; Addison's disease; reproductive system disorder;
 KW endometriosis; vasotrophic; vulnerary; cytostatic; nootropic; cardiant;
 KW anti-HIV; tranquilliser; gout; antiparasitic.
 XX Homo sapiens.
 XX Key Location/Qualifiers
 FH Key 1..21
 FT Peptide /label= Signal_peptide
 FT Protein 22..133
 FT /note= "Human mature secreted protein"
 XX US200207297-A1.
 PN 20-JUN-2002.
 XX 11-MAY-2001; 2001US-00852659.
 XX 11-SEP-1998; 98US-00152060.
 XX (RUBE/) RUBEN S M.
 PA (ROSE/) ROSEN C A.
 PA (LIYV/) LI Y.
 PA (ZENG/) ZENG Z.
 PA (KYAW/) KYAW H.
 PA (FISC/) FISCHER C L.
 PA (LIHH/) LI H.
 PA (SOPP/) SOPPET D R.
 PA (GENT/) GENTZ R L.
 PA (WEIY/) WEI Y.
 PA (MOOR/) MOORE P A.
 PA (YOUN/) YOUNG P E.
 PA (GREE/) GREENE J M.
 PA (FERR/) FERRIE A M.
 XX Ruben SM, Rosen CA, Li Y, Zeng Z, Kyaw H, Fischer CL, Li H;
 PI Soppet DR, Gentz RL, Wei Y, Moore PA, Young PE, Greene JM;
 PI Ferrie AM;
 XX WPI: 2002-598780/64.
 DR N-PSDB; AAD44659.
 XX Novel human secreted polypeptides and polynucleotides for diagnosing,
 PT preventing, treating immune, hyperproliferative, cardiovascular,
 PT neurological, reproductive disorders and identifying modulators of
 PT therapeutic use.
 XX Claim 11; Page 185-186; 209pp; English.
 XX AAD44636-AAD44676 represent cDNAs corresponding to 28 human secreted
 CC protein genes, and AAE26959-AAE26999 represent the proteins they encode.
 CC AAE27000-AAE27025 represent human secreted protein fragments or their
 CC variants. The secreted proteins and genes are useful for preventing,
 CC treating or ameliorating medical conditions, e.g., by protein or gene
 CC therapy. Specific uses are described for each of the 28 genes, based on
 CC the tissues in which they are most highly expressed and include
 CC developing products for the diagnosis or treatment of immunodeficiencies,
 CC e.g., X-linked agammaglobulinaemia, B cell immunodeficiencies, severe
 CC combined immunodeficiencies, autoimmune disorders e.g., systemic lupus
 CC erythematosus, rheumatoid arthritis, multiple sclerosis, autoimmune
 CC thyroiditis, autoimmune haemolytic anaemia, Goodpasture's syndrome,
 CC Grave's disease, diabetes mellitus, dermatitis, inflammatory conditions
 CC including septic shock, sepsis, reperfusion injury, inflammatory bowel

CC disease, Crohn's disease, haematopoietic disorders, respiratory disorders
 CC e.g., asthma and allergy, gastrointestinal disorders e.g., inflammatory
 CC bowel disease), cancers e.g., gastric, ovarian, lung, liver, bladder and
 CC breast), central nervous system (CNS) disorders e.g., ischaemic brain
 CC injury and/or stroke, neurodegenerative disorders e.g., Parkinson's
 CC disease and Alzheimer's disease, AIDS-related dementia and prion disease,
 CC cardiovascular disorders e.g., myocarditis, arrhythmias, atherosclerosis,
 CC inflammatory disorders e.g., hepatitis, gout, trauma, pancreatitis,
 CC sarcoidosis and allogenic transplant rejection, blood-related disorder
 CC (thrombosis, arterial thrombosis, atherosclerosis), hyperproliferative
 CC disorders, respiratory disorders e.g. rhinitis, sinusitis, tonsillitis,
 CC lung cancer, allergic disorders, pneumonia, renal disorders, e.g. acute
 CC glomerulonephritis, neurological diseases, liver disorders, endocrine
 CC disorders e.g., hyperthyroidism, Addison's disease, hyperlipidemia,
 CC infectious diseases and reproductive system disorders e.g. endometriosis.
 CC The present sequence represents a human secreted protein of the invention
 XX
 SQ Sequence 133 AA;

Query Match 9.2%; Score 12; DB 5; Length 133;
 Best Local Similarity 100.0%; Pred. No. 0.00025;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 107 YGCGCGNNNFQ 118
 |||||

DB 107 YGCGCGNNNFQ 118
 |||||

RESULT 37

AAE27120

ID AAE27120 standard; protein; 133 AA.

XX AC AAE27120;

XX DT 13-DEC-2002 (first entry)

XX DE Human gene 24 encoded secreted protein HTEBY11, SEQ ID NO:75.

XX KW Human; secreted protein; autoimmune disease; hyperproliferative disorder;
 KW rheumatoid arthritis; neoplasm; cerebrovascular disorder; angiogenesis;
 KW cerebral ischaemia; cardiovascular disorder; nervous system disorder;
 KW cardiac arrest; Alzheimer's disease; ocular disorder; wound healing;
 KW infection; corneal infection; skin aging; food additive; preservative;
 KW tissue regeneration; immunosuppressive; antiproliferative; cytostatic;
 KW cardiant; vasotropic; cerebroprotective; nootropic; neuroprotective;
 KW antibacterial; virucide; fungicide; ophthalmological; gene therapy;
 KW vulnerary.
 XX OS Homo sapiens.
 XX FH Key Location/Qualifiers
 FT Peptide 1..21
 FT Protein 22..133
 FT /label= Signal_peptide
 FT /note= "Mature human secreted protein"
 XX US2002076756-A1.
 XX PD 20-JUN-2002.
 XX PF 11-MAY-2001; 2001US-00853161.
 XX PR 02-FEB-2001; 2001US-0265583P.
 XX (RUBE/) RUBEN S M.
 PA (ROSE/) ROSEN C A.
 PA (LIYV/) LI Y.
 PA (ZENG/) ZENG Z.
 PA (KYAW/) KYAW H.
 PA (FISC/) FISCHER C L.
 PA (LIHH/) LI H.
 PA (SOPP/) SOPPET D R.
 PA (GENT/) GENTZ R L.

CC dementia, and prion disease), cardiovascular disorders (e.g.
 CC atherosclerosis, myocarditis, cardiovascular disease, and cardiopulmonary
 CC bypass complications), inflammation (e.g. hepatitis, gout, trauma,
 CC pancreatitis, sarcoidosis, dermatitis, allergic transplant rejection),
 CC blood-related disorders (thrombosis, arterial thrombosis),
 CC hyperproliferative disorders, renal disorders (e.g. acute
 CC glomerulonephritis), endocrine disorders (e.g. Addison's disease,
 CC hyperthyroidism, hyperpituitarism), liver diseases and disorders,
 CC reproductive system disorders (e.g. endometriosis), infectious diseases,
 CC and pancreatic disorders. Many other diseases and disorders are listed in
 CC the specification. They also useful as a vaccine adjuvant. Further they
 CC are useful to enhance or inhibit complement mediated cell lysis, for
 CC stimulating wound and tissue repair, angiogenesis, and the repair of
 CC vascular or lymphatic diseases or disorders. They are also useful to
 CC prevent hair loss, to modulate mammalian characteristics such as body
 CC height, weight, hair colour, and to increase or decrease storage
 CC capabilities, fat content, lipid, protein, carbohydrate, vitamins,
 CC minerals, cofactors or other nutritional components. The proteins are
 CC also useful for identifying binding partners. The present sequence
 CC represents a secreted protein of the invention

XX Sequence 133 AA;

Query Match 9.2%; Score 12; DB 6; Length 133;

Best Local Similarity 100.0%; Pred. No. 0.00025;

Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 107 YGGCGGNNNFQ 118

Db 107 YGGCGGNNNFQ 118

RESULT 39

ADAl9812

ID ADAl9812 standard; protein; 133 AA.

AC ADAl9812;

XX 20-NOV-2003 (first entry)

XX Human EPPIN protein SEQ ID NO:13.

XX DJ11; Kunitz-type protease inhibitor domain; antiinflammatory;
 KW anti-allergic; thrombolytic; anticoagulant; cardiant; vasotropic;
 KW antibacterial; immunosuppressive; antirheumatic; antiarthritic;
 KW nephrotropic; antipsoriatic; vulnary; protease inhibitor; gene therapy;
 KW acute pancreatitis; pulmonary injury; allergy-induced protease release;
 KW deep vein thrombosis; myocardial infarction; shock; septic shock;
 KW hyperfibrinolytic haemorrhage; inflammatory disorder; emphysema;
 KW idiopathic pulmonary fibrosis; rheumatoid arthritis; glomerulonephritis;
 KW chronic inflammatory bowel disease; psoriasis; EPPIN.

XX Homo sapiens.

XX WO2003070770-A2.

XX 28-AUG-2003.

XX 18-FEB-2003; 2003WO-BP001629.

XX 21-FEB-2002; 2002US-0358683P.

XX (GENE-) GENEPROT INC.

XX Bougueleret L, Bairoch A, Niknejad A;

XX WPI; 2003-663849/62.

XX New engineered human Kunitz-type protease inhibitor for diagnosing,
 PT preventing or treating conditions associated with excessive proteinase
 PT activity, e.g. inflammation, pulmonary injuries, myocardial infarction or
 PT hemorrhage.

PS Disclosure; Fig 1; 87pp; English.

XX The present invention describes an isolated, purified or recombinant DJ11
 CC polypeptide comprising a Kunitz-type protease inhibitor domain or its
 CC biologically active portion. The polypeptide comprises at least 98 %
 CC identity to residues 77-127 of a 131 amino acid sequence (S1, see
 CC ADA19800), or to residues 52-102 of a 106 amino acid sequence (S2, see
 CC ADA19801). DJ11 has antiinflammatory, anti-allergic, thrombolytic,
 CC anticoagulant, cardiant, vasotropic, antibacterial, immunosuppressive,
 CC antirheumatic, antiarthritic, nephrotropic, antipsoriatic and vulnary
 CC activities, and can be used as a protease inhibitor and in gene therapy.
 CC Composition and methods from the present invention can be used in
 CC diagnosing, preventing or treating conditions associated with excessive
 CC proteinase activity, such as acute pancreatitis, pulmonary injury;
 CC allergy-induced protease release, deep vein thrombosis, myocardial
 CC infarction, shock (including septic shock), hyperfibrinolytic
 CC haemorrhage, and especially, inflammatory disorders (e.g. emphysema,
 CC idiopathic pulmonary fibrosis, rheumatoid arthritis, glomerulonephritis,
 CC chronic inflammatory bowel disease or psoriasis). The DJ11 proteins may
 CC be used in preserving platelet function, organ preservation or in wound
 CC healing. The polynucleotide sequence encoding DJ11 may be used as
 CC hybridisation probes, in chromosome and gene mapping, in the generation
 CC of antisense RNA and DNA, and as targets for pharmaceutical intervention.
 CC The present sequence represents a human EPPIN protein given in comparison
 CC with DJ11 proteins in the exemplification of the present invention.

XX Sequence 133 AA;

Query Match 9.2%; Score 12; DB 7; Length 133;

Best Local Similarity 100.0%; Pred. No. 0.00025;

Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 107 YGGCGGNNNFQ 118

Db 107 YGGCGGNNNFQ 118

RESULT 40

ADG89802

ID ADG89802 standard; protein; 133 AA.

XX ADG89802;

XX 11-MAR-2004 (first entry)

XX Human protein from secreted protein gene 24 #1.

XX Secreted protein; gene therapy; neural disorder; immune system disorders;
 KW muscular disorder; reproductive disorder; gastrointestinal disorder;
 KW pulmonary disorder; cardiovascular disorder; renal disorder;
 KW proliferative disorder; cancer; systemic lupus erythematosus;
 KW rheumatoid arthritis; multiple sclerosis; thyroiditis; anaemia;
 KW Grave's disease; diabetes; hepatitis; asthma; allergy; nephritis;
 KW Parkinson's disease; Alzheimer's disease; atherosclerosis;
 KW myocardial infarction; AIDS; infection; human.

XX Homo sapiens.

XX US2003225009-A1.

XX 04-DEC-2003.

XX 30-JAN-2002; 2002US-00058993.

XX 14-MAR-1997; 97US-0040710P.

XX 14-MAR-1997; 97US-0040762P.

XX 30-MAY-1997; 97US-0048100P.

XX 30-MAY-1997; 97US-0048189P.

XX 30-MAY-1997; 97US-0048357P.

XX 30-MAY-1997; 97US-0050934P.

XX 06-JUN-1997; 97US-0048970P.

XX 05-SEP-1997; 97US-0057765P.

XX 19-DEC-1997; 97US-0068368P.

CC disease, adult respiratory distress syndrome, allergies, ankylosing
CC spondylitis and amyloidosis
XX
SQ Sequence 164 AA;

Query Match 9.2%; Score 12; DB 3; Length 164;
Best Local Similarity 100.0%; Pred. No. 0.0003;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 107 YGCGCGNNNF 118
| | | | | | | | | |
DB 138 YGCGCGNNNF 149

RESULT 42
AAE13092
ID AAE13092 standard; peptide; 54 AA.
XX
AC AAE13092;
XX
DT 28-JAN-2002 (first entry)
XX
DE Trypsin inhibitor peptide.
XX
KW BTL.009 protein; serine proteinase inhibitor; cytostatic; therapeutic;
KW nephrotropic; idiopathic pulmonary fibrosis; cystic fibrosis; emphysema;
KW rheumatoid arthritis; adult respiratory distress syndrome; angioplasty;
KW blood coagulation; glomerulonephritis; prophylactic; platelet activation;
KW neutrophil; monocyte; granulocyte; organ failure; inflammatory disease;
KW elastase inhibitor; chymotrypsin inhibitor; lung injury; vascular injury;
KW trypsin inhibitor.
XX
OS Unidentified.
XX
PN US6294648-B1.
XX
PD 25-SEP-2001.
XX
PF 20-JUL-1999; 99US-00358569.
XX
PR 20-JUL-1999; 99US-00358569.
XX
PA (FARB) BAYER CORP.
XX
PI Delaria K, Roczniak S, Davies C;
XX
DR WPI; 2001-662224/76.
XX
PT New isolated protein for inhibiting human serine proteinase activity in the
PT treatment of e.g. emphysema and adult respiratory distress syndrome.
XX
PS Disclosure; Col 5-6; 16pp; English.
XX
CC The invention relates to human BTL.009 protein, a serine proteinase
CC inhibitor of the Kunitz family that exhibits greater potency towards
CC neutral serine proteinases. BTL.009 protein is found to inhibit leukocyte
CC elastase, chymotrypsin-like protease and trypsin-like protease. BTL.009
CC protein is useful for treating emphysema, idiopathic pulmonary fibrosis,
CC adult respiratory distress syndrome, cystic fibrosis, rheumatoid
CC arthritis, organ failure, glomerulonephritis, other inflammatory diseases
CC and diseases involving lung and vascular injury. BTL.009 is also useful
CC for preventing neutrophil and monocyte activation and formation of active
CC oxygen species during the oxidative burst of stimulated granulocytes.
CC BTL.009 is useful for reducing platelet activation and blood coagulation
CC and for the prophylactic or therapeutic treatment of patients undergoing
CC angioplasty. The present sequence is trypsin inhibitor peptide related to
CC the invention
XX
SQ Sequence 54 AA;

Query Match 8.4%; Score 11; DB 4; Length 54;
Best Local Similarity 100.0%; Pred. No. 0.0013;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 107 YGCGCGNNNF 117
| | | | | | | | | |
DB 33 YGCGCGNNNF 43

RESULT 43
ADA19815
ID ADA19815 standard; protein; 136 AA.
XX
AC ADA19815;
XX
DT 20-NOV-2003 (first entry)
XX
DE Mouse DJ11 protein SEQ ID NO:16.
XX
KW DJ11; Kunitz-type protease inhibitor domain; antiinflammatory;
KW anti-allergic; thrombolytic; anticoagulant; cardiant; vasotropic;
KW antibacterial; immunosuppressive; antirheumatic; antiarthritic;
KW nephrotropic; antipsoriatic; vulnery; protease inhibitor; gene therapy;
KW acute pancreatitis; pulmonary injury; allergy-induced protease release;
KW deep vein thrombosis; myocardial infarction; shock; septic shock;
KW hyperfibrinolytic haemorrhage; inflammatory disorder; emphysema;
KW idiopathic pulmonary fibrosis; rheumatoid arthritis; glomerulonephritis;
KW chronic inflammatory bowel disease; psoriasis.
XX
OS Mus musculus.
XX
PN WO2003070770-A2.
XX
PD 28-AUG-2003.
XX
PF 18-FEB-2003; 2003WO-EP001629.
XX
PR 21-FEB-2002; 2002US-0358683P.
XX
PA (GENE-) GENEPROT INC.
XX
PI Bougueleret L, Bairoch A, Niknejad A;
XX
DR WPI; 2003-663849/62.
XX
PT New engineered human Kunitz-type protease inhibitor for diagnosing,
PT preventing or treating conditions associated with excessive proteinase
PT activity, e.g. inflammation, pulmonary injuries, myocardial infarction or
PT hemorrhage.
XX
PS Disclosure; Fig 1; 87pp; English.
XX
CC The present invention describes an isolated, purified or recombinant DJ11
CC polypeptide comprising a Kunitz-type protease inhibitor domain or its
CC biologically active portion. The polypeptide comprises at least 98 %
CC identity to residues 77-127 of a 131 amino acid sequence (S1, see
CC ADA19800), or to residues 52-102 of a 106 amino acid sequence (S2, see
CC ADA19801). DJ11 has antiinflammatory, antiallergic, thrombolytic,
CC anticoagulant, cardiant, vasotropic, antibacterial, immunosuppressive,
CC antirheumatic, antiarthritic, nephrotropic, antipsoriatic and vulnery
CC activities, and can be used as a protease inhibitor and in gene therapy.
CC Composition and methods from the present invention can be used in
CC diagnosing, preventing or treating conditions associated with excessive
CC proteinase activity, such as acute pancreatitis, pulmonary injury,
CC allergy-induced protease release, deep vein thrombosis, myocardial
CC infarction, shock (including septic shock), hyperfibrinolytic
CC haemorrhage, and especially, inflammatory disorders (e.g. emphysema,
CC idiopathic pulmonary fibrosis, rheumatoid arthritis, glomerulonephritis,
CC chronic inflammatory bowel disease or psoriasis). The DJ11 proteins may
CC be used in preserving platelet function, organ preservation or in wound
CC healing. The polynucleotide sequence encoding DJ11 may be used as
CC hybridisation probes, in chromosome and gene mapping, in the generation
CC of antisense RNA and DNA, and as targets for pharmaceutical intervention.
CC The present sequence represents a mouse DJ11 protein given in comparison
CC with DJ11 proteins in the exemplification of the present invention.
XX

SQ Sequence 136 AA;
Query Match 7.6%; Score 10; DB 7; Length 136;
Best Local Similarity 100.0%; Pred. No. 0.034;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 104 EPIYGCGQGN 113
| | | | | | | | | |
Db 104 EPIYGCGQGN 113

RESULT 44
AAR78401
ID AAR78401 standard; peptide; 58 AA.
AC AAR78401;
XX
DT 27-FEB-1996 (first entry)
XX
DE Human LACI-K1 derivative NS9.
XX
KW Human; lipoprotein-associated coagulation inhibitor; peptide library;
KW inhibitor; plasmin; bovine; pancreatic trypsin inhibitor; Kunitz domain;
KW fibrinolysis; fibrinogenolysis; bleeding; thrombolytic.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Misc-difference 17
FT /note= "residue change: Ile to Arg"
FT Misc-difference 18
FT /note= "residue change: Met to Phe"
FT Misc-difference 19
FT /note= "residue change: Lys to Glu"
FT Misc-difference 32
FT /note= "residue change: Glu to Gln"
FT Misc-difference 39
FT /note= "residue change: Glu to Gln"
XX
FN WO9518830-A2.
XX
PD 13-JUL-1995.
XX
PF 11-JAN-1995; 95WO-US000298.
XX
PR 11-JAN-1994; 94US-00179658.
PR 10-MAR-1994; 94US-00208265.
XX
PA (PROT-) PROTEIN ENG CORP.
XX
PI Markland W, Ladner RC;
XX
DR WPI; 1995-255042/33.
XX
PT Novel plasmin inhibiting protein comprising a Kunitz Domain - useful to
PT prevent/treat disorders attributable to excess plasmin activity.
XX
PS Example 2; Page 29; 59pp; English.
XX
CC The peptides AAR78391-R78425 are derivatives of the human lipoprotein-
CC associated coagulation inhibitor (LACI) Kunitz domain 1. The peptides
CC were isolated from a peptide library generated based on the human LACI-K1
CC domain (AAR78390). The peptides are mutants homologous to bovine
CC pancreatic trypsin inhibitor (BPTI) Kunitz domains that inhibit plasmin.
CC The peptides can be used to prevent or treat a clinical condition
CC exacerbated by plasmin e.g. inappropriate fibrinolysis or
CC fibrinogenolysis, excessive bleeding associated with thrombolytics
XX
SQ Sequence 58 AA;
Query Match 6.9%; Score 9; DB 2; Length 58;
Best Local Similarity 100.0%; Pred. No. 0.19;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 105 FIYGCGQGN 113
| | | | | | | | | |
Db 33 FIYGCGQGN 41

RESULT 45
ADE64021
ID ADE64021 standard; protein; 126 AA.
XX
AC ADE64021;
XX
DT 29-JAN-2004 (first entry)
XX
DE Human Protein Q15332, SEQ ID NO 9967.
XX
KW Human; pain; neuronal tissue; gene therapy;
KW spinal segmental nerve injury; chronic constriction injury; CCI;
KW spared nerve injury; SNI; Chung.
XX
OS Homo sapiens.
XX
FN WO2003016475-A2.
XX
PD 27-FEB-2003.
XX
PF 14-AUG-2002; 2002WO-US025765.
XX
PR 14-AUG-2001; 2001US-0312147P.
PR 01-NOV-2001; 2001US-0346382P.
PR 26-NOV-2001; 2001US-0333347P.
XX
PA (GEHO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
XX
PI Woolf C, D'urso D, Befort K, Costigan M;
XX
DR WPI; 2003-268312/26.
DR GENBANK; Q15332.
XX
PT New composition comprising two or more isolated polypeptides, useful for
PT preparing a medicament for treating pain in an animal.
XX
PS Claim 1; Page; 1017pp; English.
XX
CC The invention discloses a composition comprising two or more isolated rat
CC or human polynucleotides or a polynucleotide which represents a fragment,
CC derivative or allelic variation of the nucleic acid sequence. Also
CC claimed are a vector comprising the novel polynucleotide, a host cell
CC comprising the vector, a method for identifying a nucleotide sequence
CC which is differentially regulated in an animal subjected to pain and a
CC kit to perform the method, an array, a method for identifying an agent
CC that increases or decreases the expression of the polynucleotide sequence
CC that is differentially expressed in neuronal tissue of a first animal
CC subjected to pain, a method for identifying a compound which regulates
CC the expression of a polynucleotide sequence which is differentially
CC expressed in an animal subjected to pain, a method for identifying a
CC compound that regulates the activity of one or more of the
CC polynucleotides, a method for producing a pharmaceutical composition, a
CC method for identifying a compound or small molecule that regulates the
CC activity in an animal of one or more of the polypeptides given in the
CC specification, a method for identifying a compound useful in treating
CC pain and a pharmaceutical composition comprising the one or more
CC polypeptides or their antibodies. The polynucleotide or the compound that
CC modulates its activity is useful for preparing a medicament for treating
CC pain (e.g. spinal segmental nerve injury (Chung), chronic constriction
CC injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene
CC therapy). The sequence presented is a human protein (shown in Table 2 of
CC the specification) which is differentially expressed during pain. Note:
CC The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic form directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.


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SQ Sequence 126 AA;
Query Match 6.1%; Score 8; DB 7; Length 126;
Best Local Similarity 100.0%; Pred. No. 4.2;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 82 EAGPCLAS 89
Db 35 EAGPCLAS 42
|||||
35 EAGPCLAS 42

RESULT 46
AAU79498
ID AAU79498 standard; protein; 140 AA.
XX
AC AAU79498;
XX
DT 15-JUL-2002 (first entry)
XX
DE Mouse partial ADAMTS protein #1.
XX
KW Mouse; ADAMTS; cytostatic; antidiabetic; antirheumatic; antiarthritic;
KW antiulcer; vulnery; neovascularisation; angioma; diabetic omentopathy;
KW chronic rheumatoid arthritis; gene therapy; refractory skin ulcer;
KW gastric ulcer; post-operative healing failure;
KW repolysin-type 2N-metalloprotease domain; disintegrin-like domain; TSP1;
KW thrombospondin type 1 domain; sexual cycle; tumour; 5P-syndrome deletion;
KW chromosome 5p15.2-15.3; Cri-du-chat syndrome.
XX
OS Mus musculus.
XX
PN WO200231163-A1.
XX
PD 18-APR-2002.
XX
PF 11-OCT-2001; 2001WO-JP008913.
XX
PR 11-OCT-2000; 2000JP-00311309.
PR 02-APR-2001; 2001JP-00102905.
XX
PA (KAZU-) KAZUSA DNA RES INST FOUND.
PA (MITS-) MITSUBISHI PHARMA CORP.
XX
PI Ohara O, Nagase T, Nomura N, Yano K, Murakami K, Yasuda S;
PI Kanzaki K;
XX
WPI; 2002-372277/40.
DR N-PSDB; ABK49823.
XX
PT Human brain-originated ADAMTS family polypeptide and encoded gene,
PT applicable in diagnosis and screening compounds for drug compositions in
PT treating diseases due to e.g. neovascularization.
XX
PS Example 8; Page 151-152; 172pp; Japanese.
XX
CC The invention relates to a polypeptide belonging to the ADAMTS family is
CC selected from sequences appearing as AAU79496, AAU79497 and AAU79499, a
CC protein that contains the polypeptide, a protein having not less than 50%
CC homology with the amino acid sequence of the polypeptides or a
CC polypeptide modified from any of the polypeptides but with some amino
CC acids deleted, substituted, added or inserted. Also included are the
CC polynucleotides encoding the polypeptides (or their complementary strands
CC or variants), a recombinant vector containing any of the polynucleotides,
CC a transformant which is transformed with the recombinant vector,
CC producing the polypeptide, protein or peptide by culturing the
CC transformant, an antibody that can recognize the polypeptide, protein or
CC peptide and screening compounds to promote or inhibit activity of the
CC polypeptide or protein, or to promote or inhibit expression of the
CC polynucleotide by using the polypeptide, protein, peptide, the
CC polynucleotide, vector, transformant or/and antibody, particularly in the
CC presence of a test compound for contact before evaluating the activity by
CC measuring signal changes. The polypeptide and encoded gene are applicable
CC in diagnosis and screening compounds for drug compositions in treating
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CC diseases due to neovascularisation, diabetic omentopathy, chronic
CC rheumatoid arthritis, angioma, refractory skin and gastric ulcers and
CC post-operative healing failure, including gene therapy. The gene encoding
CC such polypeptide has conserved repolysin-type 2N- metalloprotease
CC domain, disintegrin-like domain and TSP1 (thrombospondin type 1) domain.
CC Its encoded protein is characterised by high expression in ovaries,
CC changes in expression dose depending on the sexual cycle, a decrease in
CC tumour cell and location of the gene on the 5P-syndrome deletion site on
CC chromosome 5p15.2-15.3 (associated with Cri-du-chat syndrome). The
CC present sequence represents a ADAMTS protein of the invention
XX
XX Sequence 140 AA;
Query Match 6.1%; Score 8; DB 5; Length 140;
Best Local Similarity 100.0%; Pred. No. 4.6;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 70 LDFRKDIC 77
Db 47 LDFRKDIC 54
|||||
47 LDFRKDIC 54

RESULT 47
AAU80150
ID AAU80150 standard; protein; 140 AA.
XX
AC AAU80150;
XX
DT 15-JUL-2002 (first entry)
XX
DE Mouse partial ADAMTS protein #3.
XX
KW Mouse; ADAMTS; cytostatic; antidiabetic; antirheumatic; antiarthritic;
KW antiulcer; vulnery; neovascularisation; angioma; diabetic omentopathy;
KW chronic rheumatoid arthritis; gene therapy; refractory skin ulcer;
KW gastric ulcer; post-operative healing failure;
KW repolysin-type 2N-metalloprotease domain; disintegrin-like domain; TSP1;
KW thrombospondin type 1 domain; sexual cycle; tumour; 5P-syndrome deletion;
KW chromosome 5p15.2-15.3; Cri-du-chat syndrome.
XX
OS Mus musculus.
XX
PN WO200231163-A1.
XX
PD 18-APR-2002.
XX
PF 11-OCT-2001; 2001WO-JP008913.
XX
PR 11-OCT-2000; 2000JP-00311309.
PR 02-APR-2001; 2001JP-00102905.
XX
PA (KAZU-) KAZUSA DNA RES INST FOUND.
PA (MITS-) MITSUBISHI PHARMA CORP.
XX
PI Ohara O, Nagase T, Nomura N, Yano K, Murakami K, Yasuda S;
PI Kanzaki K;
XX
WPI; 2002-372277/40.
DR
XX
PT Human brain-originated ADAMTS family polypeptide and encoded gene,
PT applicable in diagnosis and screening compounds for drug compositions in
PT treating diseases due to e.g. neovascularization.
XX
PS Example 8; Fig 8; 172pp; Japanese.
XX
CC The invention relates to a polypeptide belonging to the ADAMTS family is
CC selected from sequences appearing as AAU79496, AAU79497 and AAU79499, a
CC protein that contains the polypeptide, a protein having not less than 50%
CC homology with the amino acid sequence of the polypeptides or a
CC polypeptide modified from any of the polypeptides but with some amino
CC acids deleted, substituted, added or inserted. Also included are the
CC polynucleotides encoding the polypeptides (or their complementary strands
CC or variants), a recombinant vector containing any of the polynucleotides,
CC a transformant which is transformed with the recombinant vector,
CC producing the polypeptide, protein or peptide by culturing the
CC transformant, an antibody that can recognize the polypeptide, protein or
CC peptide and screening compounds to promote or inhibit activity of the
CC polypeptide or protein, or to promote or inhibit expression of the
CC polynucleotide by using the polypeptide, protein, peptide, the
CC polynucleotide, vector, transformant or/and antibody, particularly in the
CC presence of a test compound for contact before evaluating the activity by
CC measuring signal changes. The polypeptide and encoded gene are applicable
CC in diagnosis and screening compounds for drug compositions in treating
```

CC a transformant which is transformed with the recombinant vector,
 CC producing the polypeptide, protein or peptide by culturing the
 CC transformant, an antibody that can recognize the polypeptide, protein or
 CC peptide and screening compounds to promote or inhibit activity of the
 CC polypeptide or protein, or to promote or inhibit expression of the
 CC polynucleotide by using the polypeptide, protein, peptide, the
 CC polynucleotide, vector, transformant or/and antibody, particularly in the
 CC presence of a test compound for contact before evaluating the activity by
 CC measuring signal changes. The polypeptide and encoded gene are applicable
 CC in diagnosis and screening compounds for drug compositions in treating
 CC diseases due to neovascularisation, diabetic omentopathy, chronic
 CC rheumatoid arthritis, angiora, refractory skin and gastric ulcers and
 CC post-operative healing failure, including gene therapy. The gene encoding
 CC such polypeptide has conserved repressin-type ZN- metalloprotease
 CC domain, disintegrin-like domain and TSPI (Chromobospondin type I) domain.
 CC Its encoded protein is characterised by high expression in ovaries,
 CC changes in expression dose depending on the sexual cycle, a decrease in
 CC tumour cell and location of the gene on the 5p-syndrome deletion site on
 CC chromosome 5p15.2-15.3 (associated with Cri-du-chat syndrome). The
 CC present sequence represents a ADAMTS protein of the invention
 XX
 SQ Sequence 140 AA;

Query Match 6.1%; Score 8; DB 5; Length 140;
 Best Local Similarity 100.0%; Pred. No. 4.6;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 70 LDFRKDIC 77
 Db 47 LDFRKDIC 54
 |||||

RESULT 48
 AAM18394
 ID AAM18394 standard; protein; 166 AA.

XX AC AAM18394;

DT 12-OCT-2001 (first entry)

XX Peptide #4828 encoded by probe for measuring cervical gene expression.
 DE Probe: human; microarray; gene expression; cervical epithelial cell;
 KW cervical cancer.

XX OS Homo sapiens.

XX WO200157278-A2.

XX PN 09-AUG-2001.

XX PF 30-JAN-2001; 2001WO-US000670.

XX 04-FEB-2000; 2000US-0180312P.

XX 26-MAY-2000; 2000US-0207456P.

XX 30-JUN-2000; 2000US-00608408.

XX 03-AUG-2000; 2000US-00632366.

XX 21-SEP-2000; 2000US-0234687P.

XX 27-SEP-2000; 2000US-0236359P.

XX 04-OCT-2000; 2000GB-00024263.

XX (MOLE-) MOLECULAR DYNAMICS INC.

XX Penn SG, Hanzel DK, Chen W, Rank DR;

XX WPI; 2001-488901/53.

XX Human genome-derived single exon nucleic acid probes useful for analyzing

PT gene expression in human cervical epithelial cells.

XX Claim 27; SEQ ID NO 23220; 487pp; English.

XX The present invention relates to human single exon nucleic acid probes

CC (SENP: see AAI10068-AAI28459). The present sequence is a peptide encoded
 CC by one such probe. The SENPs are derived from human HeLa cells. The SENPs
 CC measuring human gene expression in a sample derived from human cervical
 CC epithelial cells. By measuring gene expression, the probes are therefore
 CC useful in grading and/or staging of diseases of the cervix, notably
 CC cervical cancer. Note: The sequence data for this patent did not form
 CC part of the printed specification, but was obtained in electronic format
 CC directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
 XX
 SQ Sequence 166 AA;

Query Match 6.1%; Score 8; DB 4; Length 166;
 Best Local Similarity 100.0%; Pred. No. 5.4;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 LVPFILLG 17
 Db 36 LVPFILLG 43
 |||||

RESULT 49
 ABB37425
 ID ABB37425 standard; peptide; 166 AA.

XX AC ABB37425;

DT 04-FEB-2002 (first entry)

DE Peptide #4931 encoded by human foetal liver single exon probe.

XX Human; foetal liver; gene expression; single exon nucleic acid probe.

XX OS Homo sapiens.

XX WO200157277-A2.

XX PN 09-AUG-2001.

XX PF 30-JAN-2001; 2001WO-US000669.

XX 04-FEB-2000; 2000US-0180312P.

XX 26-MAY-2000; 2000US-0207456P.

XX 30-JUN-2000; 2000US-00608408.

XX 03-AUG-2000; 2000US-00632366.

XX 21-SEP-2000; 2000US-0234687P.

XX 27-SEP-2000; 2000US-0236359P.

XX 04-OCT-2000; 2000GB-00024263.

XX (MOLE-) MOLECULAR DYNAMICS INC.

XX Penn SG, Hanzel DK, Chen W, Rank DR;

XX WPI; 2001-483447/52.

XX Human genome-derived single exon nucleic acid probes useful for analyzing
 PT gene expression in human fetal liver.

XX Claim 27; SEQ ID NO 30060; 639pp + Sequence Listing; English.

XX The invention relates to a single exon nucleic acid probe for measuring
 CC human gene expression in a sample derived from human foetal liver. The
 CC single exon nucleic acid probes may be used for predicting, measuring and
 CC displaying gene expression in samples derived from human fetal liver. The
 CC present sequence is a peptide encoded by a single exon nucleic acid probe
 CC of the invention. Note: The sequence data for this patent did not form
 CC part of the printed specification, but was obtained in electronic format
 CC directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
 XX
 SQ Sequence 166 AA;

Query Match 6.1%; Score 8; DB 4; Length 166;
 Best Local Similarity 100.0%; Pred. No. 5.4;

CC domain, disintegrin-like domain and TSPI (thrombospondin type 1) domain.
CC Its encoded protein is characterised by high expression in ovaries,
CC changes in expression dose depending on the sexual cycle, a decrease in
CC tumour cell and location of the gene on the 5p-syndrome deletion site on
CC chromosome 5p15.2-15.3 (associated with Cri-du-chat syndrome). The
CC present sequence represents a ADAMTS protein of the invention
XX
SQ Sequence 175 AA;
Query Match 6.1%; Score 8; DB 5; Length 175;
Best Local Similarity 100.0%; Pred. No. 5.6;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 70 LDFRKDIC 77
| | | | | | | |
Db 82 LDFRKDIC 89
Search completed: September 21, 2005, 16:47:47
Job time : 111 secs

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 10 LVPFILLG 17
| | | | | | | |
Db 36 LVPFILLG 43
RESULT 50
AAU79499
ID AAU79499 standard; protein; 175 AA.
XX
AC AAU79499;
XX
DT 15-JUL-2002 (first entry)
XX
DE Mouse partial ADAMTS protein #2.
XX
KW Mouse; ADAMTS; cytostatic; antidiabetic; antirheumatic; antiarthritic;
KW antiulcer; vulnery; neovascularisation; angioma; diabetic omentopathy;
KW chronic rheumatoid arthritis; gene therapy; refractory skin ulcer;
KW gastric ulcer; post-operative healing failure;
KW repolysin-type ZN-metalloprotease domain; disintegrin-like domain; TSPI;
KW thrombospondin type 1 domain; sexual cycle; tumour; 5p-syndrome deletion;
KW chromosome 5p15.2-15.3; Cri-du-chat syndrome.
XX
OS Mus musculus.
XX
PN WO200231163-A1.
XX
PD 18-APR-2002.
XX
PF 11-OCT-2001; 2001WO-JP008913.
XX
PR 11-OCT-2000; 2000JP-00311309.
PR 02-APR-2001; 2001JP-00102905.
XX
PA (KAZU-) KAZUSA DNA RES INST FOUND.
PA (MITS-) MITSUBISHI PHARMA CORP.
XX
PI Ohara O, Nagase T, Nomura N, Yano K, Murakami K, Yasuda S;
PI Kanzaki K;
XX
DR WPI; 2002-372277/40.
DR N-PSDB; ABK49824.
XX
PT Human brain-originated ADAMTS family polypeptide and encoded gene,
PT applicable in diagnosis and screening compounds for drug compositions in
PT treating diseases due to e.g. neovascularization.
XX
PS Claim 1; Page 154-155; 172pp; Japanese.
XX
CC The invention relates to a polypeptide belonging to the ADAMTS family is
CC selected from sequences appearing as AAU79496, AAU79497 and AAU79499, a
CC protein that contains the polypeptide, a protein having not less than 50%
CC homology with the amino acid sequence of the polypeptides or a
CC polypeptide modified from any of the polypeptides but with some amino
CC acids deleted, substituted, added or inserted. Also included are the
CC polynucleotides encoding the polypeptides (or their complementary strands
CC or variants), a recombinant vector containing any of the polynucleotides,
CC a transformant which is transformed with the recombinant vector,
CC producing the polypeptide, protein or peptide by culturing the
CC transformant, an antibody that can recognize the polypeptide, protein or
CC peptide and screening compounds to promote or inhibit activity of the
CC polypeptide or protein, or to promote or inhibit expression of the
CC polynucleotide by using the polypeptide, protein, peptide, the
CC polynucleotide, vector, transformant or/and antibody, particularly in the
CC presence of a test compound for contact before evaluating the activity by
CC measuring signal changes. The polypeptide and encoded gene are applicable
CC in diagnosis and screening compounds for drug compositions in treating
CC diseases due to neovascularisation, diabetic omentopathy, chronic
CC rheumatoid arthritis, angioma, refractory skin and gastric ulcers and
CC post-operative healing failure, including gene therapy. The gene encoding
CC such polypeptide has conserved repolysin-type ZN- metalloprotease

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OM protein - protein search, using sw model

Run on: September 21, 2005, 16:42:25 ; Search time 32 Seconds
(without alignments)
305.595 Million cell updates/sec

Title: US-10-807-204-1
Perfect score: 131
Sequence: 1 MGLSGLLPILVPFILLGDIQ.....GNNNFQTEICLVTCCKYH 131

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 513545 seqs, 74649064 residues

Word size : 0

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 50 summaries

Database : Issued Patents, AA:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	12	9.2	43	US-09-358-569D-13	Sequence 13, Appl
2	12	9.2	54	US-09-358-569D-8	Sequence 8, Appl
3	12	9.2	55	US-09-358-569D-1	Sequence 1, Appl
4	12	9.2	58	US-09-369-494-8	Sequence 8, Appl
5	12	9.2	58	US-09-569-670-8	Sequence 8, Appl
6	12	9.2	64	US-09-358-569D-10	Sequence 10, Appl
7	12	9.2	133	US-09-152-060-75	Sequence 75, Appl
8	11	8.4	54	US-09-358-569D-9	Sequence 9, Appl
9	11	8.4	67	US-08-358-160-123	Sequence 123, App
10	10	7.6	62	US-08-358-160-155	Sequence 155, App
11	10	7.6	63	US-08-358-160-159	Sequence 159, App
12	9	6.9	58	US-08-676-124-13	Sequence 13, Appl
13	9	6.9	58	US-09-414-878-13	Sequence 13, Appl
14	9	6.9	58	US-09-240-136-13	Sequence 13, Appl
15	9	6.9	58	US-09-638-770A-13	Sequence 13, Appl
16	8	6.1	77	5466783-4	Patent No. 5466783
17	8	6.1	77	5466783-4	Patent No. 5466783
18	8	6.1	767	US-09-949-016-11664	Sequence 11664, A
19	7	5.3	24	US-08-463-155A-29	Sequence 29, Appl
20	7	5.3	24	US-08-463-432B-29	Sequence 29, Appl
21	7	5.3	51	US-07-791-213D-1	Sequence 1, Appl
22	7	5.3	51	US-07-791-213D-2	Sequence 2, Appl
23	7	5.3	51	US-07-791-213D-4	Sequence 4, Appl
24	7	5.3	51	US-07-791-213D-7	Sequence 7, Appl
25	7	5.3	51	US-07-791-213D-17	Sequence 17, Appl
26	7	5.3	51	US-07-791-213D-108	Sequence 108, App
27	7	5.3	51	US-08-055-988-3	Sequence 3, Appl

ALIGNMENTS

RESULT 1

US-09-358-569D-13

; Sequence 13, Application US/09358569D

; Patent No. 6294648

; GENERAL INFORMATION:

; APPLICANT: Delaria, Kathy

; APPLICANT: Rocznik, Steve

; APPLICANT: Davies, Christopher

; TITLE OF INVENTION: Protein Having Proteinase Inhibitor Activity

; FILE REFERENCE: MSB-7259

; CURRENT APPLICATION NUMBER: US/09/358.569D

; CURRENT FILING DATE: 1999-07-20

; NUMBER OF SEQ ID NOS: 15

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 13

; LENGTH: 43

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence: Artificial

; OTHER INFORMATION: sequence derived from EST database

US-09-358-569D-13

Query Match

Best Local Similarity 9.2%; Score 12; DB 3; Length 43;

Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 107 YGGCQGNNNFQ 118

|||||

Db 21 YGGCQGNNNFQ 32

RESULT 2

US-09-358-569D-8

; Sequence 8, Application US/09358569D

; Patent No. 6294648

; GENERAL INFORMATION:

; APPLICANT: Delaria, Kathy

; APPLICANT: Rocznik, Steve

; APPLICANT: Davies, Christopher

; TITLE OF INVENTION: Protein Having Proteinase Inhibitor Activity

; FILE REFERENCE: MSB-7259

; CURRENT APPLICATION NUMBER: US/09/358.569D

; CURRENT FILING DATE: 1999-07-20

; NUMBER OF SEQ ID NOS: 15

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; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 8
; LENGTH: 54
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:derived from
; OTHER INFORMATION: EST sequence database
US-09-358-569D-8

Query Match          9.2%; Score 12; DB 3; Length 54;
Best Local Similarity 100.0%; Pred. No. 1.3e-05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 107 YGGCQGNNNNFQ 118
Db 33 YGGCQGNNNNFQ 44

RESULT 3
US-09-358-569D-1
; Sequence 1, Application US/09358569D
; Patent No. 6294648
; GENERAL INFORMATION:
; APPLICANT: Delaria, Kathy
; APPLICANT: Rocznia, Steve
; APPLICANT: Davies, Christopher
; TITLE OF INVENTION: Protein Having Proteinase Inhibitor Activity
; FILE REFERENCE: MSB-7259
; CURRENT APPLICATION NUMBER: US/09/358,569D
; CURRENT FILING DATE: 1999-07-20
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 55
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:derived from
; OTHER INFORMATION: EST sequence database
US-09-358-569D-1

Query Match          9.2%; Score 12; DB 3; Length 55;
Best Local Similarity 100.0%; Pred. No. 1.4e-05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 107 YGGCQGNNNNFQ 118
Db 35 YGGCQGNNNNFQ 46

RESULT 4
US-09-369-494-8
; Sequence 8, Application US/09369494
; Patent No. 6180607
; GENERAL INFORMATION:
; APPLICANT: Davies, Christopher
; APPLICANT: Chen, Dadong
; APPLICANT: Rocznia, Steve
; TITLE OF INVENTION: Protein Having Proteinase Inhibitor Activity
; FILE REFERENCE: MSB-7260
; CURRENT APPLICATION NUMBER: US/09/369,494
; CURRENT FILING DATE: 1999-08-05
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 8
; LENGTH: 58
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:fragment from
; OTHER INFORMATION: computer database
US-09-369-494-8

Query Match          9.2%; Score 12; DB 3; Length 58;
Best Local Similarity 100.0%; Pred. No. 1.4e-05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 107 YGGCQGNNNNFQ 118
Db 37 YGGCQGNNNNFQ 48

Query Match          9.2%; Score 12; DB 3; Length 58;
Best Local Similarity 100.0%; Pred. No. 1.5e-05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 107 YGGCQGNNNNFQ 118
Db 35 YGGCQGNNNNFQ 46

RESULT 5
US-09-569-670-8
; Sequence 8, Application US/09569670
; Patent No. 6689582
; GENERAL INFORMATION:
; APPLICANT: Davies, Christopher
; APPLICANT: Chen, Dadong
; APPLICANT: Rocznia, Steve
; TITLE OF INVENTION: Protein Having Proteinase Inhibitor Activity
; FILE REFERENCE: MSB-7260
; CURRENT APPLICATION NUMBER: US/09/569,670
; CURRENT FILING DATE: 2000-05-12
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 8
; LENGTH: 58
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:fragment from
; OTHER INFORMATION: computer database
US-09-569-670-8

Query Match          9.2%; Score 12; DB 4; Length 58;
Best Local Similarity 100.0%; Pred. No. 1.4e-05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 107 YGGCQGNNNNFQ 118
Db 35 YGGCQGNNNNFQ 46

RESULT 6
US-09-358-569D-10
; Sequence 10, Application US/09358569D
; Patent No. 6294648
; GENERAL INFORMATION:
; APPLICANT: Delaria, Kathy
; APPLICANT: Rocznia, Steve
; APPLICANT: Davies, Christopher
; TITLE OF INVENTION: Protein Having Proteinase Inhibitor Activity
; FILE REFERENCE: MSB-7259
; CURRENT APPLICATION NUMBER: US/09/358,569D
; CURRENT FILING DATE: 1999-07-20
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 10
; LENGTH: 64
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Extension of
; OTHER INFORMATION: Seq Id 1
US-09-358-569D-10

Query Match          9.2%; Score 12; DB 3; Length 64;
Best Local Similarity 100.0%; Pred. No. 1.5e-05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 107 YGGCQGNNNNFQ 118
Db 37 YGGCQGNNNNFQ 48
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RESULT 7
US-09-152-060-75
; Sequence 75, Application US/09152060
; Patent No. 6448230
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 28 Human Secreted Proteins
; FILE REFERENCE: P2003PL.US
; CURRENT APPLICATION NUMBER: US/09/152,060
; CURRENT FILING DATE: 1998-09-11
; EARLIER APPLICATION NUMBER: PCT/US98/04858
; EARLIER FILING DATE: 1998-03-12
; EARLIER APPLICATION NUMBER: 60/040,762
; EARLIER FILING DATE: 1997-03-14
; EARLIER APPLICATION NUMBER: 60/040,710
; EARLIER FILING DATE: 1997-03-14
; EARLIER APPLICATION NUMBER: 60/050,934
; EARLIER FILING DATE: 1997-05-30
; EARLIER APPLICATION NUMBER: 60/048,100
; EARLIER FILING DATE: 1997-05-30
; EARLIER APPLICATION NUMBER: 60/048,357
; EARLIER FILING DATE: 1997-05-30
; EARLIER APPLICATION NUMBER: 60/048,189
; EARLIER FILING DATE: 1997-05-30
; EARLIER APPLICATION NUMBER: 60/057,765
; EARLIER FILING DATE: 1997-09-05
; EARLIER APPLICATION NUMBER: 60/048,970
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/068,368
; EARLIER FILING DATE: 1997-12-19
; NUMBER OF SEQ ID NOS: 118
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 75
; LENGTH: 133
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-152-060-75

Query Match 9.2%; Score 12; DB 4; Length 133;
Best Local Similarity 100.0%; Pred. No. 2.9e-05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 107 YGCGCGNNNFQ 118
Db 107 YGCGCGNNNFQ 118

RESULT 8
US-09-358-569D-9
; Sequence 9, Application US/09358569D
; Patent No. 6294648
; GENERAL INFORMATION:
; APPLICANT: Delaria, Kathy
; APPLICANT: Rocznia, Steve
; APPLICANT: Davies, Christopher
; TITLE OF INVENTION: Protein Having Proteinase Inhibitor Activity
; FILE REFERENCE: MSB-7259
; CURRENT APPLICATION NUMBER: US/09/358,569D
; CURRENT FILING DATE: 1999-07-20
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 9
; LENGTH: 54
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: derived from
; OTHER INFORMATION: EST sequence database
US-09-358-569D-9

Query Match 8.4%; Score 11; DB 3; Length 54;
Best Local Similarity 100.0%; Pred. No. 0.00017;

Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 107 YGCGCGNNNF 117
Db 33 YGCGCGNNNF 43

RESULT 9
US-08-358-160-123
; Sequence 123, Application US/08358160
; Patent No. 5663143
; GENERAL INFORMATION:
; APPLICANT: LEY, Arthur C.
; APPLICANT: LADNER, Robert C.
; APPLICANT: GUTERMAN, Sonia K.
; APPLICANT: ROBERTS, Bruce L.
; APPLICANT: MARKLAND, William
; APPLICANT: KENT, Rachel B.
; TITLE OF INVENTION: ENGINEERED HUMAN-DERIVED KUNITZ
; TITLE OF INVENTION: DOMAINS THAT INHIBIT HUMAN NEUTROPHIL ELASTASE
; NUMBER OF SEQUENCES: 234
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W. Suite 300
; CITY: Washington
; STATE: District of Columbia
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/358,160
; FILING DATE: 16-DEC-1994
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/133,031
; FILING DATE: 13-OCT-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/009,319
; FILING DATE: 26-JAN-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/664,989
; FILING DATE: 01-MAR-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/487,063
; FILING DATE: 02-MAR-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/240,160
; FILING DATE: 02-SEP-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Cooper, Iver P.
; REGISTRATION NUMBER: 28,005
; REFERENCE/DOCKET NUMBER: LEY=1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; TELEX: 248633
; INFORMATION FOR SEQ ID NO: 123:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 67 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-358-160-123

Query Match 8.4%; Score 11; DB 1; Length 67;
Best Local Similarity 100.0%; Pred. No. 0.0002;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 107 YGCGCGNNNF 117
|||||
Db 38 YGCGCGNNNF 48

RESULT 10
US-08-358-160-155
; Sequence 155, Application US/08358160
; Patent No. 5663143
; GENERAL INFORMATION:
; APPLICANT: LEY, Arthur C.
; APPLICANT: LADNER, Robert C.
; APPLICANT: GUTERMAN, Sonia K.
; APPLICANT: ROBERTS, Bruce L.
; APPLICANT: MARKLAND, William
; APPLICANT: KENT, Rachel B.
; APPLICANT: KENT, Rachel B.
; TITLE OF INVENTION: ENGINEERED HUMAN-DERIVED KUNITZ
; TITLE OF INVENTION: DOMAINS THAT INHIBIT HUMAN NEUTROPHIL ELASTASE
; NUMBER OF SEQUENCES: 234
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W. Suite 300
; CITY: Washington
; STATE: District of Columbia
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/358,160
; FILING DATE: 16-DEC-1994
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/133,031
; FILING DATE: 13-OCT-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/009,319
; FILING DATE: 26-JAN-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/664,989
; FILING DATE: 01-MAR-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/487,063
; FILING DATE: 02-MAR-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/240,160
; FILING DATE: 02-SEP-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Cooper, Iver P.
; REGISTRATION NUMBER: 28,005
; REFERENCE/DOCKET NUMBER: LEY=1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; TELEX: 248633
; INFORMATION FOR SEQ ID NO: 155:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 62 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-358-160-155

Query Match 7.6%; Score 10; DB 1; Length 62;
Best Local Similarity 100.0%; Pred. No. 0.0023;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 104 EFIYGGCGN 113
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Db 37 EFIYGGCGN 46

RESULT 11
US-08-358-160-159
; Sequence 159, Application US/08358160
; Patent No. 5663143
; GENERAL INFORMATION:
; APPLICANT: LEY, Arthur C.
; APPLICANT: LADNER, Robert C.
; APPLICANT: GUTERMAN, Sonia K.
; APPLICANT: ROBERTS, Bruce L.
; APPLICANT: MARKLAND, William
; APPLICANT: KENT, Rachel B.
; APPLICANT: KENT, Rachel B.
; TITLE OF INVENTION: ENGINEERED HUMAN-DERIVED KUNITZ
; TITLE OF INVENTION: DOMAINS THAT INHIBIT HUMAN NEUTROPHIL ELASTASE
; NUMBER OF SEQUENCES: 234
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W. Suite 300
; CITY: Washington
; STATE: District of Columbia
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/358,160
; FILING DATE: 16-DEC-1994
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/133,031
; FILING DATE: 13-OCT-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/009,319
; FILING DATE: 26-JAN-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/664,989
; FILING DATE: 01-MAR-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/487,063
; FILING DATE: 02-MAR-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/240,160
; FILING DATE: 02-SEP-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Cooper, Iver P.
; REGISTRATION NUMBER: 28,005
; REFERENCE/DOCKET NUMBER: LEY=1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; TELEX: 248633
; INFORMATION FOR SEQ ID NO: 159:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 63 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-358-160-159

Query Match 7.6%; Score 10; DB 1; Length 63;
Best Local Similarity 100.0%; Pred. No. 0.0023;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 104 EFIYGGCGN 113
|||||
Db 38 EFIYGGCGN 47

RESULT 12
US-08-676-124-13
; Sequence 13, Application US/08676124
; Patent No. 6010880
; GENERAL INFORMATION:
; APPLICANT: MARKLAND, William
; APPLICANT: LADNER, Robert Charles
; TITLE OF INVENTION: INHIBITORS OF HUMAN PLASMIN DERIVED
; TITLE OF INVENTION: FROM FROM THE KUNITZ DOMAINS
; NUMBER OF SEQUENCES: 137
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Browdy and Neimark
; STREET: 419 Seventh Street N.W., Ste. 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: United States of America
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/676.124
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/00298
; FILING DATE: 11-JAN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/179,658
; FILING DATE: 11-JAN-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/208,265
; FILING DATE: 10-MAR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: COOPER, IVER P.
; REGISTRATION NUMBER: 28,005
; REFERENCE/DOCKET NUMBER: MARKLAND-3B
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 58 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-676-124-13

Query Match 6.9%; Score 9; DB 3; Length 58;
Best Local Similarity 100.0%; Pred. No. 0.027;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 105 FIYGGCQGN 113
Db 33 FIYGGCQGN 41

RESULT 13
US-09-414-878-13
; Sequence 13, Application US/09414878
; Patent No. 6071723
; GENERAL INFORMATION:
; APPLICANT: DYAX CORP
; APPLICANT: MARKLAND, William
; APPLICANT: LADNER, Robert C
; TITLE OF INVENTION: Inhibitors of Human Plasmin Derived
; TITLE OF INVENTION: From The Kunitz Domains
; NUMBER OF SEQUENCES: 139
; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Yankwich & Associates
; STREET: 130 Bishop Allen Drive
; CITY: Cambridge
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02139
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5-inch diskette
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: Microsoft Windows 98
; SOFTWARE: Microsoft Word 97 SR-1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/414.878
; FILING DATE: (concurrently herewith)
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/240,136
; FILING DATE: 29-JAN-1999
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/676,124
; FILING DATE: 07-JAN-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/00298
; FILING DATE: 11-JAN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/208,265
; FILING DATE: 10-MAR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/179,685
; FILING DATE: 11-JAN-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: YANKWICH, Leon R
; REGISTRATION NUMBER: 30,237
; NAME: ZWICKER, Kenneth P
; REGISTRATION NUMBER: 43,310
; REFERENCE/DOCKET NUMBER: DYX-007.2P US-2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-491-4343
; TELEFAX: 617-491-8801
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 58 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-414-878-13

Query Match 6.9%; Score 9; DB 3; Length 58;
Best Local Similarity 100.0%; Pred. No. 0.027;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 105 FIYGGCQGN 113
Db 33 FIYGGCQGN 41

RESULT 14
US-09-240-136-13
; Sequence 13, Application US/09240136
; Patent No. 6103499
; GENERAL INFORMATION:
; APPLICANT: DYAX CORP
; APPLICANT: MARKLAND, William
; APPLICANT: LADNER, Robert C
; TITLE OF INVENTION: Inhibitors of Human Plasmin Derived
; TITLE OF INVENTION: From The Kunitz Domains
; NUMBER OF SEQUENCES: 139
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Yankwich & Associates
; STREET: 130 Bishop Allen Drive
; CITY: Cambridge
; STATE: Massachusetts

```
;
; COUNTRY: USA
; ZIP: 02139
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5-inch diskette
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: Microsoft Windows 98
; SOFTWARE: Microsoft Word 97 SR-1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/240,136
; FILING DATE: (concurrently herewith)
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/676,124
; FILING DATE: 07-JAN-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/00298
; FILING DATE: 11-JAN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/208,265
; FILING DATE: 10-MAR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/179,685
; FILING DATE: 11-JAN-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: YANKWICH, Leon R
; REGISTRATION NUMBER: 30,237
; NAME: ZWICKER, Kenneth P
; REGISTRATION NUMBER: 43,310
; REFERENCE/DOCKET NUMBER: DYX-007.2P US-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-491-4343
; TELEFAX: 617-491-8801
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 58 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-240-136-13

Query Match 6.9%; Score 9; DB 3; Length 58;
Best Local Similarity 100.0%; Pred. No. 0.027;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 105 FYGGCQGN 113
Db 33 FYGGCQGN 41

RESULT 15
US-09-638-770A-13
; Sequence 13, Application US/09638770A
; Patent No. 6423498
; GENERAL INFORMATION:
; APPLICANT: DYAX CORP
; MARKLAND, William
; LADNER, Robert C
; TITLE OF INVENTION: Inhibitors of Human Plasmin Derived
; From The Kunitz Domains
; NUMBER OF SEQUENCES: 140
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Yankwich & Associates
; STREET: 130 Bishop Allen Drive
; CITY: Cambridge
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02139
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5-inch diskette
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: Microsoft Windows 98
; SOFTWARE: Microsoft Word 97 SR-1

;
; COUNTRY: USA
; ZIP: 02139
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5-inch diskette
; OPERATING SYSTEM: Microsoft Windows 98
; SOFTWARE: Microsoft Word 97 SR-1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/240,136
; FILING DATE: (concurrently herewith)
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/676,124
; FILING DATE: 07-JAN-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/00298
; FILING DATE: 11-JAN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/208,265
; FILING DATE: 10-MAR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/179,685
; FILING DATE: 11-JAN-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: YANKWICH, Leon R
; REGISTRATION NUMBER: 30,237
; NAME: ZWICKER, Kenneth P
; REGISTRATION NUMBER: 43,310
; REFERENCE/DOCKET NUMBER: DYX-007.2P US-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-491-4343
; TELEFAX: 617-491-8801
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 58 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-638-770A-13

Query Match 6.9%; Score 9; DB 4; Length 58;
Best Local Similarity 100.0%; Pred. No. 0.027;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 105 FYGGCQGN 113
Db 33 FYGGCQGN 41

RESULT 16
5466783-4
; Patent No. 5466783
; APPLICANT: Wun, Tze-Chuin.;Kretzmer, Kuniko K.;Broze,
; George J. Jr.
; TITLE OF INVENTION: HUMAN TISSUE FACTOR INHIBITOR
; NUMBER OF SEQUENCES: 26
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/93,285
; FILING DATE: 15-JUL-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 566,280
; FILING DATE: 13-AUG-1990
; APPLICATION NUMBER: 123,753
; FILING DATE: 23-NOV-1987
; APPLICATION NUMBER: 77,366
; FILING DATE: 23-JUL-1987
; SEQ ID NO:4:
; LENGTH: 77
; 5466783-4

Query Match 6.1%; Score 8; DB 6; Length 77;
Best Local Similarity 100.0%; Pred. No. 0.43;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 107 YGCGQGN 114
Db 38 YGCGQGN 45

RESULT 17
5466783-4
; Patent No. 5466783
; APPLICANT: Wun, Tze-Chuin.;Kretzmer, Kuniko K.;Broze,
```

;George J. Jr.
; TITLE OF INVENTION: HUMAN TISSUE FACTOR INHIBITOR
; NUMBER OF SEQUENCES: 26
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/93,285
; FILING DATE: 15-JUL-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 566,280
; FILING DATE: 13-AUG-1990
; APPLICATION NUMBER: 123,753
; FILING DATE: 23-NOV-1987
; APPLICATION NUMBER: 77,366
; FILING DATE: 23-JUL-1987
; SEQ ID NO:4:
; LENGTH: 77
5466783-4

Query Match 6.1%; Score 8; DB 6; Length 77;
Best Local Similarity 100.0%; Pred. No. 0.43;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 107 YGGCQGN 114
Db 38 YGGCQGN 45

RESULT 18
US-09-949-016-11664
; Sequence 11664, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CLO01307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11664
; LENGTH: 767
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-11664

Query Match 6.1%; Score 8; DB 4; Length 767;
Best Local Similarity 100.0%; Pred. No. 3.2;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 LVPFILLG 17
Db 340 LVPFILLG 347

RESULT 19
US-08-463-155A-29
; Sequence 29, Application US/08463155A
; Patent No. 5780265
; GENERAL INFORMATION:
; APPLICANT: Dennis, Mark S.
; APPLICANT: Lazarus, Robert A.
; TITLE OF INVENTION: KUNITZ TYPE PLASMA KALLIKREIN INHIBITORS
; NUMBER OF SEQUENCES: 72
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco

; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/463,155A
; FILING DATE: 05-Jun-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Kubinec, Jeffrey S.
; REGISTRATION NUMBER: 36,575
; REFERENCE/DOCKET NUMBER: P0944
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/225-8228
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 29:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 24 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
US-08-463-155A-29

Query Match 5.3%; Score 7; DB 1; Length 24;
Best Local Similarity 100.0%; Pred. No. 1.9;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 107 YGGCQGN 113
Db 1 YGGCQGN 7

RESULT 20
US-08-463-432B-29
; Sequence 29, Application US/08463432B
; Patent No. 5786328
; GENERAL INFORMATION:
; APPLICANT: Dennis, Mark S.
; APPLICANT: Lazarus, Robert A.
; TITLE OF INVENTION: KUNITZ TYPE PLASMA KALLIKREIN INHIBITORS
; NUMBER OF SEQUENCES: 72
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/463,432B
; FILING DATE: 05-Jun-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Kubinec, Jeffrey S.
; REGISTRATION NUMBER: 36,575
; REFERENCE/DOCKET NUMBER: P0944-2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/225-8228
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 29:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 24 amino acids
; TYPE: Amino Acid

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; TOPOLOGY: Linear
US-08-463-432B-29

Query Match          5.3%; Score 7; DB 1; Length 24;
Best Local Similarity 100.0%; Pred. No. 1.9;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 107 YGCGQGN 113
Db 1 YGCGQGN 7

RESULT 21
US-07-791-213D-1
; Sequence 1, Application US/07791213D
; Patent No. 5409895
; GENERAL INFORMATION:
; APPLICANT: MORISHITA, Hideaki
; APPLICANT: KANAMORI, Toshihori
; APPLICANT: NOBUHARA, Masahiro
; TITLE OF INVENTION: POLYPEPTIDE, DNA FRAGMENT ENCODING THE
; TITLE OF INVENTION: SAME AND PROCESS FOR PRODUCING THE SAME, AND ENZYME
; TITLE OF INVENTION: INHIBITION PROCESS, DRUG COMPOSITION AND METHODS OF
; TITLE OF INVENTION: TREATING USING THE SAME
; NUMBER OF SEQUENCES: 108
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Burns, Doane, Swecker & Mathis
; STREET: P.O. Box 1404
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: United States
; ZIP: 22313-1404
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07791,213D
; FILING DATE: 13-NOV-1991
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 2-306745
; FILING DATE: 13-NOV-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Meuth, Donna M
; REGISTRATION NUMBER: 36,607
; REFERENCE/DOCKET NUMBER: 029650-032
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 836-6620
; TELEFAX: (703) 836-2021
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 51 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 1
; OTHER INFORMATION: /note= "Xaa-1 is selected from SEQ
; OTHER INFORMATION: ID NOS:20 to 24, respectively, and 107."
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 51
; OTHER INFORMATION: /note= "Xaa-2 is selected from SEQ
; OTHER INFORMATION: ID NOS:25 to 40, respectively."
US-07-791-213D-2

Query Match          5.3%; Score 7; DB 1; Length 51;
Best Local Similarity 100.0%; Pred. No. 3.7;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 107 YGCGQGN 113
Db 31 YGCGQGN 37

RESULT 23
US-07-791-213D-4
; Sequence 4, Application US/07791213D
; Patent No. 5409895
; GENERAL INFORMATION:
; APPLICANT: MORISHITA, Hideaki
; APPLICANT: KANAMORI, Toshihori
; APPLICANT: NOBUHARA, Masahiro
; TITLE OF INVENTION: POLYPEPTIDE, DNA FRAGMENT ENCODING THE
; TITLE OF INVENTION: SAME AND PROCESS FOR PRODUCING THE SAME, AND ENZYME
; TITLE OF INVENTION: INHIBITION PROCESS, DRUG COMPOSITION AND METHODS OF
; TITLE OF INVENTION: TREATING USING THE SAME
```

; NUMBER OF SEQUENCES: 108
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Burns, Doane, Swecker & Mathis
 ; STREET: P.O. Box 1404
 ; CITY: Alexandria
 ; STATE: Virginia
 ; COUNTRY: United States
 ; ZIP: 22313-1404
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent in Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/07/791,213D
 ; FILING DATE: 13-NOV-1991
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: JP 2-306745
 ; FILING DATE: 13-NOV-1990
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Meuth, Donna M
 ; REGISTRATION NUMBER: 36,607
 ; REFERENCE/DOCKET NUMBER: 029650-032
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (703) 836-6620
 ; TELEFAX: (703) 836-2021
 ; INFORMATION FOR SEQ ID NO: 4:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 51 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: peptide
 ; FEATURE:
 ; NAME/KEY: Modified-site
 ; LOCATION: 15
 ; OTHER INFORMATION: /note= "Xaa-1 is Gln or Lys."
 ; FEATURE:
 ; NAME/KEY: Modified-site
 ; LOCATION: 42
 ; OTHER INFORMATION: /note= "Xaa-2 is Tyr when Xaa-1 is
 ; OTHER INFORMATION: Lys; and Xaa-2 is Glu when Xaa-1 is Gln."
 ; US-07-791-213D-4

Query Match 5.3%; Score 7; DB 1; Length 51;
 Best Local Similarity 100.0%; Pred. No. 3.7;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 107 YGGCQGN 113
 DB 31 YGGCQGN 37

RESULT 24
 ; US-07-791-213D-7
 ; Sequence 7, Application US/07791213D
 ; Patent No. 5409895
 ; GENERAL INFORMATION:
 ; APPLICANT: MORISHITA, Hideaki
 ; APPLICANT: KANAMORI, Toshinori
 ; APPLICANT: NOBUHARA, Masahiro
 ; TITLE OF INVENTION: POLYPEPTIDE, DNA FRAGMENT ENCODING THE
 ; TITLE OF INVENTION: SAME AND PROCESS FOR PRODUCING THE SAME, AND ENZYME
 ; TITLE OF INVENTION: INHIBITION PROCESS, DRUG COMPOSITION AND METHODS OF
 ; TITLE OF INVENTION: TREATING USING THE SAME
 ; NUMBER OF SEQUENCES: 108
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Burns, Doane, Swecker & Mathis
 ; STREET: P.O. Box 1404
 ; CITY: Alexandria
 ; STATE: Virginia
 ; COUNTRY: United States
 ; ZIP: 22313-1404

; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent in Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/07/791,213D
 ; FILING DATE: 13-NOV-1991
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: JP 2-306745
 ; FILING DATE: 13-NOV-1990
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Meuth, Donna M
 ; REGISTRATION NUMBER: 36,607
 ; REFERENCE/DOCKET NUMBER: 029650-032
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (703) 836-6620
 ; TELEFAX: (703) 836-2021
 ; INFORMATION FOR SEQ ID NO: 7:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 51 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: peptide
 ; FEATURE:
 ; NAME/KEY: Modified-site
 ; LOCATION: 1
 ; OTHER INFORMATION: /note= "Xaa-1 is selected from SEQ
 ; OTHER INFORMATION: ID NOS:20 to 24, respectively."
 ; FEATURE:
 ; NAME/KEY: Modified-site
 ; LOCATION: 51
 ; OTHER INFORMATION: /note= "Xaa-2 is selected from SEQ
 ; OTHER INFORMATION: ID NOS:25-40, respectively."
 ; US-07-791-213D-7

Query Match 5.3%; Score 7; DB 1; Length 51;
 Best Local Similarity 100.0%; Pred. No. 3.7;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 107 YGGCQGN 113
 DB 31 YGGCQGN 37

RESULT 25
 ; US-07-791-213D-17
 ; Sequence 17, Application US/07791213D
 ; Patent No. 5409895
 ; GENERAL INFORMATION:
 ; APPLICANT: MORISHITA, Hideaki
 ; APPLICANT: KANAMORI, Toshinori
 ; APPLICANT: NOBUHARA, Masahiro
 ; TITLE OF INVENTION: POLYPEPTIDE, DNA FRAGMENT ENCODING THE
 ; TITLE OF INVENTION: SAME AND PROCESS FOR PRODUCING THE SAME, AND ENZYME
 ; TITLE OF INVENTION: INHIBITION PROCESS, DRUG COMPOSITION AND METHODS OF
 ; TITLE OF INVENTION: TREATING USING THE SAME
 ; NUMBER OF SEQUENCES: 108
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Burns, Doane, Swecker & Mathis
 ; STREET: P.O. Box 1404
 ; CITY: Alexandria
 ; STATE: Virginia
 ; COUNTRY: United States
 ; ZIP: 22313-1404
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent in Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/07/791,213D

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; FILING DATE: 13-NOV-1991
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 2-306745
; FILING DATE: 13-NOV-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Meuth, Donna M
; REGISTRATION NUMBER: 36,607
; REFERENCE/DOCKET NUMBER: 029650-032
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 836-6620
; TELEFAX: (703) 836-2021
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 51 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-07-791-213D-17

Query Match 5.3%; Score 7; DB 1; Length 51;
Best Local Similarity 100.0%; Pred. No. 3.7;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 107 YGGCQGN 113
Db 30 YGGCQGN 36

RESULT 26
US-07-791-213D-108
; Sequence 108, Application US/07791213D
; Patent No. 5409895
; GENERAL INFORMATION:
; APPLICANT: MORISHITA, Hideaki
; APPLICANT: KANAMORI, Toshinori
; APPLICANT: NOBUHARA, Masahiro
; TITLE OF INVENTION: POLYPEPTIDE, DNA FRAGMENT ENCODING THE
; TITLE OF INVENTION: SAME AND PROCESS FOR PRODUCING THE SAME, AND ENZYME
; TITLE OF INVENTION: INHIBITION PROCESS, DRUG COMPOSITION AND METHODS OF
; TITLE OF INVENTION: TREATING USING THE SAME
; NUMBER OF SEQUENCES: 108
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Burns, Doane, Swecker & Mathis
; STREET: P.O. Box 1404
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: United States
; ZIP: 22313-1404
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07791.213D
; FILING DATE: 13-NOV-1991
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 2-306745
; FILING DATE: 13-NOV-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Meuth, Donna M
; REGISTRATION NUMBER: 36,607
; REFERENCE/DOCKET NUMBER: 029650-032
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 836-6620
; TELEFAX: (703) 836-2021
; INFORMATION FOR SEQ ID NO: 108:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 51 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
```

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; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 1
; OTHER INFORMATION: /note= "Xaa-1 is selected from SEQ
; OTHER INFORMATION: ID NO:20 to 24 and 107."
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 15
; OTHER INFORMATION: /note= "Xaa-2 is Gln or Lys."
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 42
; OTHER INFORMATION: /note= "Xaa-3 is Glu or Tyr."
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 51
; OTHER INFORMATION: /note= "Xaa-4 is selected from SEQ
; OTHER INFORMATION: ID NOS:25 to 40."
US-07-791-213D-108

Query Match 5.3%; Score 7; DB 1; Length 51;
Best Local Similarity 100.0%; Pred. No. 3.7;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 107 YGGCQGN 113
Db 31 YGGCQGN 37

RESULT 27
US-08-055-988-3
; Sequence 3, Application US/08055988
; Patent No. 5427937
; GENERAL INFORMATION:
; APPLICANT: Michael Capello
; APPLICANT: Peter J. Hotez
; APPLICANT: Frank F. Richards
; TITLE OF INVENTION: Hookworm Anticoagulant
; NUMBER OF SEQUENCES: 7;
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MacArthur Center for Molecular
; ADDRESSEE: Parasitology
; ADDRESSEE: Yale Parasitology and Tropical Medicine
; ADDRESSEE: Center, 700 Laboratory of Epidemiology
; ADDRESSEE: and Public Health
; STREET: 60 College Street
; CITY: New Haven
; STATE: CT
; COUNTRY: USA
; ZIP: 06510
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 5.25" 360 Kb diskette
; COMPUTER: IBM PC
; OPERATING SYSTEM: MS DOS
; SOFTWARE: Word Processing
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/055,988
; FILING DATE: 19930430
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Mary M. Krinsky, St. Onge Steward Johnston & Reens
; REGISTRATION NUMBER: 32423
; REFERENCE/DOCKET NUMBER: 1751-003
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 203-324-6155
; TELEFAX: 203-327-1096
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 51 residues
; TYPE: AMINO ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
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MOLECULE TYPE: polypeptide
DESCRIPTION: internal fragment
FEATURE:
NAME/KEY: Extrinsic Pathway Inhibitor, Tail I
PUBLICATION INFORMATION:
AUTHORS: Rapoport, S.I.
TITLE: The Extrinsic Pathway
JOURNAL: Thrombosis and Haemostasis
VOLUME: 66
ISSUE: 1
PAGES: 6-15, Figure 5
DATE: 1991
RELEVANT RESIDUES IN SEQ ID NO: segment corresponding to
RELEVANT RESIDUES IN SEQ ID NO: peptide residues 26 to 76
US-08-055-988-3
Query Match 5.3%; Score 7; DB 1; Length 51;
Best Local Similarity 100.0%; Pred. No. 3.7;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 104 EFIGGC 110
Db 28 EFIGGC 34
RESULT 28
US-07-972-387-67
; Sequence 67, Application US/07972387
; Patent No. 5451659
; GENERAL INFORMATION:
; APPLICANT: Morishita, Hideaki
; APPLICANT: Kanamori, Toshinori
; APPLICANT: No. 5451659unara, Masahiro
; TITLE OF INVENTION: Polypeptide, DNA Fragment Encoding the
; TITLE OF INVENTION: Same, Drug Composition Containing the Same and Process for
; TITLE OF INVENTION: Producing the Same
; NUMBER OF SEQUENCES: 76
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Birch, Stewart, Kolasch & Birch
; STREET: 301 N. Washington St.
; CITY: Falls Church
; STATE: Virginia
; COUNTRY: USA
; ZIP: 22046-0747
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/972,387
; FILING DATE: 19921105
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Murphy Jr., Gerald M.
; REGISTRATION NUMBER: 28,977
; REFERENCE/DOCKET NUMBER: 1110-124P
; TELEPHONE: 703-241-1300
; TELEFAX: 703-241-2848
; TELEX: 248345
; INFORMATION FOR SEQ ID NO: 67:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 51 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-07-972-387-67
Query Match 5.3%; Score 7; DB 1; Length 51;
Best Local Similarity 100.0%; Pred. No. 3.7;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 107 YGCGGN 113
Db 31 YGCGGN 37
RESULT 29
US-08-437-841-1
; Sequence 1, Application US/08437841
; Patent No. 5563123
; GENERAL INFORMATION:
; APPLICANT: Innis, Michael
; APPLICANT: Creasey, Abia
; TITLE OF INVENTION: Chimeric Proteins
; NUMBER OF SEQUENCES: 37
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Chiron Corporation
; STREET: 4560 Horton St.
; CITY: Emeryville
; STATE: CA
; COUNTRY: USA
; ZIP: 94608
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30B
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/437,841
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/286,521
; FILING DATE: 05-AUG-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Savereide, Paul B.
; REGISTRATION NUMBER: 36,914
; REFERENCE/DOCKET NUMBER: 0990.001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 510-601-2585
; TELEFAX: 510-655-3542
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 51 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-437-841-1
Query Match 5.3%; Score 7; DB 1; Length 51;
Best Local Similarity 100.0%; Pred. No. 3.7;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 104 EFIGGC 110
Db 28 EFIGGC 34
RESULT 30
US-08-286-521-1
; Sequence 1, Application US/08286521
; Patent No. 5589359
; GENERAL INFORMATION:
; APPLICANT: Innis, Michael
; APPLICANT: Creasey, Abia
; TITLE OF INVENTION: Chimeric Proteins
; NUMBER OF SEQUENCES: 37
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Chiron Corporation
; STREET: 4560 Horton St.
; CITY: Emeryville

STATE: CA
 COUNTRY: USA
 ZIP: 94608
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30B
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/286,521
 FILING DATE: 05-AUG-1994
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: Saveriede, Paul B.
 REGISTRATION NUMBER: 36,914
 REFERENCE/DOCKET NUMBER: 0990.001
 TELEPHONE: 510-601-2585
 TELEFAX: 510-655-3542
 INFORMATION FOR SEQ ID NO: 1:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 51 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 US-08-286-521-1

Query Match 5.3%; Score 7; DB 1; Length 51;
 Best Local Similarity 100.0%; Pred. No. 3.7;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 104 EFYGGC 110
 Db 28 EFYGGC 34

RESULT 31

US-08-431-412-67
 Sequence 67, Application US/08431412
 Patent No. 5589360
 GENERAL INFORMATION:
 APPLICANT: Morishita, Hideaki
 APPLICANT: Kanamori, Toshinori
 APPLICANT: No. 5589360uhara, Masahiro
 TITLE OF INVENTION: Polypeptide, DNA Fragment Encoding the
 TITLE OF INVENTION: Same, Drug Composition Containing the Same and Process for
 NUMBER OF SEQUENCES: 76
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Birch, Stewart, Kolasch & Birch
 STREET: 301 N. Washington St.
 CITY: Falls Church
 STATE: Virginia
 COUNTRY: USA
 ZIP: 22046-0747
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/431,412
 FILING DATE: 28-APR-1995
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/972,387
 FILING DATE: 05-NOV-1992
 ATTORNEY/AGENT INFORMATION:
 NAME: Murphy Jr., Gerald M.
 REGISTRATION NUMBER: 28,977
 REFERENCE/DOCKET NUMBER: 1110-124P
 TELECOMMUNICATION INFORMATION:

TELEPHONE: 703-241-1300
 TELEFAX: 703-241-2848
 TELEX: 248345
 INFORMATION FOR SEQ ID NO: 67:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 51 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-431-412-67

Query Match 5.3%; Score 7; DB 1; Length 51;
 Best Local Similarity 100.0%; Pred. No. 3.7;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 107 YGGCQGN 113
 Db 31 YGGCQGN 37

RESULT 32

US-08-057-971-67
 Sequence 67, Application US/08057971
 Patent No. 5679770
 GENERAL INFORMATION:
 APPLICANT: Morishita, Hideaki
 APPLICANT: Kanamori, Toshinori
 APPLICANT: No. 5679770uhara, Masahiro
 TITLE OF INVENTION: Polypeptide, DNA Fragment Encoding the
 TITLE OF INVENTION: Same, Drug Composition Containing the Same and Process for
 NUMBER OF SEQUENCES: 81
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Birch, Stewart, Kolasch & Birch
 STREET: P.O. Box 747
 CITY: Falls Church
 STATE: Virginia
 COUNTRY: USA
 ZIP: 22040-0747
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/057,971
 FILING DATE: 06-MAY-1993
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: Murphy Jr., Gerald M.
 REGISTRATION NUMBER: 28,977
 REFERENCE/DOCKET NUMBER: 1110-129P
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 703-205-8000
 TELEFAX: 703-205-8050
 TELEX:
 INFORMATION FOR SEQ ID NO: 67:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 51 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-057-971-67

Query Match 5.3%; Score 7; DB 1; Length 51;
 Best Local Similarity 100.0%; Pred. No. 3.7;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 107 YGGCQGN 113
 Db 31 YGGCQGN 37

RESULT 33
US-08-436-175-1
; Sequence 1, Application US/08436175
; Patent No. 5696088
; GENERAL INFORMATION:
; APPLICANT: Innis, Michael
; APPLICANT: Creasey, Abia
; TITLE OF INVENTION: Chimeric Proteins
; NUMBER OF SEQUENCES: 37
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Chiron Corporation
; STREET: 4560 Horton St.
; CITY: Emeryville
; STATE: CA
; COUNTRY: USA
; ZIP: 94608
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30B
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/436,175
; FILING DATE: 09-MAY-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/286,521
; FILING DATE: 05-AUG-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Savereide, Paul B.
; REGISTRATION NUMBER: 36,914
; REFERENCE/DOCKET NUMBER: 0990.001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 510-601-2585
; TELEFAX: 510-655-3542
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 51 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-436-175-1

Query Match 5.3%; Score 7; DB 1; Length 51;
Best Local Similarity 100.0%; Pred. No. 3.7;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 104 EPIYGC 110
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DB 28 EPIYGC 34

RESULT 34
US-08-293-150A-1
; Sequence 1, Application US/08293150A
; Patent No. 5792629
; GENERAL INFORMATION:
; APPLICANT: MORISHITA, Hideaki
; APPLICANT: KANAMORI, Toshinori
; APPLICANT: NOBUHARA, Masahiro
; TITLE OF INVENTION: POLYPEPTIDE, DNA FRAGMENT ENCODING THE
; TITLE OF INVENTION: SAME AND PROCESS FOR PRODUCING THE SAME, AND ENZYME
; TITLE OF INVENTION: INHIBITION PROCESS, DRUG COMPOSITION AND METHODS OF
; TITLE OF INVENTION: TREATING USING THE SAME
; NUMBER OF SEQUENCES: 110
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
; STREET: P.O. Box 1404
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: United States
; ZIP: 22313-1404

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/293,150A
; FILING DATE: 19-AUG-1994
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/791,213
; FILING DATE: 13-NOV-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 2-306745
; FILING DATE: 13-NOV-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Meuth, Donna M.
; REGISTRATION NUMBER: 36,607
; REFERENCE/DOCKET NUMBER: 029650-049
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 836-6620
; TELEFAX: (703) 836-2021
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 51 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-293-150A-1

Query Match 5.3%; Score 7; DB 1; Length 51;
Best Local Similarity 100.0%; Pred. No. 3.7;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 107 YGGCQGN 113
|||
DB 31 YGGCQGN 37

RESULT 35
US-08-293-150A-2
; Sequence 2, Application US/08293150A
; Patent No. 5792629
; GENERAL INFORMATION:
; APPLICANT: MORISHITA, Hideaki
; APPLICANT: KANAMORI, Toshinori
; APPLICANT: NOBUHARA, Masahiro
; TITLE OF INVENTION: POLYPEPTIDE, DNA FRAGMENT ENCODING THE
; TITLE OF INVENTION: SAME AND PROCESS FOR PRODUCING THE SAME, AND ENZYME
; TITLE OF INVENTION: INHIBITION PROCESS, DRUG COMPOSITION AND METHODS OF
; TITLE OF INVENTION: TREATING USING THE SAME
; NUMBER OF SEQUENCES: 110
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
; STREET: P.O. Box 1404
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: United States
; ZIP: 22313-1404
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/293,150A
; FILING DATE: 19-AUG-1994
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/791,213
; FILING DATE: 13-NOV-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 2-306745

```
; FILING DATE: 13-NOV-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Meuth, Donna M.
; REGISTRATION NUMBER: 36,607
; REFERENCE/DOCKET NUMBER: 029650-049
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 836-6620
; TELEFAX: (703) 836-2021
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 51 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 1
; OTHER INFORMATION: /note= "Xaa-1 is selected from SEQ
; OTHER INFORMATION: ID NOS:20 to 24, respectively, and 107."
;
; NAME/KEY: Modified-site
; LOCATION: 51
; OTHER INFORMATION: /note= "Xaa-2 is selected from SEQ
; OTHER INFORMATION: ID NOS:25 to 40, respectively."
;
US-08-293-150A-2

Query Match 5.3%; Score 7; DB 1; Length 51;
Best Local Similarity 100.0%; Pred. No. 3.7;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 107 YGGCQGN 113
Db 31 YGGCQGN 37

RESULT 36
US-08-293-150A-4
; Sequence 4, Application US/08293150A
; Patent No. 5792629
; GENERAL INFORMATION:
; APPLICANT: MORISHITA, Hideaki
; APPLICANT: KANAMORI, Toshinori
; APPLICANT: NOBUHARA, Masahiro
; TITLE OF INVENTION: POLYPEPTIDE, DNA FRAGMENT ENCODING THE
; TITLE OF INVENTION: SAME AND PROCESS FOR PRODUCING THE SAME, AND ENZYME
; TITLE OF INVENTION: INHIBITION PROCESS, DRUG COMPOSITION AND METHODS OF
; TITLE OF INVENTION: TREATING USING THE SAME
; NUMBER OF SEQUENCES: 110
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
; STREET: P.O. Box 1404
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: United States
; ZIP: 22313-1404
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/293,150A
; FILING DATE: 19-AUG-1994
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/791,213
; FILING DATE: 13-NOV-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 2-306745
; FILING DATE: 13-NOV-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Meuth, Donna M.
; REGISTRATION NUMBER: 36,607
```

```
; REFERENCE/DOCKET NUMBER: 029650-049
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 836-6620
; TELEFAX: (703) 836-2021
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 51 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 15
; OTHER INFORMATION: /note= "Xaa-1 is Gln or Lys."
;
; NAME/KEY: Modified-site
; LOCATION: 42
; OTHER INFORMATION: /note= "Xaa-2 is Tyr when Xaa-1 is
; OTHER INFORMATION: Lys; and Xaa-2 is Glu when Xaa-1 is Gln."
;
US-08-293-150A-4

Query Match 5.3%; Score 7; DB 1; Length 51;
Best Local Similarity 100.0%; Pred. No. 3.7;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 107 YGGCQGN 113
Db 31 YGGCQGN 37

RESULT 37
US-08-293-150A-7
; Sequence 7, Application US/08293150A
; Patent No. 5792629
; GENERAL INFORMATION:
; APPLICANT: MORISHITA, Hideaki
; APPLICANT: KANAMORI, Toshinori
; APPLICANT: NOBUHARA, Masahiro
; TITLE OF INVENTION: POLYPEPTIDE, DNA FRAGMENT ENCODING THE
; TITLE OF INVENTION: SAME AND PROCESS FOR PRODUCING THE SAME, AND ENZYME
; TITLE OF INVENTION: INHIBITION PROCESS, DRUG COMPOSITION AND METHODS OF
; TITLE OF INVENTION: TREATING USING THE SAME
; NUMBER OF SEQUENCES: 110
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
; STREET: P.O. Box 1404
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: United States
; ZIP: 22313-1404
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/293,150A
; FILING DATE: 19-AUG-1994
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/791,213
; FILING DATE: 13-NOV-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 2-306745
; FILING DATE: 13-NOV-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Meuth, Donna M.
; REGISTRATION NUMBER: 36,607
; REFERENCE/DOCKET NUMBER: 029650-049
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 836-6620
; TELEFAX: (703) 836-2021
; INFORMATION FOR SEQ ID NO: 7:
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; MOLECULE TYPE: peptide
US-08-293-150A-17

Query Match      5.3%; Score 7; DB 1; Length 51;
Best Local Similarity 100.0%; Pred. No. 3.7;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0

QY      107 YGCGCQN 113
        |||||
DB       30 YGCGCQN 36

RESULT 39
US-08-293-150A-108
; Sequence 108, Application US/08293150A
; Patent No. 5792629
; GENERAL INFORMATION:
; APPLICANT: MORISHITA, Hideaki
; APPLICANT: KANAMORI, Toshinori
; APPLICANT: NOBUHARA, Masahiro
; TITLE OF INVENTION: POLYPEPTIDE, DNA FRAGMENT ENCODING THE
; SAME AND PROCESS FOR PRODUCING THE SAME, AND ENZYME
; TITLE OF INVENTION: INHIBITION PROCESS, DRUG COMPOSITION AND METHODS OF
; TREATING USING THE SAME
; NUMBER OF SEQUENCES: 110
; CORRESPONDENCE ADDRESS:
; ADDRESSES: BURNS, DOANE, SWECKER & MATHIS
; STREET: P.O. Box 1404
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: United States
; ZIP: 22313-1404
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/293,150A
; FILING DATE: 19-AUG-1994
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/791,213
; FILING DATE: 13-NOV-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 2-306745
; FILING DATE: 13-NOV-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Meuth, Donna M.
; REGISTRATION NUMBER: 36,607
; REFERENCE/DOCKET NUMBER: 029650-049
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 836-6620
; TELEFAX: (703) 836-2021
; INFORMATION FOR SEQ ID NO: 108:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 51 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 1
; OTHER INFORMATION: /note= "Xaa-1 is selected from SEQ
; ID NO:20 to 24 and 107."
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 15
; OTHER INFORMATION: /note= "Xaa-2 is Glu or Lys."
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 42
; OTHER INFORMATION: /note= "Xaa-3 is Glu or Tyr."

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; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 51
; OTHER INFORMATION: /note= "Xaa-4 is selected from SEQ
; OTHER INFORMATION: ID NOS:25 to 40."
; US-08-293-150A-108

Query Match 5.3%; Score 7; DB 1; Length 51;
Best Local Similarity 100.0%; Pred. No. 3.7;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 107 YGGCQGN 113
Db 31 YGGCQGN 37

RESULT 40

US-08-943-682-1

; Sequence 1, Application US/08943682

; Patent No. 6174721

; GENERAL INFORMATION:

; APPLICANT: Innis, Michael

; APPLICANT: Creasey, Adla

; TITLE OF INVENTION: Chimeric Proteins

; NUMBER OF SEQUENCES: 37

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Chiron Corporation

; STREET: 4560 Horton St.

; CITY: Emeryville

; STATE: CA

; COUNTRY: USA

; ZIP: 94608

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30B

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/943,682

; FILING DATE: 03-OCT-1997

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/438,184

; FILING DATE: 09-MAY-1995

; APPLICATION NUMBER: US 08/286,521

; FILING DATE: 05-AUG-1994

; ATTORNEY/AGENT INFORMATION:

; NAME: Savereide, Paul B.

; REGISTRATION NUMBER: 36,914

; REFERENCE/DOCKET NUMBER: 0990.001

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 510-601-2585

; TELEFAX: 510-655-3542

; INFORMATION FOR SEQ ID NO: 1:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 51 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: peptide

; US-08-943-682-1

Query Match 5.3%; Score 7; DB 3; Length 51;
Best Local Similarity 100.0%; Pred. No. 3.7;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 104 EFIYGGC 110
Db 28 EFIYGGC 34

RESULT 41

US-09-013-896A-4

Query Match 5.3%; Score 7; DB 4; Length 51;
Best Local Similarity 100.0%; Pred. No. 3.7;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

; Sequence 4, Application US/09013896A
; Patent No. 6262233
; GENERAL INFORMATION:
; APPLICANT: GENIZ, REINER
; TITLE OF INVENTION: TISSUE FACTOR PATHWAY INHIBITOR-3
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
; STREET: 1100 NEW YORK AVE., NW, STE. 600
; CITY: WASHINGTON
; STATE: DC
; COUNTRY: US
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/013,896A
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: STEFFE, ERIC K.
; REGISTRATION NUMBER: 36,688
; REFERENCE/DOCKET NUMBER: 1488.1290001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 309-8504
; TELEFAX: (301) 309-8439
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 51 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-013-896A-4

Query Match 5.3%; Score 7; DB 3; Length 51;
Best Local Similarity 100.0%; Pred. No. 3.7;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 104 EFIYGGC 110
Db 28 EFIYGGC 34

RESULT 42

US-09-101-272G-19

; Sequence 19, Application US/09101272G

; Patent No. 6509445

; GENERAL INFORMATION:

; APPLICANT: Nissin Food Products Co., Ltd.

; TITLE OF INVENTION: CANCEROUS METASTASIS INHIBITOR

; FILE REFERENCE: Q50979

; CURRENT APPLICATION NUMBER: US/09/101,272G

; CURRENT FILING DATE: 1998-07-08

; PRIOR APPLICATION NUMBER: JP 1059/1996

; PRIOR FILING DATE: 1996-01-08

; NUMBER OF SEQ ID NOS: 107

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 19

; LENGTH: 51

; TYPE: PRT

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: misc feature

; OTHER INFORMATION: residues 5-55 of HI-8 domain of UTI (formula II)

; US-09-101-272G-19

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; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 51 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-741-106-1

Query Match          5.3%; Score 7; DB 4; Length 51;
Best Local Similarity 100.0%; Pred. No. 3.7;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 104 EPIYGGC 110
Db 28 EPIYGGC 34

RESULT 43
US-09-827-948-4
; Sequence 4, Application US/09827948
; Patent No. 6548262
; GENERAL INFORMATION:
; APPLICANT: Gentz, Reiner, L.
; APPLICANT: Hsu, Teu-An
; APPLICANT: Rosen, Craig A.
; APPLICANT: Ni, Jian
; TITLE OF INVENTION: Tissue Factor Pathway Inhibitor-3
; FILE REFERENCE: 1488.1290002
; CURRENT APPLICATION NUMBER: US/09/827,948
; CURRENT FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: US 09/013,896
; PRIOR FILING DATE: 1998-01-27
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 4
; LENGTH: 51
; TYPE: PRT
; ORGANISM: Human
US-09-827-948-4

Query Match          5.3%; Score 7; DB 4; Length 51;
Best Local Similarity 100.0%; Pred. No. 3.7;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 104 EPIYGGC 110
Db 28 EPIYGGC 34

RESULT 44
US-09-741-106-1
; Sequence 1, Application US/09741106
; Patent No. 6783960
; GENERAL INFORMATION:
; APPLICANT: Innis, Michael
; APPLICANT: Creasey, Abba
; TITLE OF INVENTION: Chimeric Proteins
; NUMBER OF SEQUENCES: 37
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Chiron Corporation
; STREET: 4560 Horton St.
; CITY: Emeryville
; STATE: CA
; COUNTRY: USA
; ZIP: 94608
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30B
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/741,106
; FILING DATE: 12-Dec-2000
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/286,521
; FILING DATE: 1994-08-05
; ATTORNEY/AGENT INFORMATION:
; NAME: Saveriede, Paul B.
; REGISTRATION NUMBER: 36,914
; REFERENCE/DOCKET NUMBER: 0990.001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 510-601-2585
; TELEFAX: 510-655-3542

; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 51 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 1:
PCT-US95-09464-1

Query Match          5.3%; Score 7; DB 5; Length 51;
Best Local Similarity 100.0%; Pred. No. 3.7;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 104 EPIYGGC 110
Db 28 EPIYGGC 34

RESULT 45
PCT-US95-09464-1
; Sequence 1, Application PC/TUS9509464
; GENERAL INFORMATION:
; APPLICANT: CHIRON CORPORATION
; TITLE OF INVENTION: Chimeric Proteins
; NUMBER OF SEQUENCES: 37
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Chiron Corporation
; STREET: 4560 Horton St.
; CITY: Emeryville
; STATE: CA
; COUNTRY: USA
; ZIP: 94608
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30B
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/09464
; FILING DATE: 25-JULY-1995
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Saveriede, Paul B.
; REGISTRATION NUMBER: 36,914
; REFERENCE/DOCKET NUMBER: 0990.100
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 510-601-2585
; TELEFAX: 510-655-3542
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 51 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 1:
PCT-US95-09464-1

Query Match          5.3%; Score 7; DB 5; Length 51;
Best Local Similarity 100.0%; Pred. No. 3.7;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 104 EPIYGGC 110
Db 28 EPIYGGC 34

RESULT 46
US-07-791-213D-16
; Sequence 16, Application US/07791213D
; Patent No. 5409895
; GENERAL INFORMATION:
; APPLICANT: MORISHITA, Hideaki
```

```
; APPLICANT: KANAMORI, Toshinori
; APPLICANT: NOBUHARA, Masahiro
; TITLE OF INVENTION: POLYPEPTIDE, DNA FRAGMENT ENCODING THE
; TITLE OF INVENTION: SAME AND PROCESS FOR PRODUCING THE SAME, AND ENZYME
; TITLE OF INVENTION: INHIBITION PROCESS, DRUG COMPOSITION AND METHODS OF
; TITLE OF INVENTION: TREATING USING THE SAME
; NUMBER OF SEQUENCES: 108
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Burns, Doane, Swecker & Mathis
; STREET: P.O. Box 1404
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: United States
; ZIP: 22313-1404
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/791,213D
; FILING DATE: 13-NOV-1991
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 2-306745
; FILING DATE: 13-NOV-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Meuth, Donna M
; REGISTRATION NUMBER: 36,607
; REFERENCE/DOCKET NUMBER: 029650-032
; TELEPHONE: (703) 836-6620
; TELEFAX: (703) 836-2021
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 54 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-07-791-213D-16

Query Match 5.3%; Score 7; DB 1; Length 54;
Best Local Similarity 100.0%; Pred. No. 3.9;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 107 YGGCQGN 113
Db 35 YGGCQGN 41

RESULT 47
US-08-293-150A-16
; Sequence 16, Application US/08293150A
; Patent No. 5792629
; GENERAL INFORMATION:
; APPLICANT: MORISHITA, Hideaki
; APPLICANT: KANAMORI, Toshinori
; APPLICANT: NOBUHARA, Masahiro
; TITLE OF INVENTION: POLYPEPTIDE, DNA FRAGMENT ENCODING THE
; TITLE OF INVENTION: SAME AND PROCESS FOR PRODUCING THE SAME, AND ENZYME
; TITLE OF INVENTION: INHIBITION PROCESS, DRUG COMPOSITION AND METHODS OF
; TITLE OF INVENTION: TREATING USING THE SAME
; NUMBER OF SEQUENCES: 110
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
; STREET: P.O. Box 1404
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: United States
; ZIP: 22313-1404
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
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; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/293,150A
; FILING DATE: 19-AUG-1994
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/791,213
; FILING DATE: 13-NOV-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 2-306745
; FILING DATE: 13-NOV-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Meuth, Donna M.
; REGISTRATION NUMBER: 36,607
; REFERENCE/DOCKET NUMBER: 029650-049
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 836-6620
; TELEFAX: (703) 836-2021
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 54 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-293-150A-16

Query Match 5.3%; Score 7; DB 1; Length 54;
Best Local Similarity 100.0%; Pred. No. 3.9;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 107 YGGCQGN 113
Db 35 YGGCQGN 41

RESULT 48
US-08-358-160-19
; Sequence 19, Application US/08358160
; Patent No. 5663143
; GENERAL INFORMATION:
; APPLICANT: LEY, Arthur C.
; APPLICANT: LADNER, Robert C.
; APPLICANT: GUTERMAN, Sonia K.
; APPLICANT: ROBERTS, Bruce L.
; APPLICANT: MARKLAND, William
; APPLICANT: KENT, Rachel B.
; TITLE OF INVENTION: ENGINEERED HUMAN-DERIVED KUNITZ
; TITLE OF INVENTION: DOMAINS THAT INHIBIT HUMAN NEUTROPHIL ELASTASE
; NUMBER OF SEQUENCES: 234
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W. Suite 300
; CITY: Washington
; STATE: District of Columbia
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/358,160
; FILING DATE: 16-DEC-1994
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/133,031
; FILING DATE: 13-OCT-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/009,319
; FILING DATE: 26-JAN-1993
; PRIOR APPLICATION DATA:
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Thu Sep 22 07:16:41 2005

; APPLICATION NUMBER: US 07/664,989
; FILING DATE: 01-MAR-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/487,063
; FILING DATE: 02-MAR-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/240,160
; FILING DATE: 02-SEP-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Cooper, Iver P.
; REGISTRATION NUMBER: 28,005
; REFERENCE/DOCKET NUMBER: LEY=1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; TELEX: 248633
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 56 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-358-160-19

Query Match 5.3%; Score 7; DB 1; Length 56;
Best Local Similarity 100.0%; Pred. No. 4;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 107 YGGCQGN 113
Db 33 YGGCQGN 39

RESULT 49
US-08-358-160-20
; Sequence 20, Application US/08358160
; Patent No. 5663143
; GENERAL INFORMATION:
; APPLICANT: LEY, Arthur C.
; APPLICANT: LADNER, Robert C.
; APPLICANT: GUTERMAN, Sonia K.
; APPLICANT: ROBERTS, Bruce L.
; APPLICANT: MARKLAND, William
; APPLICANT: KENT, Rachel B.
; TITLE OF INVENTION: ENGINEERED HUMAN-DERIVED KUNITZ
; TITLE OF INVENTION: DOMAINS THAT INHIBIT HUMAN NEUTROPHIL ELASTASE
; NUMBER OF SEQUENCES: 234
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W. Suite 300
; CITY: Washington
; STATE: District of Columbia
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/358,160
; FILING DATE: 16-DEC-1994
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/133,031
; FILING DATE: 13-OCT-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/009,319
; FILING DATE: 26-JAN-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/664,989
; FILING DATE: 01-MAR-1991

; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/487,063
; FILING DATE: 02-MAR-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/240,160
; FILING DATE: 02-SEP-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Cooper, Iver P.
; REGISTRATION NUMBER: 28,005
; REFERENCE/DOCKET NUMBER: LEY=1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; TELEX: 248633
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 56 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-358-160-20

Query Match 5.3%; Score 7; DB 1; Length 56;
Best Local Similarity 100.0%; Pred. No. 4;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 107 YGGCQGN 113
Db 33 YGGCQGN 39

RESULT 50
US-08-358-160-87
; Sequence 87, Application US/08358160
; Patent No. 5663143
; GENERAL INFORMATION:
; APPLICANT: LEY, Arthur C.
; APPLICANT: LADNER, Robert C.
; APPLICANT: GUTERMAN, Sonia K.
; APPLICANT: ROBERTS, Bruce L.
; APPLICANT: MARKLAND, William
; APPLICANT: KENT, Rachel B.
; TITLE OF INVENTION: ENGINEERED HUMAN-DERIVED KUNITZ
; TITLE OF INVENTION: DOMAINS THAT INHIBIT HUMAN NEUTROPHIL ELASTASE
; NUMBER OF SEQUENCES: 234
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W. Suite 300
; CITY: Washington
; STATE: District of Columbia
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/358,160
; FILING DATE: 16-DEC-1994
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/133,031
; FILING DATE: 13-OCT-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/009,319
; FILING DATE: 26-JAN-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/664,989
; FILING DATE: 01-MAR-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/487,063

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; FILING DATE: 02-MAR-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/240,160
; FILING DATE: 02-SEP-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Cooper, Iver P.
; REGISTRATION NUMBER: 28,005
; REFERENCE/DOCKET NUMBER: LEV=1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; TELEX: 248633
; INFORMATION FOR SEQ ID NO: 87:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 56 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-358-160-87

Query Match      5.3%; Score 7; DB 1; Length 56;
Best Local Similarity 100.0%; Pred.No. 4;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 107 YGGCQGN 113
Db 33 YGGCQGN 39

Search completed: September 21, 2005, 16:51:21
Job time : 33 secs

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OM protein - protein search, using sw model

Run on: September 21, 2005, 16:46:12 ; Search time 109 Seconds
(without alignments)
489.161 Million cell updates/sec

Title: US-10-807-204-1
Perfect score: 131
Sequence: 1 MGLSGLLPILVPFILLGDIQ.....GNNNFQTEAICLVTKCKYH 131

Scoring table: OLIGO

Searched: 1826521 seqs, 407012169 residues

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Total number of hits satisfying chosen parameters: 1826521

Minimum DB seq length: 0

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Post-processing: Listing first 50 summaries

Database : Published Applications AA:*

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- 3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep.*
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- 6: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep.*
- 7: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep.*
- 8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep.*
- 9: /cgn2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pep.*
- 10: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep.*
- 11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep.*
- 12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep.*
- 13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep.*
- 14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep.*
- 15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep.*
- 16: /cgn2_6/ptodata/2/pubpaa/US10D_PUBCOMB.pep.*
- 17: /cgn2_6/ptodata/2/pubpaa/US10E_PUBCOMB.pep.*
- 18: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep.*
- 19: /cgn2_6/ptodata/2/pubpaa/US11A_PUBCOMB.pep.*
- 20: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep.*
- 21: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*
- 22: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	131	100.0	131	16	US-10-807-204-1
2	131	100.0	131	16	US-10-807-204-12
3	106	80.9	106	16	US-10-807-204-2
4	64	48.9	86	17	US-10-480-988-21
5	64	48.9	98	16	US-10-807-204-9
6	64	48.9	101	15	US-10-276-774-2606
7	64	48.9	131	16	US-10-807-204-15
8	43	32.8	43	16	US-10-807-204-5
9	30	22.9	30	16	US-10-807-204-4
10	24	18.3	24	16	US-10-807-204-6
11	21	16.0	33	16	US-10-807-204-7

12	21	16.0	33	16	US-10-807-204-10	Sequence 10, Appl
13	14	10.7	134	16	US-10-807-204-14	Sequence 14, Appl
14	12	9.2	51	15	US-10-588-993-118	Sequence 118, App
15	12	9.2	58	16	US-10-361-997-5	Sequence 5, Appl1
16	12	9.2	58	17	US-10-931-153-21	Sequence 21, Appl
17	12	9.2	102	9	US-09-852-659A-120	Sequence 120, App
18	12	9.2	102	15	US-10-058-993-121	Sequence 121, App
19	12	9.2	117	9	US-09-852-659A-119	Sequence 119, App
20	12	9.2	117	15	US-10-058-993-120	Sequence 120, App
21	12	9.2	133	9	US-09-853-161-75	Sequence 75, Appl
22	12	9.2	133	9	US-09-852-659A-75	Sequence 75, Appl
23	12	9.2	133	9	US-09-852-797-75	Sequence 75, Appl
24	12	9.2	133	15	US-10-058-993-75	Sequence 75, Appl
25	12	9.2	133	16	US-10-807-204-13	Sequence 13, Appl
26	11	8.4	67	10	US-09-896-095-147	Sequence 147, App
27	11	8.4	67	14	US-10-038-722-90	Sequence 90, Appl
28	11	8.4	67	15	US-10-115-134-4	Sequence 4, Appl1
29	10	7.6	63	14	US-09-896-095-176	Sequence 176, App
30	10	7.6	63	14	US-10-038-722-119	Sequence 119, App
31	10	7.6	63	15	US-10-115-134-33	Sequence 33, Appl
32	10	7.6	136	16	US-10-807-204-16	Sequence 16, Appl
33	9	6.9	58	14	US-10-167-351-13	Sequence 13, Appl
34	9	6.9	58	20	US-11-083-742-13	Sequence 13, Appl
35	8	6.1	166	9	US-09-864-761-47670	Sequence 47670, A
36	8	6.1	324	18	US-10-213-974-24	Sequence 24, Appl
37	8	6.1	449	17	US-10-732-923-22254	Sequence 2254, A
38	8	6.1	746	14	US-10-205-823-66	Sequence 66, Appl
39	8	6.1	746	20	US-11-051-454-66	Sequence 2643, Ap
40	8	6.1	816	15	US-10-094-749-2643	Sequence 35830, A
41	8	6.1	1203	18	US-10-450-763-35830	Sequence 34348, A
42	8	6.1	1597	18	US-10-450-763-34348	Sequence 40612, A
43	8	6.1	1597	18	US-10-450-763-40612	Sequence 41171, A
44	8	6.1	1597	18	US-10-450-763-41171	Sequence 50261, A
45	8	6.1	1597	18	US-10-450-763-50261	Sequence 38243, A
46	8	6.1	1599	18	US-10-450-763-38243	Sequence 44809, A
47	8	6.1	1599	18	US-10-450-763-44809	Sequence 39507, A
48	8	6.1	1784	18	US-10-450-763-39507	Sequence 23, Appl
49	7	5.3	18	17	US-10-753-078A-23	Sequence 263879,
50	7	5.3	30	16	US-10-425-115-263879	

ALIGNMENTS

RESULT 1
US-10-807-204-1
; Sequence 1, Application US/10807204
; Publication No. US20040229312A1
; GENERAL INFORMATION:
; APPLICANT: Bougueleret, Lydie
; APPLICANT: Baïroch, Amos
; APPLICANT: Niknejad, Anne
; TITLE OF INVENTION: Engineered Human Kunitz-Type Protease
; TITLE OF INVENTION: Inhibitor
; FILE REFERENCE: 54720-8015.US00
; CURRENT APPLICATION NUMBER: US/10/807,204
; CURRENT FILING DATE: 2004-03-22
; PRIOR APPLICATION NUMBER: PCT/EP03/01629
; PRIOR FILING DATE: 2003-02-18
; PRIOR APPLICATION NUMBER: US 60/358,683
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 131
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (1)...(131)
; OTHER INFORMATION: eppin-like precursor
; FEATURE:
; NAME/KEY: SIGNAL


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; FEATURE:
; NAME/KEY: DISULFID
; LOCATION: (52)...(102)
; OTHER INFORMATION: predicted disulfide bond
; FEATURE:
; NAME/KEY: DISULFID
; LOCATION: (61)...(85)
; OTHER INFORMATION: predicted disulfide bond
; FEATURE:
; NAME/KEY: DISULFID
; LOCATION: (77)...(98)
; OTHER INFORMATION: predicted disulfide bond
; US-10-807-204-2

Query Match      80.9%; Score 106; DB 16; Length 106;
Best Local Similarity 100.0%; Pred. No. 1.7e-97;
Matches 106; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 26 EGILGKPCPKIKVECEVEEIDQCTKPRDCPENMKCCPFSCGKKCLDFRDKICSMPPQEAGP 85
Db 1 EGILGKPCPKIKVECEVEEIDQCTKPRDCPENMKCCPFSCGKKCLDFRDKICSMPPQEAGP 60

Qy 86 CLASIPHHWYKTKICSEFYGGCGNNNNFQTEAICLVTCCKYH 131
Db 61 CLASIPHHWYKTKICSEFYGGCGNNNNFQTEAICLVTCCKYH 106

RESULT 4
US-10-480-988-21
; Sequence 21, Application US/10480988
; Publication No. US20050069877A1
; GENERAL INFORMATION:
; APPLICANT: GANDHI, Ameena R.; KABLE, Amy E.;
; APPLICANT: SWARNAKAR, Anita; HAPALIA, April J.A.;
; APPLICANT: TRAN, Bao; DUGGAN, Brendan M.;
; APPLICANT: WARREN, Bridget A.; ISON, Craig H.;
; APPLICANT: HONCHELL, Cynthia D.; NGUYEN, Dannel B.;
; APPLICANT: LU, Dyung Aina M.; LEE, Ernestine A.;
; APPLICANT: YUE, Henry; FORSYTHE, Ian J.;
; APPLICANT: BARROSO, Ines; RAMKUMAR, Javalaxmi;
; APPLICANT: GRIFFIN, Jennifer A.; LI, Joana X.;
; APPLICANT: YANG, Junming; THANGAVELU, Kavitha;
; APPLICANT: GIETZEN, Kimberly J.; DING, Li;
; APPLICANT: BAUGHN, Mariah R.; BOROWSKY, Mark L.;
; APPLICANT: YAO, Monique G.; CHAWLA, Narinder K.;
; APPLICANT: MASON, Patricia M.; GURURAJAN, Rajagopal;
; APPLICANT: LEE, Sally; BECHA, Shanya D.;
; APPLICANT: LEE, Soo Yeun; TRAN, Uyen K.;
; APPLICANT: ELLIOTT, Vicki S.; LUO, Wen;
; APPLICANT: SPRAGUE, William W.; TANG, Y. Tom;
; APPLICANT: LU, Yan; ZEBARJADIAN, Yeganeh
; TITLE OF INVENTION: PROTEIN MODIFICATION AND MAINTENANCE MOLECULES
; FILE REFERENCE: PF-1040 USN
; CURRENT APPLICATION NUMBER: US/10/480,988
; PRIOR FILING DATE: 2003-12-16
; PRIOR APPLICATION NUMBER: PCT/US02/19360
; PRIOR FILING DATE: 2002-06-18
; PRIOR APPLICATION NUMBER: US 60/300,508
; PRIOR FILING DATE: 2001-06-22
; PRIOR APPLICATION NUMBER: US 60/303,445
; PRIOR FILING DATE: 2001-07-06
; PRIOR APPLICATION NUMBER: US 60/305,405
; PRIOR FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: US 60/311,442
; PRIOR FILING DATE: 2001-08-09
; PRIOR APPLICATION NUMBER: US 60/314,821
; PRIOR FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: US 60/315,992
; PRIOR FILING DATE: 2001-08-29
; PRIOR APPLICATION NUMBER: US 60/378,205
; PRIOR FILING DATE: 2002-05-03
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: PERL Program

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; SEQ ID NO 21
; LENGTH: 86
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No: 7675588CD1
; US-10-480-988-21

Query Match      48.9%; Score 64; DB 17; Length 86;
Best Local Similarity 100.0%; Pred. No. 1e-55;
Matches 64; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MGLSGLLPILVPFILLGDIQSPGHAEGILGKPCPKIKVECEVEEIDQCTKPRDCPENMKC 60
Db 1 MGLSGLLPILVPFILLGDIQSPGHAEGILGKPCPKIKVECEVEEIDQCTKPRDCPENMKC 60

Qy 61 CPFS 64
Db 61 CPFS 64

RESULT 5
US-10-807-204-9
; Sequence 9, Application US/10807204
; Publication No. US20040229312A1
; GENERAL INFORMATION:
; APPLICANT: Bougueleret, Lydie
; APPLICANT: Bairoch, Amos
; APPLICANT: Niknejad, Anne
; TITLE OF INVENTION: Engineered Human Kunitz-Type Protease
; FILE REFERENCE: 54720-8015.US00
; CURRENT APPLICATION NUMBER: US/10/807,204
; CURRENT FILING DATE: 2004-03-22
; PRIOR APPLICATION NUMBER: PCT/EP03/01629
; PRIOR FILING DATE: 2003-02-18
; PRIOR APPLICATION NUMBER: US 60/358,683
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 98
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-807-204-9

Query Match      48.9%; Score 64; DB 16; Length 98;
Best Local Similarity 100.0%; Pred. No. 1.1e-55;
Matches 64; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MGLSGLLPILVPFILLGDIQSPGHAEGILGKPCPKIKVECEVEEIDQCTKPRDCPENMKC 60
Db 1 MGLSGLLPILVPFILLGDIQSPGHAEGILGKPCPKIKVECEVEEIDQCTKPRDCPENMKC 60

Qy 61 CPFS 64
Db 61 CPFS 64

RESULT 6
US-10-276-774-2606
; Sequence 2606, Application US/10276774
; Publication No. US20040053245A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; APPLICANT: Tang, Y. Tom et al
; TITLE OF INVENTION: No. US20040053245A1el Nucleic Acids and Polypeptides
; FILE REFERENCE: 21272-030
; CURRENT APPLICATION NUMBER: US/10/276,774
; CURRENT FILING DATE: 2002-11-18
; PRIOR APPLICATION NUMBER: 09/560,875
; PRIOR FILING DATE: 2000-04-27

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; PRIOR APPLICATION NUMBER: 09/496,914
; PRIOR FILING DATE: 2000-02-03
; NUMBER OF SEQ ID NOS: 2700
; SOFTWARE: Custom
; SEQ ID NO 2606
; LENGTH: 101
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-276-774-2606

Query Match      48.9%; Score 64; DB 15; Length 101;
Best Local Similarity 100.0%; Pred. No. 1.1e-55;
Matches 64; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MGLSGLLPILVPFILLGDIQBPFGHAEGLGKPCPKIKVECEVEIDQCTKPRDCPENMKC 60
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 16 MGLSGLLPILVPFILLGDIQBPFGHAEGLGKPCPKIKVECEVEIDQCTKPRDCPENMKC 75
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy 61 CPFS 64
    ||||
Db 76 CPFS 79

RESULT 7
US-10-807-204-15
; Sequence 15, Application US/10807204
; Publication No. US20040229312A1
; GENERAL INFORMATION:
; APPLICANT: Bougueleret, Lydie
; APPLICANT: Bairoch, Amos
; APPLICANT: Niknejad, Anne
; TITLE OF INVENTION: Engineered Human Kunitz-Type Protease
; TITLE OF INVENTION: Inhibitor
; FILE REFERENCE: 54720-8015.US00
; CURRENT APPLICATION NUMBER: US/10/807,204
; CURRENT FILING DATE: 2004-03-22
; PRIOR APPLICATION NUMBER: PCT/EP03/01629
; PRIOR FILING DATE: 2003-02-18
; PRIOR APPLICATION NUMBER: US 60/358,683
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 15
; LENGTH: 131
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-807-204-15

Query Match      48.9%; Score 64; DB 16; Length 131;
Best Local Similarity 100.0%; Pred. No. 1.4e-55;
Matches 64; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MGLSGLLPILVPFILLGDIQBPFGHAEGLGKPCPKIKVECEVEIDQCTKPRDCPENMKC 60
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1 MGLSGLLPILVPFILLGDIQBPFGHAEGLGKPCPKIKVECEVEIDQCTKPRDCPENMKC 60
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy 61 CPFS 64
    ||||
Db 61 CPFS 64

RESULT 8
US-10-807-204-5
; Sequence 5, Application US/10807204
; Publication No. US20040229312A1
; GENERAL INFORMATION:
; APPLICANT: Bougueleret, Lydie
; APPLICANT: Bairoch, Amos
; APPLICANT: Niknejad, Anne
; TITLE OF INVENTION: Engineered Human Kunitz-Type Protease
; TITLE OF INVENTION: Inhibitor
; FILE REFERENCE: 54720-8015.US00
; CURRENT APPLICATION NUMBER: US/10/807,204
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; CURRENT FILING DATE: 2004-03-22
; PRIOR APPLICATION NUMBER: PCT/EP03/01629
; PRIOR FILING DATE: 2003-02-18
; PRIOR APPLICATION NUMBER: US 60/358,683
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 43
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-807-204-5

Query Match      32.8%; Score 43; DB 16; Length 43;
Best Local Similarity 100.0%; Pred. No. 4.7e-35;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 32 PCPKIKVECEVEIDQCTKPRDCPENMKCCPFSCGKKCLDFRK 74
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1 PCPKIKVECEVEIDQCTKPRDCPENMKCCPFSCGKKCLDFRK 43
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||

RESULT 9
US-10-807-204-4
; Sequence 4, Application US/10807204
; Publication No. US20040229312A1
; GENERAL INFORMATION:
; APPLICANT: Bougueleret, Lydie
; APPLICANT: Bairoch, Amos
; APPLICANT: Niknejad, Anne
; TITLE OF INVENTION: Engineered Human Kunitz-Type Protease
; TITLE OF INVENTION: Inhibitor
; FILE REFERENCE: 54720-8015.US00
; CURRENT APPLICATION NUMBER: US/10/807,204
; CURRENT FILING DATE: 2004-03-22
; PRIOR APPLICATION NUMBER: PCT/EP03/01629
; PRIOR FILING DATE: 2003-02-18
; PRIOR APPLICATION NUMBER: US 60/358,683
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 30
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-807-204-4

Query Match      22.9%; Score 30; DB 16; Length 30;
Best Local Similarity 100.0%; Pred. No. 3.2e-22;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MGLSGLLPILVPFILLGDIQBPFGHAEGLG 30
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1 MGLSGLLPILVPFILLGDIQBPFGHAEGLG 30
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||

RESULT 10
US-10-807-204-6
; Sequence 6, Application US/10807204
; Publication No. US20040229312A1
; GENERAL INFORMATION:
; APPLICANT: Bougueleret, Lydie
; APPLICANT: Bairoch, Amos
; APPLICANT: Niknejad, Anne
; TITLE OF INVENTION: Engineered Human Kunitz-Type Protease
; TITLE OF INVENTION: Inhibitor
; FILE REFERENCE: 54720-8015.US00
; CURRENT APPLICATION NUMBER: US/10/807,204
; CURRENT FILING DATE: 2004-03-22
; PRIOR APPLICATION NUMBER: PCT/EP03/01629
; PRIOR FILING DATE: 2003-02-18
; PRIOR APPLICATION NUMBER: US 60/358,683
; PRIOR FILING DATE: 2002-02-21
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; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 24
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-807-204-6

Query Match      18.3%; Score 24; DB 16; Length 24;
Best Local Similarity 100.0%; Pred. No. 2.5e-16;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 75 DCSMPQEGAGPCLASIPHWYNNK 98
Db 1 DCSMPQEGAGPCLASIPHWYNNK 24

RESULT 11
US-10-807-204-7
; Sequence 7, Application US/10807204
; Publication No. US20040229312A1
; GENERAL INFORMATION:
; APPLICANT: Bougueleret, Lydie
; APPLICANT: Bairoch, Amos
; APPLICANT: Niknejad, Anne
; TITLE OF INVENTION: Engineered Human Kunitz-Type Protease
; FILE REFERENCE: 54720-8015.US00
; CURRENT APPLICATION NUMBER: US/10/807,204
; PRIOR FILING DATE: 2004-03-22
; PRIOR APPLICATION NUMBER: PCT/EP03/01629
; PRIOR FILING DATE: 2003-02-18
; PRIOR APPLICATION NUMBER: US 60/358,683
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 33
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-807-204-7

Query Match      16.0%; Score 21; DB 16; Length 33;
Best Local Similarity 100.0%; Pred. No. 3.2e-13;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 111 QGNNNFQTEAICLVTCCKYH 131
Db 13 QGNNNFQTEAICLVTCCKYH 33

RESULT 12
US-10-807-204-10
; Sequence 10, Application US/10807204
; Publication No. US20040229312A1
; GENERAL INFORMATION:
; APPLICANT: Bougueleret, Lydie
; APPLICANT: Bairoch, Amos
; APPLICANT: Niknejad, Anne
; TITLE OF INVENTION: Engineered Human Kunitz-Type Protease
; FILE REFERENCE: 54720-8015.US00
; CURRENT APPLICATION NUMBER: US/10/807,204
; PRIOR FILING DATE: 2004-03-22
; PRIOR APPLICATION NUMBER: PCT/EP03/01629
; PRIOR FILING DATE: 2003-02-18
; PRIOR APPLICATION NUMBER: US 60/358,683
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 33
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-807-204-10

Query Match      16.0%; Score 21; DB 16; Length 33;
Best Local Similarity 100.0%; Pred. No. 3.2e-13;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 111 QGNNNFQTEAICLVTCCKYH 131
Db 13 QGNNNFQTEAICLVTCCKYH 33

RESULT 13
US-10-807-204-14
; Sequence 14, Application US/10807204
; Publication No. US20040229312A1
; GENERAL INFORMATION:
; APPLICANT: Bougueleret, Lydie
; APPLICANT: Bairoch, Amos
; APPLICANT: Niknejad, Anne
; TITLE OF INVENTION: Engineered Human Kunitz-Type Protease
; FILE REFERENCE: 54720-8015.US00
; CURRENT APPLICATION NUMBER: US/10/807,204
; PRIOR FILING DATE: 2004-03-22
; PRIOR APPLICATION NUMBER: PCT/EP03/01629
; PRIOR FILING DATE: 2003-02-18
; PRIOR APPLICATION NUMBER: US 60/358,683
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14
; LENGTH: 134
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-807-204-14

Query Match      10.7%; Score 14; DB 16; Length 134;
Best Local Similarity 100.0%; Pred. No. 9.9e-06;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 105 FIYGCQCGNNNFQ 118
Db 105 FIYGCQCGNNNFQ 118

RESULT 14
US-10-058-993-118
; Sequence 118, Application US/10058993
; Publication No. US20030225009A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 28 Human Secreted Proteins
; FILE REFERENCE: P2003P5
; CURRENT APPLICATION NUMBER: US/10/058,993
; CURRENT FILING DATE: 2002-01-30
; PRIOR APPLICATION NUMBER: 09/852,659
; PRIOR FILING DATE: 2001-05-11
; PRIOR APPLICATION NUMBER: 09/852,797
; PRIOR FILING DATE: 2001-05-11
; PRIOR APPLICATION NUMBER: 09/853,161
; PRIOR FILING DATE: 2001-05-11
; PRIOR APPLICATION NUMBER: 60/265,583
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: 09/152,060
; PRIOR FILING DATE: 1998-09-11
; PRIOR APPLICATION NUMBER: PCT/US98/04858
; PRIOR FILING DATE: 1998-03-12
; PRIOR APPLICATION NUMBER: 60/068,368
; PRIOR FILING DATE: 1997-12-19
; PRIOR APPLICATION NUMBER: 60/057,765
; PRIOR FILING DATE: 1997-09-05
; PRIOR APPLICATION NUMBER: 60/048,970
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; PRIOR FILING DATE: 1997-06-05
; PRIOR APPLICATION NUMBER: 60/050,934
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/048,100
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/048,189
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/048,357
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/040,710
; PRIOR FILING DATE: 1997-03-14
; PRIOR APPLICATION NUMBER: 60/040,762
; PRIOR FILING DATE: 1997-03-14
; NUMBER OF SEQ ID NOS: 122
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 118
; LENGTH: 51
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-058-993-118

Query Match 9.2%; Score 12; DB 15; Length 51;
Best Local Similarity 100.0%; Pred. No. 0.00043;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 107 YGGCGGNNNNFQ 118
Db 31 YGGCGGNNNNFQ 42

RESULT 15
US-10-361-997-5
; Sequence 5, Application US/10361997
; Publication No. US20040171794A1
; GENERAL INFORMATION:
; APPLICANT: Ladner, Robert Charles
; APPLICANT: Lev, Arthur C.
; TITLE OF INVENTION: KUNITZ DOMAIN PEPTIDES
; FILE REFERENCE: 3421.1015-000
; CURRENT APPLICATION NUMBER: US/10/361,997
; CURRENT FILING DATE: 2003-02-07
; PRIOR APPLICATION NUMBER: US 60/355,547
; PRIOR FILING DATE: 2002-02-07
; NUMBER OF SEQ ID NOS: 84
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 58
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-361-997-5

Query Match 9.2%; Score 12; DB 16; Length 58;
Best Local Similarity 100.0%; Pred. No. 0.00048;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 107 YGGCGGNNNNFQ 118
Db 35 YGGCGGNNNNFQ 46

RESULT 16
US-10-931-153-21
; Sequence 21, Application US/10931153
; Publication No. US20050089515A1
; GENERAL INFORMATION:
; APPLICANT: Ley, Arthur C.
; APPLICANT: Sato, Aaron K.
; APPLICANT: Ladner, Robert C.
; APPLICANT: Stochl, Mark
; TITLE OF INVENTION: POLY-PEGYLATED PROTEASE INHIBITORS
; FILE REFERENCE: 10280-119001
; CURRENT APPLICATION NUMBER: US/10/931,153
; CURRENT FILING DATE: 2004-08-30

; PRIOR APPLICATION NUMBER: US 60/498,845
; PRIOR FILING DATE: 2003-08-29
; PRIOR APPLICATION NUMBER: US 60/598,967
; PRIOR FILING DATE: 2004-08-04
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 21
; LENGTH: 58
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-931-153-21

Query Match 9.2%; Score 12; DB 17; Length 58;
Best Local Similarity 100.0%; Pred. No. 0.00048;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 107 YGGCGGNNNNFQ 118
Db 35 YGGCGGNNNNFQ 46

RESULT 17
US-09-852-659A-120
; Sequence 120, Application US/09852659A
; Patent No. US20020077287A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 28 Human Secreted Proteins
; FILE REFERENCE: P2003P4
; CURRENT APPLICATION NUMBER: US/09/852,659A
; CURRENT FILING DATE: 2001-05-11
; PRIOR APPLICATION NUMBER: 60/265,583
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: 09/152,060
; PRIOR FILING DATE: 1998-09-11
; PRIOR APPLICATION NUMBER: PCT/US98/04858
; PRIOR FILING DATE: 1998-03-12
; PRIOR APPLICATION NUMBER: 60/040,762
; PRIOR FILING DATE: 1997-03-14
; PRIOR APPLICATION NUMBER: 60/040,710
; PRIOR FILING DATE: 1997-03-14
; PRIOR APPLICATION NUMBER: 60/050,934
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/048,100
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/048,357
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/048,189
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/057,765
; PRIOR FILING DATE: 1997-09-05
; PRIOR APPLICATION NUMBER: 60/048,970
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/068,368
; PRIOR FILING DATE: 1997-12-19
; NUMBER OF SEQ ID NOS: 121
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 120
; LENGTH: 102
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-852-659A-120

Query Match 9.2%; Score 12; DB 9; Length 102;
Best Local Similarity 100.0%; Pred. No. 0.00077;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 107 YGGCGGNNNNFQ 118
Db 76 YGGCGGNNNNFQ 87

RESULT 18

```
US-10-058-993-121
; Sequence 121, Application US/10058993
; Publication No. US20030225009A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 28 Human Secreted Proteins
; FILE REFERENCE: PZ003P5
; CURRENT APPLICATION NUMBER: US/10/058,993
; CURRENT FILING DATE: 2002-01-30
; PRIOR APPLICATION NUMBER: 09/852,659
; PRIOR FILING DATE: 2001-05-11
; PRIOR APPLICATION NUMBER: 09/852,797
; PRIOR FILING DATE: 2001-05-11
; PRIOR APPLICATION NUMBER: 09/853,161
; PRIOR FILING DATE: 2001-05-11
; PRIOR APPLICATION NUMBER: 60/265,583
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: 09/152,060
; PRIOR FILING DATE: 1998-09-11
; PRIOR APPLICATION NUMBER: PCT/US98/04858
; PRIOR FILING DATE: 1998-03-12
; PRIOR APPLICATION NUMBER: 60/068,368
; PRIOR FILING DATE: 1997-12-19
; PRIOR APPLICATION NUMBER: 60/057,765
; PRIOR FILING DATE: 1997-09-05
; PRIOR APPLICATION NUMBER: 60/048,970
; PRIOR FILING DATE: 1997-06-05
; PRIOR APPLICATION NUMBER: 60/048,189
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/050,934
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/048,100
; PRIOR FILING DATE: 1997-03-14
; Query Match
; Best Local Similarity 100.0%; Pred. No. 0.00077;
; Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 107 YGCGCGNNNFQ 118
DB 76 YGCGCGNNNFQ 87

RESULT 19
US-09-852-659A-119
; Sequence 119, Application US/09852659A
; Patent No. US2002007287A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 28 Human Secreted Proteins
; FILE REFERENCE: PZ003P4
; CURRENT APPLICATION NUMBER: US/09/852,659A
; CURRENT FILING DATE: 2001-05-11
; PRIOR APPLICATION NUMBER: 60/265,583
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: 09/152,060
; PRIOR FILING DATE: 1998-09-11
; PRIOR APPLICATION NUMBER: PCT/US98/04858
; PRIOR FILING DATE: 1998-03-12
; PRIOR APPLICATION NUMBER: 60/040,762

US-10-058-993-121
; Sequence 121, Application US/10058993
; Publication No. US20030225009A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 28 Human Secreted Proteins
; FILE REFERENCE: PZ003P5
; CURRENT APPLICATION NUMBER: US/10/058,993
; CURRENT FILING DATE: 2002-01-30
; PRIOR APPLICATION NUMBER: 09/852,659
; PRIOR FILING DATE: 2001-05-11
; PRIOR APPLICATION NUMBER: 09/852,797
; PRIOR FILING DATE: 2001-05-11
; PRIOR APPLICATION NUMBER: 09/853,161
; PRIOR FILING DATE: 2001-05-11
; PRIOR APPLICATION NUMBER: 60/265,583
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: 09/152,060
; PRIOR FILING DATE: 1998-09-11
; PRIOR APPLICATION NUMBER: PCT/US98/04858
; PRIOR FILING DATE: 1998-03-12
; PRIOR APPLICATION NUMBER: 60/068,368
; PRIOR FILING DATE: 1997-12-19
; PRIOR APPLICATION NUMBER: 60/057,765
; PRIOR FILING DATE: 1997-09-05
; PRIOR APPLICATION NUMBER: 60/048,970
; PRIOR FILING DATE: 1997-06-05
; PRIOR APPLICATION NUMBER: 60/048,189
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/050,934
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/048,100
; PRIOR FILING DATE: 1997-03-14
; Query Match
; Best Local Similarity 100.0%; Pred. No. 0.00087;
; Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 107 YGCGCGNNNFQ 118
DB 91 YGCGCGNNNFQ 102

RESULT 20
US-10-058-993-120
; Sequence 120, Application US/10058993
; Publication No. US20030225009A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 28 Human Secreted Proteins
; FILE REFERENCE: PZ003P5
; CURRENT APPLICATION NUMBER: US/10/058,993
; CURRENT FILING DATE: 2002-01-30
; PRIOR APPLICATION NUMBER: 09/852,659
; PRIOR FILING DATE: 2001-05-11
; PRIOR APPLICATION NUMBER: 09/852,797
; PRIOR FILING DATE: 2001-05-11
; PRIOR APPLICATION NUMBER: 09/853,161
; PRIOR FILING DATE: 2001-05-11
; PRIOR APPLICATION NUMBER: 60/265,583
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: 09/152,060
; PRIOR FILING DATE: 1998-09-11
; PRIOR APPLICATION NUMBER: PCT/US98/04858
; PRIOR FILING DATE: 1998-03-12
; PRIOR APPLICATION NUMBER: 60/068,368
; PRIOR FILING DATE: 1997-12-19
; PRIOR APPLICATION NUMBER: 60/057,765
; PRIOR FILING DATE: 1997-09-05
; PRIOR APPLICATION NUMBER: 60/048,970
; PRIOR FILING DATE: 1997-06-05
; PRIOR APPLICATION NUMBER: 60/050,934
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/048,100
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/048,189
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/048,357
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/040,710
; PRIOR FILING DATE: 1997-03-14
; PRIOR APPLICATION NUMBER: 60/040,762
; NUMBER OF SEQ ID NOS: 122
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 121
; LENGTH: 102
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-058-993-121
```

; PRIOR FILING DATE: 1997-03-14
; NUMBER OF SEQ ID NOS: 122
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 120
; LENGTH: 117
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-058-993-120

Query Match 9.2%; Score 12; DB 15; Length 117;
Best Local Similarity 100.0%; Pred. No. 0.00087;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 107 YGGCQGNNNFQ 118
| | | | | | | | | |
Db 91 YGGCQGNNNFQ 102

RESULT 21
US-09-853-161-75
; Sequence 75, Application US/09853161
; Patent No. US20020076756A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 28 Human Secreted Proteins
; FILE REFERENCE: P2003P1
; CURRENT APPLICATION NUMBER: US/09/853,161
; CURRENT FILING DATE: 2001-05-11
; PRIOR APPLICATION NUMBER: 60/265,583
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: 09/152,060
; PRIOR FILING DATE: 1998-09-11
; PRIOR APPLICATION NUMBER: PCT/US98/04858
; PRIOR FILING DATE: 1998-03-12
; PRIOR APPLICATION NUMBER: 60/040,762
; PRIOR FILING DATE: 1997-03-14
; PRIOR APPLICATION NUMBER: 60/040,710
; PRIOR FILING DATE: 1997-03-14
; PRIOR APPLICATION NUMBER: 60/050,934
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/048,100
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/048,189
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/057,765
; PRIOR FILING DATE: 1997-09-05
; PRIOR APPLICATION NUMBER: 60/048,970
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/068,368
; PRIOR FILING DATE: 1997-12-19
; NUMBER OF SEQ ID NOS: 118
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 75
; LENGTH: 133
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-853-161-75

Query Match 9.2%; Score 12; DB 9; Length 133;
Best Local Similarity 100.0%; Pred. No. 0.00097;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 107 YGGCQGNNNFQ 118
| | | | | | | | | |
Db 107 YGGCQGNNNFQ 118

RESULT 22
US-09-852-659A-75
; Sequence 75, Application US/09852659A
; Patent No. US2002007287A1

; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 28 Human Secreted Proteins
; FILE REFERENCE: P2003P4
; CURRENT APPLICATION NUMBER: US/09/852,659A
; CURRENT FILING DATE: 2001-05-11
; PRIOR APPLICATION NUMBER: 60/265,583
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: 09/152,060
; PRIOR FILING DATE: 1998-09-11
; PRIOR APPLICATION NUMBER: PCT/US98/04858
; PRIOR FILING DATE: 1998-03-12
; PRIOR APPLICATION NUMBER: 60/040,762
; PRIOR FILING DATE: 1997-03-14
; PRIOR APPLICATION NUMBER: 60/040,710
; PRIOR FILING DATE: 1997-03-14
; PRIOR APPLICATION NUMBER: 60/050,934
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/048,100
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/048,357
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/048,189
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/057,765
; PRIOR FILING DATE: 1997-09-05
; PRIOR APPLICATION NUMBER: 60/048,970
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/068,368
; PRIOR FILING DATE: 1997-12-19
; NUMBER OF SEQ ID NOS: 121
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 75
; LENGTH: 133
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-852-659A-75

Query Match 9.2%; Score 12; DB 9; Length 133;
Best Local Similarity 100.0%; Pred. No. 0.00097;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 107 YGGCQGNNNFQ 118
| | | | | | | | | |
Db 107 YGGCQGNNNFQ 118

RESULT 23
US-09-852-797-75
; Sequence 75, Application US/09852797
; Patent No. US20020172994A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 28 Human Secreted Proteins
; FILE REFERENCE: P2003P2
; CURRENT APPLICATION NUMBER: US/09/852,797
; CURRENT FILING DATE: 2001-05-11
; PRIOR APPLICATION NUMBER: 60/265,583
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: 09/152,060
; PRIOR FILING DATE: 1998-09-11
; PRIOR APPLICATION NUMBER: PCT/US98/04858
; PRIOR FILING DATE: 1998-03-12
; PRIOR APPLICATION NUMBER: 60/040,762
; PRIOR FILING DATE: 1997-03-14
; PRIOR APPLICATION NUMBER: 60/040,710
; PRIOR FILING DATE: 1997-03-14
; PRIOR APPLICATION NUMBER: 60/050,934
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/048,100
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/048,357
; PRIOR FILING DATE: 1997-05-30

; PRIOR APPLICATION NUMBER: 60/048,189
 ; PRIOR FILING DATE: 1997-05-30
 ; PRIOR APPLICATION NUMBER: 60/057,765
 ; PRIOR FILING DATE: 1997-09-05
 ; PRIOR APPLICATION NUMBER: 60/048,970
 ; PRIOR FILING DATE: 1997-06-06
 ; PRIOR APPLICATION NUMBER: 60/068,368
 ; PRIOR FILING DATE: 1997-12-19
 ; NUMBER OF SEQ ID NOS: 118
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 75
 ; LENGTH: 133
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-09-852-797-75

Query Match 9.2%; Score 12; DB 9; Length 133;
 Best Local Similarity 100.0%; Pred. No. 0.00097;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 107 YGGCGGNNNFQ 118
 Db 107 YGGCGGNNNFQ 118

RESULT 24
 US-10-058-993-75
 ; Sequence 75, Application US/10058993
 ; Publication No. US20030225009A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Rosen et al.
 ; TITLE OF INVENTION: 28 Human Secreted Proteins
 ; FILE REFERENCE: P2003P5
 ; CURRENT APPLICATION NUMBER: US/10/058,993
 ; CURRENT FILING DATE: 2002-01-30
 ; PRIOR APPLICATION NUMBER: 09/852,659
 ; PRIOR FILING DATE: 2001-05-11
 ; PRIOR APPLICATION NUMBER: 09/852,797
 ; PRIOR FILING DATE: 2001-05-11
 ; PRIOR APPLICATION NUMBER: 09/853,161
 ; PRIOR FILING DATE: 2001-05-11
 ; PRIOR APPLICATION NUMBER: 60/265,583
 ; PRIOR FILING DATE: 2001-02-02
 ; PRIOR APPLICATION NUMBER: 09/152,060
 ; PRIOR FILING DATE: 1998-09-11
 ; PRIOR APPLICATION NUMBER: PCT/US98/04858
 ; PRIOR FILING DATE: 1998-03-12
 ; PRIOR APPLICATION NUMBER: 60/068,368
 ; PRIOR FILING DATE: 1997-12-19
 ; PRIOR APPLICATION NUMBER: 60/057,765
 ; PRIOR FILING DATE: 1997-09-05
 ; PRIOR APPLICATION NUMBER: 60/048,970
 ; PRIOR FILING DATE: 1997-06-05
 ; PRIOR APPLICATION NUMBER: 60/050,934
 ; PRIOR FILING DATE: 1997-05-30
 ; PRIOR APPLICATION NUMBER: 60/048,100
 ; PRIOR FILING DATE: 1997-05-30
 ; PRIOR APPLICATION NUMBER: 60/048,189
 ; PRIOR FILING DATE: 1997-05-30
 ; PRIOR APPLICATION NUMBER: 60/048,357
 ; PRIOR FILING DATE: 1997-05-30
 ; PRIOR APPLICATION NUMBER: 60/040,710
 ; PRIOR FILING DATE: 1997-03-14
 ; PRIOR APPLICATION NUMBER: 60/040,762
 ; PRIOR FILING DATE: 1997-03-14
 ; NUMBER OF SEQ ID NOS: 122
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 75
 ; LENGTH: 133
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-10-058-993-75

Query Match 9.2%; Score 12; DB 15; Length 133;
 Best Local Similarity 100.0%; Pred. No. 0.00097;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 107 YGGCGGNNNFQ 118
 Db 107 YGGCGGNNNFQ 118
 RESULT 25
 US-10-807-204-13
 ; Sequence 13, Application US/10807204
 ; Publication No. US20040229312A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Bougueleret, Lydie
 ; APPLICANT: Bairoch, Amos
 ; APPLICANT: Niknejad, Anne
 ; TITLE OF INVENTION: Engineered Human Kunitz-Type Protease
 ; TITLE OF INVENTION: Inhibitor
 ; FILE REFERENCE: 54720-8015.US00
 ; CURRENT APPLICATION NUMBER: US/10/807,204
 ; CURRENT FILING DATE: 2004-03-22
 ; PRIOR APPLICATION NUMBER: PCT/EP03/01629
 ; PRIOR FILING DATE: 2003-02-18
 ; PRIOR APPLICATION NUMBER: US 60/358,683
 ; PRIOR FILING DATE: 2002-02-21
 ; NUMBER OF SEQ ID NOS: 16
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 13
 ; LENGTH: 133
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-10-807-204-13

Query Match 9.2%; Score 12; DB 16; Length 133;
 Best Local Similarity 100.0%; Pred. No. 0.00097;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 107 YGGCGGNNNFQ 118
 Db 107 YGGCGGNNNFQ 118

RESULT 26
 US-09-896-095-147
 ; Sequence 147, Application US/09896095
 ; Publication No. US20030219886A1
 ; GENERAL INFORMATION:
 ; APPLICANT: LADNER, Charles C.
 ; APPLICANT: GUTERMAN, Sonia K.
 ; APPLICANT: ROBERTS, Bruce L.
 ; APPLICANT: MARKLAND, William
 ; APPLICANT: LEY, Arthur C.
 ; APPLICANT: KENT, Rachel B.
 ; TITLE OF INVENTION: DIRECTED EVOLUTION OF NOVEL BINDING PROTEINS
 ; FILE REFERENCE: LADNER-7L
 ; CURRENT APPLICATION NUMBER: US/09/896,095
 ; CURRENT FILING DATE: 2001-05-29
 ; PRIOR APPLICATION NUMBER: 08/415,922
 ; PRIOR FILING DATE: 1995-03-04
 ; PRIOR APPLICATION NUMBER: 08/009,319
 ; PRIOR FILING DATE: 1993-01-26
 ; PRIOR APPLICATION NUMBER: 07/664,989
 ; PRIOR FILING DATE: 1991-03-01
 ; PRIOR APPLICATION NUMBER: 08/993,776
 ; PRIOR FILING DATE: 1997-12-18
 ; NUMBER OF SEQ ID NOS: 274
 ; SOFTWARE: PatentIn version 3.2
 ; SEQ ID NO 147
 ; LENGTH: 67
 ; TYPE: PRT
 ; ORGANISM: Bos taurus
 US-09-896-095-147

Query Match 8.4%; Score 11; DB 10; Length 67;
Best Local Similarity 100.0%; Pred. No. 0.0054;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 107 YGCGCGNNNF 117
| | | | | | | | | |
Db 38 YGCGCGNNNF 48

RESULT 27

US-10-038-722-90
; Sequence 90, Application US/10038722
; Publication No. US20030175919A1
; GENERAL INFORMATION:
; APPLICANT: LEY, Arthur C.
; APPLICANT: GUTERMAN, Sonia K.
; APPLICANT: MARKLAND, William
; APPLICANT: KENT, Rachel B.
; APPLICANT: ROBERTS, Bruce L.
; APPLICANT: LADNER, Robert C.
; TITLE OF INVENTION: ITI-D1 KUNITZ DOMAIN MUTANTS AS THE INHIBITORS
; FILE REFERENCE: LEY=1B
; CURRENT APPLICATION NUMBER: US/10/038.722
; CURRENT FILING DATE: 2002-01-08
; PRIOR APPLICATION NUMBER: US 08/849,406
; PRIOR FILING DATE: 1999-07-21
; PRIOR APPLICATION NUMBER: PCT/US95/16349
; PRIOR FILING DATE: 1995-12-15
; PRIOR APPLICATION NUMBER: US 08/358,160
; PRIOR FILING DATE: 1994-12-16
; NUMBER OF SEQ ID NOS: 129
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 90
; LENGTH: 67
; TYPE: PRT
; ORGANISM: Bos taurus
US-10-038-722-90

Query Match 8.4%; Score 11; DB 14; Length 67;
Best Local Similarity 100.0%; Pred. No. 0.0054;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 107 YGCGCGNNNF 117
| | | | | | | | | |
Db 38 YGCGCGNNNF 48

RESULT 28

US-10-115-134-4
; Sequence 4, Application US/10115134
; Publication No. US20030223977A1
; GENERAL INFORMATION:
; APPLICANT: LEY, Arthur Charles
; APPLICANT: GUTERMAN, Sonia Kosow
; APPLICANT: MARKLAND, William
; APPLICANT: KENT, Rachel Baribault
; APPLICANT: ROBERTS, Bruce Lindsay
; APPLICANT: LADNER, Robert Charles
; TITLE OF INVENTION: DOMAIN MUTANTS AS CATHEPSIN G INHIBITORS
; FILE REFERENCE: LEY=1C
; CURRENT APPLICATION NUMBER: US/10/115.134
; CURRENT FILING DATE: 2002-04-04
; PRIOR APPLICATION NUMBER: 08/849,406
; PRIOR FILING DATE: 2001-07-21
; NUMBER OF SEQ ID NOS: 92
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 4
; LENGTH: 67
; TYPE: PRT
; ORGANISM: Bos taurus
US-10-115-134-4

Query Match 8.4%; Score 11; DB 15; Length 67;
Best Local Similarity 100.0%; Pred. No. 0.0054;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 107 YGCGCGNNNF 117
| | | | | | | | | |
Db 38 YGCGCGNNNF 48

RESULT 29

US-09-896-095-176
; Sequence 176, Application US/09896095
; Publication No. US20030219886A1
; GENERAL INFORMATION:
; APPLICANT: LADNER, Charles C.
; APPLICANT: GUTERMAN, Sonia K.
; APPLICANT: ROBERTS, Bruce L.
; APPLICANT: MARKLAND, William
; APPLICANT: LEY, Arthur C.
; APPLICANT: KENT, Rachel B.
; TITLE OF INVENTION: DIRECTED EVOLUTION OF NOVEL BINDING PROTEINS
; FILE REFERENCE: LADNER=7L
; CURRENT APPLICATION NUMBER: US/09/896,095
; CURRENT FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: 08/415,922
; PRIOR FILING DATE: 1995-03-04
; PRIOR APPLICATION NUMBER: 08/009,319
; PRIOR FILING DATE: 1993-01-26
; PRIOR APPLICATION NUMBER: 07/664,989
; PRIOR FILING DATE: 1991-03-01
; PRIOR APPLICATION NUMBER: 08/993,776
; PRIOR FILING DATE: 1997-12-18
; NUMBER OF SEQ ID NOS: 274
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 176
; LENGTH: 63
; TYPE: PRT
; ORGANISM: Bombyx mori
US-09-896-095-176

Query Match 7.6%; Score 10; DB 10; Length 63;
Best Local Similarity 100.0%; Pred. No. 0.051;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 104 EFYGGCGGN 113
| | | | | | | | | |
Db 38 EFYGGCGGN 47

RESULT 30

US-10-038-722-119
; Sequence 119, Application US/10038722
; Publication No. US20030175919A1
; GENERAL INFORMATION:
; APPLICANT: LEY, Arthur C.
; APPLICANT: GUTERMAN, Sonia K.
; APPLICANT: MARKLAND, William
; APPLICANT: KENT, Rachel B.
; APPLICANT: ROBERTS, Bruce L.
; APPLICANT: LADNER, Robert C.
; TITLE OF INVENTION: ITI-D1 KUNITZ DOMAIN MUTANTS AS THE INHIBITORS
; FILE REFERENCE: LEY=1B
; CURRENT APPLICATION NUMBER: US/10/038,722
; CURRENT FILING DATE: 2002-01-08
; PRIOR APPLICATION NUMBER: US 08/849,406
; PRIOR FILING DATE: 1999-07-21
; PRIOR APPLICATION NUMBER: PCT/US95/16349
; PRIOR FILING DATE: 1995-12-15
; PRIOR APPLICATION NUMBER: US 08/358,160
; PRIOR FILING DATE: 1994-12-16
; NUMBER OF SEQ ID NOS: 129
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 119

```

; LENGTH: 63
; TYPE: PRT
; ORGANISM: Bombyx mori
US-10-038-722-119

Query Match          7.6%; Score 10; DB 14; Length 63;
Best Local Similarity 100.0%; Pred. No. 0.051;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 104 EFIYGGCGQN 113
DB 38 EFIYGGCGQN 47

RESULT 31
US-10-115-134-33
; Sequence 33, Application US/10115134
; Publication No. US2003022397A1
; GENERAL INFORMATION:
; APPLICANT: LEY, Arthur Charles
; APPLICANT: GUTERMAN, Sonia Kosow
; APPLICANT: MARKLAND, William
; APPLICANT: KENT, Rachel Baribault
; APPLICANT: ROBERTS, Bruce Lindsey
; APPLICANT: LADNER, Robert Charles
; TITLE OF INVENTION: DOMAIN MUTANTS AS CATHEPSIN G INHIBITORS
; FILE REFERENCE: LEY-1C
; CURRENT APPLICATION NUMBER: US/10/115,134
; PRIOR FILING DATE: 2002-04-04
; PRIOR APPLICATION NUMBER: 08/849,406
; PRIOR FILING DATE: 2001-07-21
; NUMBER OF SEQ ID NOS: 92
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 33
; LENGTH: 63
; TYPE: PRT
; ORGANISM: Bombyx mori
US-10-115-134-33

Query Match          7.6%; Score 10; DB 15; Length 63;
Best Local Similarity 100.0%; Pred. No. 0.051;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 104 EFIYGGCGQN 113
DB 38 EFIYGGCGQN 47

RESULT 32
US-10-807-204-16
; Sequence 16, Application US/10807204
; Publication No. US20040229312A1
; GENERAL INFORMATION:
; APPLICANT: Bougueleret, Lydie
; APPLICANT: Bairoch, Amos
; APPLICANT: Niknejad, Anne
; TITLE OF INVENTION: Engineered Human Kunitz-Type Protease
; TITLE OF INVENTION: Inhibitor
; FILE REFERENCE: 54720-8015.US00
; CURRENT APPLICATION NUMBER: US/10/807,204
; CURRENT FILING DATE: 2004-03-22
; PRIOR APPLICATION NUMBER: PCT/EP03/01629
; PRIOR FILING DATE: 2003-02-18
; PRIOR APPLICATION NUMBER: US 60/358,683
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 16
; LENGTH: 136
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-807-204-16

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Query Match          7.6%; Score 10; DB 16; Length 136;
Best Local Similarity 100.0%; Pred. No. 0.097;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 104 EFIYGGCGQN 113
DB 104 EFIYGGCGQN 113

RESULT 33
US-10-167-351-13
; Sequence 13, Application US/10167351
; Publication No. US20030165896A1
; GENERAL INFORMATION:
; APPLICANT: DYAX CORP.
; APPLICANT: Markland, William
; APPLICANT: Ladner, Robert C.
; TITLE OF INVENTION: Inhibitors of Human Plasmin Derived From The Kunitz Domains
; FILE REFERENCE: DYX-007.2P US-4
; CURRENT APPLICATION NUMBER: US/10/167,351
; CURRENT FILING DATE: 2002-06-11
; PRIOR APPLICATION NUMBER: 09/638,770
; PRIOR FILING DATE: 2000-08-15
; PRIOR APPLICATION NUMBER: 09/414,878
; PRIOR FILING DATE: 1999-10-08
; PRIOR APPLICATION NUMBER: 09/240,136
; PRIOR FILING DATE: 1999-01-29
; PRIOR APPLICATION NUMBER: 08/676,124
; PRIOR FILING DATE: 1997-01-07
; PRIOR APPLICATION NUMBER: PCT/US95/00298
; PRIOR FILING DATE: 1995-01-11
; PRIOR APPLICATION NUMBER: 08/208,265
; PRIOR FILING DATE: 1994-03-10
; PRIOR APPLICATION NUMBER: 08/179,658
; PRIOR FILING DATE: 1994-01-11
; NUMBER OF SEQ ID NOS: 137
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 13
; LENGTH: 58
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: mutant Kunitz domain selectants
US-10-167-351-13

Query Match          6.9%; Score 9; DB 14; Length 58;
Best Local Similarity 100.0%; Pred. No. 0.47;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 105 FIYGGCGQN 113
DB 33 FIYGGCGQN 41

RESULT 34
US-11-083-742-13
; Sequence 13, Application US/11083742
; Publication No. US20050186649A1
; GENERAL INFORMATION:
; APPLICANT: DYAX CORP.
; APPLICANT: Markland, William
; APPLICANT: Ladner, Robert C.
; TITLE OF INVENTION: Inhibitors of Human Plasmin Derived From The Kunitz Domains
; FILE REFERENCE: DYX-007.2P US-4
; CURRENT APPLICATION NUMBER: US/11/083,742
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/167,351
; PRIOR FILING DATE: 2002-06-11
; PRIOR APPLICATION NUMBER: 09/638,770
; PRIOR FILING DATE: 2000-08-15
; PRIOR APPLICATION NUMBER: 09/414,878
; PRIOR FILING DATE: 1999-10-08
; PRIOR APPLICATION NUMBER: 09/240,136

```

```
; PRIOR FILING DATE: 1999-01-29
; PRIOR APPLICATION NUMBER: 08/676,124
; PRIOR FILING DATE: 1997-01-07
; PRIOR APPLICATION NUMBER: PCT/US95/00298
; PRIOR FILING DATE: 1995-01-11
; PRIOR APPLICATION NUMBER: 08/208,265
; PRIOR FILING DATE: 1994-03-10
; PRIOR APPLICATION NUMBER: 08/179,658
; PRIOR FILING DATE: 1994-01-11
; NUMBER OF SEQ ID NOS: 137
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 13
; LENGTH: 58
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: mutant Kunitz domain selectants
US-11-083-742-13

Query Match          6.9%; Score 9; DB 20; Length 58;
Best Local Similarity 100.0%; Pred. No. 0.47;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      105 FIYGGCQGN 113
Db      33 FIYGGCQGN 41

RESULT 35
US-09-864-761-47670
; Sequence 47670, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharron G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; FILE REFERENCE: Aeomica-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
```

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; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Annonax Sequence Listing Engine vers. 1.1
; SEQ ID NO 47670
; LENGTH: 166
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AJ239323.2
; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 8.9
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 3.9
; OTHER INFORMATION: EST HUMAN HIT: AUI33286.1, EVALUE 1.00e-60
; OTHER INFORMATION: SWISSPROT HIT: P51795, EVALUE 5.00e-82
US-09-864-761-47670

Query Match          6.1%; Score 8; DB 9; Length 166;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      10 LVPFILLG 17
Db      36 LVPFILLG 43

RESULT 36
US-10-213-974-24
; Sequence 24, Application US/10213974
; Publication No. US20050125159A1
; GENERAL INFORMATION:
; APPLICANT: Stein, Joshua C
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Methods for Analyzing Biological Elements
; FILE REFERENCE: 38-10(52045)B
; CURRENT APPLICATION NUMBER: US/10/213,974
; CURRENT FILING DATE: 2002-08-06
; PRIOR APPLICATION NUMBER: US 60/325,537
; PRIOR FILING DATE: 2001-10-01
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 24
; LENGTH: 324
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-10-213-974-24

Query Match          6.1%; Score 8; DB 18; Length 324;
Best Local Similarity 100.0%; Pred. No. 20;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      10 LVPFILLG 17
Db      221 LVPFILLG 228

RESULT 37
US-10-732-923-22254
; Sequence 22254, Application US/10732923
; Publication No. US20050108791A1
; GENERAL INFORMATION:
; APPLICANT: Edgerton, Michael D
; TITLE OF INVENTION: TRANSGENIC PLANTS WITH IMPROVED PHENOTYPES
; FILE REFERENCE: 38-15(52796)C
; CURRENT APPLICATION NUMBER: US/10/732,923
; CURRENT FILING DATE: 2003-12-10
; PRIOR APPLICATION NUMBER: 10/310,154
; PRIOR FILING DATE: 2002-12-04
; NUMBER OF SEQ ID NOS: 24149
; SEQ ID NO 22254
; LENGTH: 449
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; TYPE: PRT
; ORGANISM: Sinorhizobium meliloti
US-10-7332-22254

Query Match          6.1%; Score 8; DB 17; Length 449;
Best Local Similarity 100.0%; Pred. No. 26;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      5 GLLPILVP 12
Db      391 GLLPILVP 398

RESULT 38
US-10-205-823-66
; Sequence 66, Application US/10205823
; Publication No. US20030108963A1
; GENERAL INFORMATION:
; APPLICANT: Schlegel, Robert
; APPLICANT: Monahan, John E.
; APPLICANT: Endege, Wilson O.
; APPLICANT: Gannavarapu, Manjula
; APPLICANT: Gorbacheva, Bella
; APPLICANT: Hoersch, Sebastian
; APPLICANT: Kamatkar, Shubhangi
; APPLICANT: Wonsey, Angela M.
; APPLICANT: Glatt, Karen
; APPLICANT: Zhao, Xumei
; APPLICANT: Anderson, Dustin
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND
; TITLE OF INVENTION: METHODS FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
; TITLE OF INVENTION: THERAPY OF PROSTATE CANCER
; FILE REFERENCE: MRI-044
; CURRENT APPLICATION NUMBER: US/10/205,823
; PRIOR FILING DATE: 2002-07-25
; PRIOR APPLICATION NUMBER: 60/307,982
; PRIOR FILING DATE: 2001-07-25
; PRIOR APPLICATION NUMBER: 60/314,356
; PRIOR FILING DATE: 2001-08-22
; PRIOR APPLICATION NUMBER: 60/325,020
; PRIOR FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: 60/341,746
; PRIOR FILING DATE: 2001-12-12
; PRIOR APPLICATION NUMBER: 60/362,158
; PRIOR FILING DATE: 2002-03-05
; NUMBER OF SEQ ID NOS: 455
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 66
; LENGTH: 746
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-051-454-66

Query Match          6.1%; Score 8; DB 20; Length 746;
Best Local Similarity 100.0%; Pred. No. 41;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      10 LVPFILLG 17
Db      319 LVPFILLG 326

RESULT 40
US-10-094-749-2643
; Sequence 2643, Application US/10094749
; Publication No. US20030219741A1
; GENERAL INFORMATION:
; APPLICANT: ISOGAI, TAKAO
; APPLICANT: SUGIYAMA, TOMOYASU
; APPLICANT: OTSUKI, TETSUJI
; APPLICANT: WAKAMATSU, AI
; APPLICANT: SATO, HIROYUKI
; APPLICANT: ISHII, SHIZUKO
; APPLICANT: YAMAMOTO, JUN-ICHI
; APPLICANT: ISONO, YUUKO
; APPLICANT: HIO, YURI
; APPLICANT: OTSUKA, KAORU
; APPLICANT: NAGAI, KEIICHI
; APPLICANT: IRIE, RYOTARO
; APPLICANT: TAMECHIKA, ICHIRO
; APPLICANT: SEKI, NAOHICO
; APPLICANT: YOSHIKAWA, TSUTOMU
; APPLICANT: OTSUKA, MOTOYUKI
; APPLICANT: NAGAHARI, KENJI
; APPLICANT: MASUHO, YASUHIKO
; TITLE OF INVENTION: NOVEL FULL-LENGTH cDNA
; FILE REFERENCE: 084335/0160
; CURRENT APPLICATION NUMBER: US/10/094,749
; CURRENT FILING DATE: 2002-03-12
; PRIOR APPLICATION NUMBER: 60/350,435
; PRIOR FILING DATE: 2002-01-24
; PRIOR APPLICATION NUMBER: JP 2001-328381
; PRIOR FILING DATE: 2001-09-14
; NUMBER OF SEQ ID NOS: 3381
; SOFTWARE: PatentIn Ver. 2.1

; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-205-823-66

Query Match          6.1%; Score 8; DB 14; Length 746;
Best Local Similarity 100.0%; Pred. No. 41;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      10 LVPFILLG 17
Db      319 LVPFILLG 326

RESULT 39
US-11-051-454-66
; Sequence 66, Application US/11051454
; Publication No. US20050191673A1
; GENERAL INFORMATION:
; APPLICANT: Schlegel, Robert
; APPLICANT: Monahan, John E.
; APPLICANT: Endege, Wilson O.
; APPLICANT: Gannavarapu, Manjula
; APPLICANT: Gorbacheva, Bella
; APPLICANT: Hoersch, Sebastian
```

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; SEQ ID NO 2643
; LENGTH: 816
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-094-749-2643

Query Match          6.1%; Score 8; DB 15; Length 816;
Best Local Similarity 100.0%; Pred. No. 44;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 LVPFILLG 17
   |||||
Db 389 LVPFILLG 396

RESULT 41
US-10-450-763-35830
; Sequence 35830, Application US/10450763
; Publication No. US20050196754A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc
; TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
; FILE REFERENCE: 790CIP3/US
; CURRENT FILING DATE: 2003-06-11
; PRIOR APPLICATION NUMBER: PCT/US01/08631
; PRIOR FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: 09/540,217
; PRIOR FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: 09/649,167
; PRIOR FILING DATE: 2000-08-23
; NUMBER OF SEQ ID NOS: 60736
; SOFTWARE: Custom
; SEQ ID NO 35830
; LENGTH: 1203
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (675)..(693)
; OTHER INFORMATION: CHLORIDE CHANNEL SIGNATURE domain identified by eMATRIX,
; OTHER INFORMATION: accession number PR00762A, p-value=4.000e-22, raw score of 14.22
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (663)..(1029)
; OTHER INFORMATION: Voltage gated chloride channels domain identified by Pfam,
; OTHER INFORMATION: accession name voltage_CLC, E-value=1.1e-169, Pfam score of 576.2
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(1203)
; OTHER INFORMATION: Xaa = X or * as defined in Table 2
US-10-450-763-35830

Query Match          6.1%; Score 8; DB 18; Length 1203;
Best Local Similarity 100.0%; Pred. No. 61;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 LVPFILLG 17
   |||||
Db 836 LVPFILLG 843

RESULT 42
US-10-450-763-34348
; Sequence 34348, Application US/10450763
; Publication No. US20050196754A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc
; TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
; FILE REFERENCE: 790CIP3/US
; CURRENT APPLICATION NUMBER: US/10/450.763
; CURRENT FILING DATE: 2003-06-11
; PRIOR APPLICATION NUMBER: PCT/US01/08631
```

```
; PRIOR FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: 09/540,217
; PRIOR FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: 09/649,167
; PRIOR FILING DATE: 2000-08-23
; NUMBER OF SEQ ID NOS: 60736
; SOFTWARE: Custom
; SEQ ID NO 34348
; LENGTH: 1597
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (272)..(317)
; OTHER INFORMATION: kw TRANSCRIPTASE REVERSE II ORF2 domain identified by
; OTHER INFORMATION: eMATRIX, accession number DM01354N, p-value=1.000e-40, raw score
; OTHER INFORMATION: 13.17
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (1057)..(1423)
; OTHER INFORMATION: Voltage gated chloride channels domain identified by Pfam,
; OTHER INFORMATION: accession name voltage_CLC, E-value=1.1e-169, Pfam score of 576.2
US-10-450-763-34348

Query Match          6.1%; Score 8; DB 18; Length 1597;
Best Local Similarity 100.0%; Pred. No. 78;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 LVPFILLG 17
   |||||
Db 1230 LVPFILLG 1237

RESULT 43
US-10-450-763-40612
; Sequence 40612, Application US/10450763
; Publication No. US20050196754A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc
; TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
; FILE REFERENCE: 790CIP3/US
; CURRENT APPLICATION NUMBER: US/10/450,763
; CURRENT FILING DATE: 2003-06-11
; PRIOR APPLICATION NUMBER: PCT/US01/08631
; PRIOR FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: 09/540,217
; PRIOR FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: 09/649,167
; PRIOR FILING DATE: 2000-08-23
; NUMBER OF SEQ ID NOS: 60736
; SOFTWARE: Custom
; SEQ ID NO 40612
; LENGTH: 1597
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (272)..(317)
; OTHER INFORMATION: kw TRANSCRIPTASE REVERSE II ORF2 domain identified by
; OTHER INFORMATION: eMATRIX, accession number DM01354N, p-value=1.000e-40, raw score
; OTHER INFORMATION: 13.17
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (1058)..(1424)
; OTHER INFORMATION: Voltage gated chloride channels domain identified by Pfam,
; OTHER INFORMATION: accession name voltage_CLC, E-value=1.1e-169, Pfam score of 576.2
US-10-450-763-40612

Query Match          6.1%; Score 8; DB 18; Length 1597;
Best Local Similarity 100.0%; Pred. No. 78;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 LVPFILLG 17
```

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; OTHER INFORMATION: kw TRANSCRIPTASE REVERSE II ORF2 domain identified by
; OTHER INFORMATION: eMATRIX, accession number DM01354N, p-value=1.000e-40, raw score
; OTHER INFORMATION: 13.17
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (1057)..(1423)
; OTHER INFORMATION: Voltage gated chloride channels domain identified by Pfam,
; OTHER INFORMATION: accession name voltage_CLC, E-value=1.1e-169, Pfam score of 576.2
US-10-450-763-50261

Query Match      6.1%; Score 8; DB 18; Length 1597;
Best Local Similarity 100.0%; Pred. No. 78;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      10 LVPFILLG 17
      |||||
Db      1230 LVPFILLG 1237

RESULT 44
US-10-450-763-41171
; Sequence 41171, Application US/10450763
; Publication No. US20050196754A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc
; TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
; FILE REFERENCE: 790CIP3/US
; CURRENT APPLICATION NUMBER: US/10/450,763
; CURRENT FILING DATE: 2003-06-11
; PRIOR APPLICATION NUMBER: PCT/US01/08631
; PRIOR FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: 09/540,217
; PRIOR FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: 09/649,167
; PRIOR FILING DATE: 2000-08-23
; NUMBER OF SEQ ID NOS: 60736
; SOFTWARE: Custom
; SEQ ID NO 41171
; LENGTH: 1597
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (272)..(317)
; OTHER INFORMATION: kw TRANSCRIPTASE REVERSE II ORF2 domain identified by
; OTHER INFORMATION: eMATRIX, accession number DM01354N, p-value=1.000e-40, raw score
; OTHER INFORMATION: 13.17
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (1057)..(1423)
; OTHER INFORMATION: Voltage gated chloride channels domain identified by Pfam,
; OTHER INFORMATION: accession name voltage_CLC, E-value=1.1e-169, Pfam score of 576.2
US-10-450-763-41171

Query Match      6.1%; Score 8; DB 18; Length 1597;
Best Local Similarity 100.0%; Pred. No. 78;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      10 LVPFILLG 17
      |||||
Db      1230 LVPFILLG 1237

RESULT 45
US-10-450-763-50261
; Sequence 50261, Application US/10450763
; Publication No. US20050196754A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc
; TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
; FILE REFERENCE: 790CIP3/US
; CURRENT APPLICATION NUMBER: US/10/450,763
; CURRENT FILING DATE: 2003-06-11
; PRIOR APPLICATION NUMBER: PCT/US01/08631
; PRIOR FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: 09/540,217
; PRIOR FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: 09/649,167
; PRIOR FILING DATE: 2000-08-23
; NUMBER OF SEQ ID NOS: 60736
; SOFTWARE: Custom
; SEQ ID NO 50261
; LENGTH: 1597
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (272)..(317)

```

```

; OTHER INFORMATION: kw TRANSCRIPTASE REVERSE II ORF2 domain identified by
; OTHER INFORMATION: eMATRIX, accession number DM01354N, p-value=1.000e-40, raw score
; OTHER INFORMATION: 13.17
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (1057)..(1423)
; OTHER INFORMATION: Voltage gated chloride channels domain identified by Pfam,
; OTHER INFORMATION: accession name voltage_CLC, E-value=1.1e-169, Pfam score of 576.2
US-10-450-763-50261

Query Match      6.1%; Score 8; DB 18; Length 1597;
Best Local Similarity 100.0%; Pred. No. 78;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      10 LVPFILLG 17
      |||||
Db      1230 LVPFILLG 1237

RESULT 46
US-10-450-763-38243
; Sequence 38243, Application US/10450763
; Publication No. US20050196754A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc
; TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
; FILE REFERENCE: 790CIP3/US
; CURRENT APPLICATION NUMBER: US/10/450,763
; CURRENT FILING DATE: 2003-06-11
; PRIOR APPLICATION NUMBER: PCT/US01/08631
; PRIOR FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: 09/540,217
; PRIOR FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: 09/649,167
; PRIOR FILING DATE: 2000-08-23
; NUMBER OF SEQ ID NOS: 60736
; SOFTWARE: Custom
; SEQ ID NO 38243
; LENGTH: 1599
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (272)..(317)
; OTHER INFORMATION: kw TRANSCRIPTASE REVERSE II ORF2 domain identified by
; OTHER INFORMATION: eMATRIX, accession number DM01354N, p-value=1.000e-40, raw score
; OTHER INFORMATION: 13.17
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (1061)..(1427)
; OTHER INFORMATION: Voltage gated chloride channels domain identified by Pfam,
; OTHER INFORMATION: accession name voltage_CLC, E-value=1.1e-169, Pfam score of 576.2
US-10-450-763-38243

Query Match      6.1%; Score 8; DB 18; Length 1599;
Best Local Similarity 100.0%; Pred. No. 78;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      10 LVPFILLG 17
      |||||
Db      1232 LVPFILLG 1239

RESULT 47
US-10-450-763-44809
; Sequence 44809, Application US/10450763
; Publication No. US20050196754A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc
; TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
; FILE REFERENCE: 790CIP3/US
; CURRENT APPLICATION NUMBER: US/10/450,763
; CURRENT FILING DATE: 2003-06-11

```

```
; PRIOR APPLICATION NUMBER: PCT/US01/08631
; PRIOR FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: 09/540,217
; PRIOR FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: 09/649,167
; PRIOR FILING DATE: 2000-08-23
; NUMBER OF SEQ ID NOS: 60736
; SOFTWARE: Custom
; SEQ ID NO 44809
; LENGTH: 1599
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (272)..(317)
; OTHER INFORMATION: kw TRANSCRIPTASE REVERSE II ORF2 domain identified by
; OTHER INFORMATION: eMATRix, accession number DM01354N, p-value=1.000e-40, raw score
; OTHER INFORMATION: 13.17
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(1599)
; OTHER INFORMATION: Xaa = X or * as defined in Table 2
US-10-450-763-44809

Query Match          6.1%; Score 8; DB 18; Length 1599;
Best Local Similarity 100.0%; Pred. No. 78;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      10 LVPFILLG 17
Db      1232 LVPFILLG 1239

RESULT 48
US-10-450-763-39507
; Sequence 39507, Application US/10450763
; Publication No. US20050196754A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc
; TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
; FILE REFERENCE: 790CIP3/US
; CURRENT APPLICATION NUMBER: US/10/450,763
; CURRENT FILING DATE: 2003-06-11
; PRIOR APPLICATION NUMBER: PCT/US01/08631
; PRIOR FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: 09/540,217
; PRIOR FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: 09/649,167
; PRIOR FILING DATE: 2000-08-23
; NUMBER OF SEQ ID NOS: 60736
; SOFTWARE: Custom
; SEQ ID NO 39507
; LENGTH: 1784
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (297)..(338)
; OTHER INFORMATION: kw TRANSCRIPTASE REVERSE II ORF2 domain identified by
; OTHER INFORMATION: eMATRix, accession number DM01354I, p-value=1.000e-40, raw score
; OTHER INFORMATION: 15.55
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (1246)..(1612)
; OTHER INFORMATION: Voltage gated chloride channels domain identified by PFam,
; OTHER INFORMATION: accession name voltage_CLC, E-value=1.1e-169, Pfam score of 576.3
US-10-450-763-39507

Query Match          6.1%; Score 8; DB 18; Length 1784;
Best Local Similarity 100.0%; Pred. No. 85;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      10 LVPFILLG 17
```

```
Db      1417 LVPFILLG 1424

RESULT 49
US-10-753-078A-23
; Sequence 23, Application US/10753078A
; Publication No. US20050037475A1
; GENERAL INFORMATION:
; APPLICANT: Reifsnnyder, David
; APPLICANT: Inlow, Duane
; APPLICANT: Dorin, Glenn
; APPLICANT: Riquelme, Patricia
; APPLICANT: Cowgill, Cynthia
; APPLICANT: Bolesch, Doug
; APPLICANT: Gustafson, Mark
; TITLE OF INVENTION: Improved Method of Purifying TFPI and
; TITLE OF INVENTION: TFPI Analogs
; FILE REFERENCE: 012441.00050
; CURRENT APPLICATION NUMBER: US/10/753,078A
; CURRENT FILING DATE: 2004-01-08
; PRIOR APPLICATION NUMBER: US 60/494,546
; PRIOR FILING DATE: 2003-08-13
; PRIOR APPLICATION NUMBER: US 60/509,277
; PRIOR FILING DATE: 2003-10-08
; PRIOR APPLICATION NUMBER: US 60/512,199
; PRIOR FILING DATE: 2003-10-20
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 23
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-753-078A-23

Query Match          5.3%; Score 7; DB 17; Length 18;
Best Local Similarity 100.0%; Pred. No. 17;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      104 EFYGGC 110
Db       5 EFYGGC 11

RESULT 50
US-10-425-115-263879
; Sequence 263879, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 263879
; LENGTH: 30
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_172271C.1.pep
US-10-425-115-263879

Query Match          5.3%; Score 7; DB 16; Length 30;
Best Local Similarity 100.0%; Pred. No. 26;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy       4 SGLLPIL 10
```


Db 15 SGLLPIL 21

Search completed: September 21, 2005, 16:53:19
Job time : 112 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 21, 2005, 16:41:20 ; Search time 31 Seconds
(without alignments)
406.593 Million cell updates/sec

Title: US-10-807-204-1
Perfect score: 131
Sequence: 1 MGLSGLLPILVPFILLGDIQ.....GNNNNFQTEAICLVCKKYH 131

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 283416 seqs, 96216763 residues

Word size : 0

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 50 summaries

Database : PIR 79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	10	7.6	62	2 S01802	chymotrypsin inhib
2	10	7.6	63	1 TIMTC3	chymotrypsin inhib
3	8	6.1	67	1 TIBOC	trypsin inhibitor,
4	8	6.1	126	2 S54159	probable sodium po
5	8	6.1	324	2 B96738	probable ABC trans
6	8	6.1	449	2 G95876	probable permease
7	8	6.1	1515	2 T52081	MRP-like ABC trans
8	7	5.3	53	2 B29235	hemolymph trypsin
9	7	5.3	57	1 TIMJVC	venom basic protei
10	7	5.3	62	2 S01803	chymotrypsin inhib
11	7	5.3	211	2 F95851	probable nitrateni
12	7	5.3	215	2 D84382	hypothetical prote
13	7	5.3	272	2 AC0140	probable membrane
14	7	5.3	299	2 I49337	tissue factor path
15	7	5.3	300	2 S12143	lipoprotein-associ
16	7	5.3	302	1 TIRTKG	tissue factor path
17	7	5.3	304	1 JC2264	tissue factor path
18	7	5.3	304	1 TIHUGI	tissue factor path
19	7	5.3	337	2 F83839	hypothetical prote
20	7	5.3	337	2 A72042	conserved hypothet
21	7	5.3	337	2 H86582	CT 368 hypothetical
22	7	5.3	337	2 T19885	hypothetical prote
23	7	5.3	348	2 T19885	alpha-1-microglobu
24	7	5.3	352	1 HCHU	myb-related protei
25	7	5.3	374	2 T05891	myb-related protei
26	7	5.3	376	2 T53673	tissue factor path
27	7	5.3	396	2 S53325	tissue factor path
28	7	5.3	497	2 F83634	hypothetical prote
29	7	5.3	564	2 F72268	ABC transporter, A

30	7	5.3	602	2 D90557	hypothetical prote
31	7	5.3	615	2 S74277	probable membrane
32	7	5.3	615	2 S40624	probable membrane
33	7	5.3	988	2 B96621	hypothetical prote
34	7	5.3	1030	2 T37868	probable helicase
35	7	5.3	1073	1 S56822	SKI2 protein homol
36	7	5.3	1117	2 T11667	probable RNA helic
37	6	4.6	43	2 C47447	calcium channel pr
38	6	4.6	53	2 C90850	fimbrial minor pil
39	6	4.6	55	2 S30332	proteinase inhibit
40	6	4.6	56	2 JN0380	trypsin inhibitor
41	6	4.6	57	1 TIRIV2	venom basic protei
42	6	4.6	57	2 S13846	venom animal Kunit
43	6	4.6	58	1 TIHABK	isoinhibitor K (BP
44	6	4.6	61	1 TIVIT1	venom basic protei
45	6	4.6	62	2 S07451	proteinase inhibit
46	6	4.6	62	2 A44180	taicatoxin serine
47	6	4.6	62	2 S19327	venom basic protei
48	6	4.6	63	2 T34799	probable transcrip
49	6	4.6	65	1 TIVIVC	venom basic protei
50	6	4.6	71	2 D42506	F-ORF-E protein -

ALIGNMENTS

RESULT 1

S01802
chymotrypsin inhibitor I - silkworm
C:Species: Bombyx mori (silkworm)
C:Date: 30-Sep-1989 #sequence_revision 30-Sep-1989 #text_change 09-Jul-2004
C:Accession: S01802
R:Sasaki, T.
Biol. Chem. Hoppe-Seyler 369, 1235-1241, 1988
A:Title: Amino-acid sequences of two basic chymotrypsin inhibitors from silkworm larval
A:Reference number: S01802; MUID:89228538; PMID:3072972
A:Accession: S01802
A:Molecule type: protein
A:Residues: 1-62 <SAS>
A:Cross-references: UNIPROT:P10831
C:Superfamily: basic proteinase inhibitor; animal Kunitz-type proteinase inhibitor homol
C:Keywords: serine proteinase inhibitor
F:9-60/Domain: animal Kunitz-type proteinase inhibitor homology <BPI>

Query Match 7.6%; Score 10; DB 2; Length 62;
Best Local Similarity 100.0%; Pred. No. 0.0024;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 104 EFIYGGCQGN 113
|||||
Db 37 EFIYGGCQGN 46

RESULT 2

TIMTC3
chymotrypsin inhibitor III - silkworm
N:Alternate names: SCI-III
C:Species: Bombyx mori (silkworm)
C:Date: 22-Jul-1987 #sequence_revision 22-Jul-1994 #text_change 09-Jul-2004
C:Accession: A25740
R:Sasaki, T.
FEBS Lett. 168, 227-230, 1984
A:Title: Amino acid sequence of a novel Kunitz-type chymotrypsin inhibitor from hemolymph
A:Reference number: A25740
A:Accession: A25740
A:Molecule type: protein
A:Residues: 1-63 <SAS>
A:Cross-references: UNIPROT:P07481
A:Experimental source: larval hemolymph
C:Comment: In contrast to chymotrypsin inhibitors I and II, which are basic, this inhibi
C:Superfamily: basic proteinase inhibitor; animal Kunitz-type proteinase inhibitor homol
C:Keywords: serine proteinase inhibitor
F:10-61/Domain: animal Kunitz-type proteinase inhibitor homology <BPI>

F;10-61.20-44.36-57/disulfide bonds: #status predicted
F;21/Inhibitory site: Phe (chymotrypsin) #status predicted

Query Match 7.6%; Score 10; DB 1; Length 63;
Best Local Similarity 100.0%; Pred. No. 0.0024;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 104 EFIYGGCGGN 113
|||||

Db 38 EFIYGGCGGN 47
|||||

RESULT 3

TIBOC

trypsin inhibitor, colostrum (BPI type) - bovine

C;Species: Bos primigenius taurus (cattle)

C;Date: 24-Apr-1984 #sequence_revision 31-Dec-1993 #text_change 09-Jul-2004

C;Accession: A01207

R;Cechova, D.; Jonakova, V.; Sorm, F.

Collect. Czech. Chem. Commun. 36, 3342-3357, 1971

A;Title: Primary structure of trypsin inhibitor from cow colostrum (component B2).

A;Reference number: A90928

A;Accession: A01207

A;Molecule type: protein

A;Residues: 1-26, 'B', 28-67 <CEC>

A;Cross-references: UNIPROT:P00976

A;Note: the residue identified as Asx is bound to carbohydrate; therefore, we have shown

R;Cechova, D.; Ber, E.

Collect. Czech. Chem. Commun. 39, 680-688, 1974

A;Title: Disulfide bonds of trypsin inhibitor from cow colostrum.

A;Reference number: A90929

A;Contents: annotation; disulfide bonds

R;Cechova, D.; Muszynska, G.

FEBS Lett. 8, 84-86, 1970

A;Title: Role of lysine 18 in active center of cow colostrum trypsin inhibitor.

A;Reference number: A91440

A;Contents: annotation

A;Note: the inhibitory site was determined

C;Superfamily: basic proteinase inhibitor; animal Kunitz-type proteinase inhibitor homol

C;Keywords: colostrum; glycoprotein; serine proteinase inhibitor

F;8-58/Domain: animal Kunitz-type proteinase inhibitor homology <BPI>

F;8-58,17-41,33-54/Disulfide bonds: #status experimental

F;18/Inhibitory site: Lys (trypsin) #status experimental

F;27/Binding site: carbohydrate (Asn) (covalent) #status experimental

Query Match 6.1%; Score 8; DB 1; Length 67;
Best Local Similarity 100.0%; Pred. No. 0.37;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 107 YGGCGQGN 114
|||||

Db 38 YGGCGQGN 45
|||||

RESULT 4

S54159

probable sodium potassium ATPase gamma chain - human

C;Species: Homo sapiens (man)

C;Date: 08-Jul-1995 #sequence_revision 21-Jul-1995 #text_change 09-Jul-2004

C;Accession: S54159

R;Austrey, E.; Belley, L.; Millasot, P.; Junten, C.; Jeanpierre, C.

submitted to the EMBL Data Library, April 1995

A;Description: Characterization of the human cDNA for L-arginine:glycine amidinotransfer

A;Reference number: S54159

A;Accession: S54159

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-126 <AUS>

A;Cross-references: UNIPROT:Q15332; EMBL:X86400; NID:g791046; PID:CAA60152.1; PID:g7910

Query Match 6.1%; Score 8; DB 2; Length 126;
Best Local Similarity 100.0%; Pred. No. 0.61;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 82 EAGPCLAS 89
|||||

Db 35 EAGPCLAS 42
|||||

RESULT 5

B96738

Probable ABC transporter F3117.2 [imported] - Arabidopsis thaliana

C;Species: Arabidopsis thaliana (mouse-ear cress)

C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004

C;Accession: B96738

R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,

Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.

ansen, N.F.; Hughes, B.; Huizar, L.

Nature 408, 816-820, 2000

A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.

C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziani,

Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.

A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, I.

ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.

A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.

A;Reference number: A86141; MUID:21016719; PMID:11130712

A;Accession: B96738

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-324 <STO>

A;Cross-references: UNIPROT:Q9PVV9; GB:AE005173; NID:g6714334; PIDN:AAF26026.1; GSPDB:GN

C;Genetics:

A;Gene: F3117.2

A;Map position: 1

Query Match 6.1%; Score 8; DB 2; Length 324;
Best Local Similarity 100.0%; Pred. No. 1.3;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 LVPFILLG 17
|||||

Db 221 LVPFILLG 228
|||||

RESULT 6

G95876

probable permealase protein [imported] - Sinorhizobium meliloti

C;Species: Sinorhizobium meliloti

C;Date: 24-Aug-2001 #sequence_revision 24-Aug-2001 #text_change 09-Jul-2004

C;Accession: G95876

R;Finan, T.M.; Weidner, S.; Wong, K.; Buhrmester, J.; Chain, P.; Vorholter, F.J.; Hernan

Proc. Natl. Acad. Sci. U.S.A. 98, 9889-9894, 2001

A;Title: The complete sequence of the 1.683-kb pSymB megaplasmid from the N2-fixing endo

A;Reference number: A95842; MUID:21396508; PMID:11481431

A;Accession: G95876

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-449 <KUR>

A;Cross-references: UNIPROT:Q92WQ0; GB:AL591985; PIDN:CAC48679.1; PID:g15140151; GSPDB:GN

A;Experimental source: strain 1021, megaplasmid pSymB

R;Galibert, F.; Finan, T.M.; Long, S.R.; Puhler, A.; Abola, P.; Ampe, F.; Barloy-Hubler,

pela, D.; Chain, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Federspiel, N.A.; Fisher, R.F.;

Li; Hyman, R.W.; Jones, T.

Science 293, 668-672, 2001

A;Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, C.; Lelaure,

heault, P.; Vandenbol, M.; Vorholter, F.J.; Weidner, S.; Wells, D.H.; Wong, K.; Yeh, K.C.

A;Title: The composite genome of the legume symbiont Sinorhizobium meliloti.

A;Reference number: A96039; MUID:21368234; PMID:11474104

A;Contents: annotation

C;Genetics:

A;Gene: SMD20289

A;Genome: plasmid

Query Match 6.1%; Score 8; DB 2; Length 449;
Best Local Similarity 100.0%; Pred. No. 1.7;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 GLLPILVP 12
|||||
Db 391 GLLPILVP 398

RESULT 7

T52081
MRP-like ABC transporter [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 20-Oct-2000 #sequence_revision 20-Oct-2000 #text_change 09-Jul-2004
C:Accession: T52081
R:Tommasini, R.; Vogt, E.; Schmid, J.; Fromentau, M.; Amrhein, N.; Martinoia, E.
FEBS Lett. 411, 206-210, 1997
A:Title: Differential expression of genes coding for ABC transporters after treatment of
A:Reference number: Z25942; MUID:97415407; PMID:9271206
A:Accession: T52081
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-1515 <TOM>
A:Cross-references: UNIPROT:Q24510; EMBL:U92650; PIDN:AAC49791.1
A:Experimental source: cultivar Columbia
C:Superfamily: human multidrug resistance protein cMOAT2; ATP-binding cassette homology

Query Match 6.1%; Score 8; DB 2; Length 1515;
Best Local Similarity 100.0%; Pred. No. 4.4;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 LVPFILLG 17
|||||
Db 949 LVPFILLG 956

RESULT 8

B29235
hemolymph trypsin inhibitor B (BPI type) - tobacco hornworm (fragment)
C:Species: Manduca sexta (tobacco hornworm)
C:Date: 30-Jun-1989 #sequence_revision 30-Jun-1989 #text_change 09-Jul-2004
C:Accession: B29235
R:Ramesh, N.; Sugumaran, M.; Mole, J.E.
J. Biol. Chem. 263, 11523-11527, 1988
A:Title: Purification and characterization of two trypsin inhibitors from the hemolymph
A:Reference number: A92663; MUID:88298810; PMID:3165377
A:Accession: B29235
A:Molecule type: protein
A:Residues: 1-53 <RAM>

A:Cross-references: UNIPROT:P26227
C:Superfamily: basic proteinase inhibitor; animal Kunitz-type proteinase inhibitor homol
C:Keywords: serine proteinase inhibitor
F:4-53/Domain: animal Kunitz-type proteinase inhibitor homology (fragment) <BPI>

Query Match 5.3%; Score 7; DB 2; Length 53;
Best Local Similarity 100.0%; Pred. No. 3.8;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 107 YGCGQGN 113
|||||
Db 34 YGCGQGN 40

RESULT 9

TINJVC
venom basic proteinase inhibitor II - Cape cobra
C:Species: Naja nivea (Cape cobra)
C:Date: 30-Nov-1980 #sequence_revision 30-Nov-1980 #text_change 09-Jul-2004
C:Accession: A01217
R:Hokama, Y.; Iwanaga, S.; Tatsuki, T.; Suzuki, T.
J. Biochem. 79, 559-578, 1976
A:Title: Snake venom proteinase inhibitors. III. Isolation of five polypeptide inhibitor
o acid sequences of two of them.
A:Reference number: A91942; MUID:76237547; PMID:950337
A:Accession: A01217
A:Molecule type: protein

A:Residues: 1-57 <HOK>
A:Cross-references: UNIPROT:P00986

C:Comment: The activity of this inhibitor is probably similar to that of bovine basic pr
C:Superfamily: basic proteinase inhibitor; animal Kunitz-type proteinase inhibitor homol
C:Keywords: serine proteinase inhibitor; venom
F:5-55/Domain: animal Kunitz-type proteinase inhibitor homology <BPI>
F:5-55,14-38,30-51/Disulfide bonds: #status predicted

Query Match 5.3%; Score 7; DB 1; Length 57;
Best Local Similarity 100.0%; Pred. No. 4;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 104 EFIYGGC 110
|||||
Db 32 EFIYGGC 38

RESULT 10

S01803
chymotrypsin inhibitor II - silkworm
C:Species: Bombyx mori (silkworm)
C:Date: 30-Sep-1989 #sequence_revision 30-Sep-1989 #text_change 09-Jul-2004
C:Accession: S01803
R:Sasaki, T.
Biol. Chem. Hoppe-Seyler 369, 1235-1241, 1988
A:Title: Amino-acid sequences of two basic chymotrypsin inhibitors from silkworm larval
A:Reference number: S01802; MUID:89228538; PMID:3072972
A:Accession: S01803
A:Molecule type: protein
A:Residues: 1-62 <SAS>
A:Cross-references: UNIPROT:P10832
C:Superfamily: basic proteinase inhibitor; animal Kunitz-type proteinase inhibitor homol
C:Keywords: serine proteinase inhibitor
F:9-60/Domain: animal Kunitz-type proteinase inhibitor homology <BPI>

Query Match 5.3%; Score 7; DB 2; Length 62;
Best Local Similarity 100.0%; Pred. No. 4.3;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 104 EFIYGGC 110
|||||
Db 37 EFIYGGC 43

RESULT 11

P95851
probable nitrate/nitrite response regulator protein [imported] - Sinorhizobium meliloti (C:Species: Sinorhizobium meliloti
C:Date: 24-Aug-2001 #sequence_revision 24-Aug-2001 #text_change 09-Jul-2004
C:Accession: P95851
R:Finan, T.M.; Weidner, S.; Wong, K.; Buhrmester, J.; Chain, P.; Vorholter, F.J.; Hernan
Proc. Natl. Acad. Sci. U.S.A. 98, 9889-9894, 2001
A:Title: The complete sequence of the 1,683-kb pSymB megaplasmid from the N2-fixing endo
A:Reference number: A95842; MUID:21396508; PMID:11481431
A:Accession: P95851
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-211 <KUR>
A:Cross-references: UNIPROT:Q92X84; GB:AL591985; PIDN:CAC48478.1; PID:gi15139950; GSPDB:G
A:Experimental source: strain 1021, megaplasmid pSymB
R:Galibert, F.; Finan, T.M.; Long, S.R.; Puhler, A.; Abola, P.; Ampe, F.; Barloy-Hubler,
pela, D.; Chain, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Federspiel, N.A.; Fisher, R.F.,
L.; Hyman, R.W.; Jones, T.
Science 293, 668-672, 2001
A:Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, C.; Lelaure,
heault, P.; Vandenbol, M.; Vorholter, F.J.; Weidner, S.; Welle, D.H.; Wong, K.; Yeh, K.
A:Title: The composite genome of the legume symbiont Sinorhizobium meliloti.
A:Reference number: A96039; MUID:21368234; PMID:11474104
C:Contents: annotation
C:Genetics:
A:Gene: Smb20078
A:Genome: plasmid
C:Superfamily: response regulator with HTH DNA-binding domain, NarL type; response regul

Query Match 5.3%; Score 7; DB 2; Length 211;
 Best Local Similarity 100.0%; Pred. No. 11; Mismatches 0; Gaps 0;
 Matches 7; Conservative 0; Indels 0; Gaps 0;

Qy 1 MGLSGLL 7
 |||||
 Db 96 MGLSGLL 102

RESULT 12
 D84382
 hypothetical protein Vng3314h [imported] - Halobacterium sp. NRC-1
 C:Species: Halobacterium sp. NRC-1
 C:Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 09-Jul-2004
 C:Accession: D84382
 R;Ng, W.V.; Kennedy, S.P.; Mahairas, G.G.; Berquist, B.; Pan, M.; Shukla, H.D.; Lasky, S.; Leithausner, B.; Keller, K.; Cruz, R.; Danson, M.J.; Hough, D.W.; Maddocks, D.G.; Jablon, K.H.; Alam, M.; Freitas, T.
 Proc. Natl. Acad. Sci. U.S.A. 97, 12176-12181, 2000
 A:Authors: Hou, S.; Daniels, C.J.; Dennis, P.P.; Omer, A.D.; Ebhardt, H.; Lowe, T.M.; Li
 A:Title: Genome sequence of Halobacterium species NRC-1.
 A:Reference number: A84160; MUID:20504483; PMID:11016950
 A:Accession: D84382
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-215 <STO>
 A:Cross-references: UNIPROT:Q9HMZ7; GB:AE004437; NID:gl0581728; PIDN:AAG20424.1; GSPDB:G
 C:Genetics:
 A:Gene: VNG2314H

Query Match 5.3%; Score 7; DB 2; Length 215;
 Best Local Similarity 100.0%; Pred. No. 11; Mismatches 0; Gaps 0;
 Matches 7; Conservative 0; Indels 0; Gaps 0;

Qy 5 GLLPILV 11
 |||||
 Db 92 GLLPILV 98

RESULT 13
 AC0140
 probable membrane protein YP01140 [imported] - Yersinia pestis (strain CO92)
 C:Species: Yersinia pestis
 C:Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 09-Jul-2004
 C:Accession: AC0140
 R;Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B.; deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.; Il, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrell, Nature 413, 523-527, 2001
 A:Title: Genome sequence of Yersinia pestis, the causative agent of plague.
 A:Reference number: AB0001; MUID:21470413; PMID:11586360
 A:Accession: AC0140
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-272 <KUR>
 A:Cross-references: UNIPROT:Q8ZGY1; GB:AL590842; PIDN:CAC89982.1; PID:g15979204; GSPDB:G
 C:Genetics:
 A:Gene: YP01140

Query Match 5.3%; Score 7; DB 2; Length 272;
 Best Local Similarity 100.0%; Pred. No. 14; Mismatches 0; Gaps 0;
 Matches 7; Conservative 0; Indels 0; Gaps 0;

Qy 10 LVPFILL 16
 |||||
 Db 114 LVPFILL 120

RESULT 14
 I46937
 tissue factor pathway inhibitor - rabbit
 C:Species: Oryctolagus cuniculus (domestic rabbit)
 A:Title: cDNA cloning and expression of rat tissue factor pathway inhibitor (TFPI).

C:Date: 04-Sep-1997 #sequence_revision 04-Sep-1997 #text_change 09-Jul-2004
 C:Accession: I46937
 R;Belaouaj, A.; Kuppusewamy, M.N.; Birktoft, J.J.; Bajaj, S.P.
 Thromb. Res. 69, 547-553, 1993
 A:Title: Revised cDNA sequence of rabbit tissue factor pathway inhibitor.
 A:Reference number: I46937; MUID:93276427; PMID:8503123
 A:Accession: I46937
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-299 <BEL>
 A:Cross-references: UNIPROT:P19761; GB:S61902; NID:g386015; PIDN:AAB26836.1; PID:g386016
 C:Superfamily: tissue factor pathway inhibitor; animal Kunitz-type proteinase inhibitor
 F:45-99/Domain: animal Kunitz-type proteinase inhibitor homology <BP11>
 F:120-170/Domain: animal Kunitz-type proteinase inhibitor homology <BP1>
 F:212-262/Domain: animal Kunitz-type proteinase inhibitor homology <BP12>

Query Match 5.3%; Score 7; DB 2; Length 299;
 Best Local Similarity 100.0%; Pred. No. 15; Mismatches 0; Gaps 0;
 Matches 7; Conservative 0; Indels 0; Gaps 0;

Qy 104 EFIYGGC 110
 |||||
 Db 76 EFIYGGC 82

RESULT 15
 S12143
 lipoprotein-associated coagulation inhibitor precursor - rabbit
 N:Alternate names: endothelial cell coagulation inhibitor; endothelial cell tissue factor
 C:Species: Oryctolagus cuniculus (domestic rabbit)
 C:Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 16-Jul-1999
 C:Accession: S12143; A61373
 R;Wesselschmidt, R.L.; Girard, T.J.; Broze Jr., G.J.
 Nucleic Acids Res. 18, 6440, 1990
 A:Title: cDNA sequence of rabbit lipoprotein-associated coagulation inhibitor.
 A:Reference number: S12143; MUID:91057146; PMID:2136251
 A:Accession: S12143
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-300 <WES>
 A:Cross-references: EMBL:X54708; NID:gl612; PIDN:CAA38515.1; PID:g1613
 R;Colburn, P.; Crabb, J.W.; Buonassisi, V.
 J. Cell. Physiol. 148, 320-326, 1991
 A:Title: Enhanced inhibition of tissue factor by the extended form of an endothelial cell
 A:Reference number: A61373; MUID:91349227; PMID:1880157
 A:Accession: A61373
 A:Molecule type: protein
 A:Residues: 25-33,'X',35-46 <COL>
 C:Superfamily: tissue factor pathway inhibitor; animal Kunitz-type proteinase inhibitor
 C:Keywords: anticoagulant; glycoprotein
 F:50-100/Domain: animal Kunitz-type proteinase inhibitor homology <BP1>
 F:121-171/Domain: animal Kunitz-type proteinase inhibitor homology <BP2>
 F:213-263/Domain: animal Kunitz-type proteinase inhibitor homology <BP3>

Query Match 5.3%; Score 7; DB 2; Length 300;
 Best Local Similarity 100.0%; Pred. No. 15; Mismatches 0; Gaps 0;
 Matches 7; Conservative 0; Indels 0; Gaps 0;

Qy 104 EFIYGGC 110
 |||||
 Db 77 EFIYGGC 83

RESULT 16
 TIRYTK
 tissue factor pathway inhibitor precursor - rat
 N:Alternate names: extrinsic pathway inhibitor; lipoprotein-associated coagulation inhibi
 C:Species: Rattus norvegicus (Norway rat)
 C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 09-Jul-2004
 C:Accession: JX0213
 R;Enjyoji, K.; Emi, M.; Mukai, T.; Kato, H.
 J. Biochem. 111, 681-687, 1992
 A:Title: cDNA cloning and expression of rat tissue factor pathway inhibitor (TFPI).

A;Reference number: JX0213; MUID:92348361; PMID:1639767
A;Accession: JX0213
A;Molecule type: mRNA
A;Residues: 1-302 <ENJ>
A;Cross-references: UNIPROT:Q02445; DDBJ:D10926; NID:G220916; PIDN:BAA01724.1; PID:G2209
A;Experimental source: liver
C;Comment: This serine proteinase inhibitor regulates clotting by factor Xa-dependent in
C;Comment: The first Kunitz-type domain binds the factor VIIa/tissue factor complex; the
C;Superfamily: tissue factor pathway inhibitor; animal Kunitz-type proteinase inhibitor
C;Keywords: anticoagulant; blood coagulation; duplication; glycoprotein; heparin binding
F;1-28/Domain: signal sequence #status predicted <SIG>
F;29-304/Product: tissue factor pathway inhibitor #status predicted <MAT>
F;53-103/Domain: animal Kunitz-type proteinase inhibitor homology <BP1>
F;124-174/Domain: animal Kunitz-type proteinase inhibitor homology <BP2>
F;222-272/Domain: animal Kunitz-type proteinase inhibitor homology <BP3>
F;288-291/Region: heparin binding #status predicted
F;53/Inhibitory site: Lys (coagulation factor VII/tissue factor complex) #status predicted
F;134/Inhibitory site: Arg (coagulation factor XI) #status predicted
F;144,251,261/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;232/Inhibitory site: Lys (unidentified proteinase) #status predicted

Query Match 5.3%; Score 7; DB 1; Length 302;
Best Local Similarity 100.0%; Pred. No. 15;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 104 EPIYGGC 110
|||||
Db 80 EPIYGGC 86

RESULT 17
JC2264
tissue factor pathway inhibitor precursor - rhesus macaque
N;Alternate names: extrinsic pathway inhibitor; lipoprotein-associated coagulation inhib
C;Species: Macaca mulatta (rhesus macaque)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C;Accession: JC2264
R;Kamei, S.; Kamikubo, Y.; Hamuro, T.; Fujimoto, H.; Yonemura, H.; Miyamoto
J. Biochem. 115, 708-714, 1994
A;Title: Amino acid sequence and inhibitory activity of rhesus monkey tissue factor path
A;Reference number: JC2264; MUID:94375417; PMID:8089087
A;Accession: JC2264
A;Molecule type: mRNA
A;Residues: 1-304 <KAM>
A;Cross-references: UNIPROT:Q28864; GB:S73337; NID:G685016; PIDN:AAB31955.1; PID:G685017
A;Experimental source: liver
C;Comment: This protein inhibits the activities of factor Xa and tissue factor-factor VI
C;Superfamily: tissue factor pathway inhibitor; animal Kunitz-type proteinase inhibitor
C;Keywords: anticoagulant; glycoprotein; serine proteinase inhibitor
F;1-28/Domain: signal sequence #status predicted <SIG>
F;29-304/Product: tissue factor pathway inhibitor #status predicted <MAT>
F;54-104/Domain: animal Kunitz-type proteinase inhibitor homology <BP1>
F;125-175/Domain: animal Kunitz-type proteinase inhibitor homology <BP2>
F;217-267/Domain: animal Kunitz-type proteinase inhibitor homology <BP3>
F;54-104, 63-87, 79-100, 125-175, 134-158, 150-171, 217-267, 226-250, 242-263/Diulfide bonds: #
F;54-104, 63-87, 79-100, 125-175, 134-158, 150-171, 217-267, 226-250, 242-263/Diulfide bonds: #
F;64/Inhibitory site: Lys (coagulation factor VII/tissue factor complex) #status predicted
F;135/Inhibitory site: Arg (coagulation factor XI) #status predicted
F;145,195,256/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;227/Inhibitory site: Arg (unidentified proteinase) #status predicted

Query Match 5.3%; Score 7; DB 1; Length 304;
Best Local Similarity 100.0%; Pred. No. 15;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 104 EPIYGGC 110
|||||
Db 81 EPIYGGC 87

RESULT 18
TIHUGK
tissue factor pathway inhibitor precursor [validated] - human

N;Alternate names: extrinsic pathway inhibitor; lipoprotein-associated coagulation inhib
C;Species: Homo sapiens (man)
C;Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 09-Jul-2004
C;Accession: A23712; A39176; A28650; A60433; B60433; S13034; A34315; A38294; S03903
R;Girard, T.J.; Eddy, R.; Wesselschmidt, R.L.; MacPhail, L.A.; Likert, K.M.; Byers, M.G.
J. Biol. Chem. 266, 5036-5041, 1991
A;Title: Structure of the human lipoprotein-associated coagulation inhibitor gene. Intro
A;Reference number: A23712; MUID:91161593; PMID:2002045
A;Accession: A23712
A;Molecule type: DNA
A;Residues: 1-304 <GR>
A;Cross-references: UNIPROT:P10646; GB:M59493; GB:M59499; NID:G187204; PIDN:AAA59526.1;
R;van der Logt, C.P.E.; Reitsma, P.H.; Bertina, R.M.
Biochemistry 30, 1571-1577, 1991
A;Title: Intron-exon organization of the human gene coding for the lipoprotein-associated
A;Reference number: A39176; MUID:91129227; PMID:1993173
A;Accession: A39176
A;Molecule type: DNA
A;Residues: 1-304 <VAN>
A;Cross-references: GB:M58650; GB:J05312; NID:G186827; PIDN:AAA59480.1; PID:G186829
R;Wun, T.C.; Kretzmer, K.K.; Girard, T.J.; Miletich, J.P.; Broze Jr., G.J.
J. Biol. Chem. 263, 6001-6004, 1988
A;Title: Cloning and characterization of a cDNA coding for the lipoprotein-associated co
A;Reference number: A28650; MUID:88198127; PMID:2452157
A;Accession: A28650
A;Molecule type: mRNA
A;Residues: 1-304 <WUN>
A;Cross-references: GB:J03225; NID:G180545; PIDN:AAA52022.1; PID:G180546
A;Note: part of this sequence, including the amino end of the mature protein, was confil
R;Girard, T.J.; Warren, L.A.; Novotny, W.F.; Bejcek, B.E.; Miletich, J.P.; Broze Jr., G.J.
Thromb. Res. 55, 37-50, 1989
A;Title: Identification of the 1.4 KB and 4.0 KB messages for the lipoprotein associated
A;Reference number: A60433; MUID:89388722; PMID:2781520
A;Accession: A60433
A;Status: not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 1-304 <G12>
A;Experimental source: endothelial cells
A;Accession: B60433
A;Molecule type: protein
A;Residues: 'XX', 31-53, 'X', 55-56 <G13>
A;Experimental source: recombinant material from mouse C137 cells
R;Girard, T.J.; McCourt, D.; Novotny, W.F.; MacPhail, L.A.; Likert, K.M.; Broze Jr., G.J.
Biochem. J. 270, 621-625, 1990
A;Title: Endogenous phosphorylation of the lipoprotein-associated coagulation inhibitor
A;Reference number: S13034; MUID:91054349; PMID:2122883
A;Accession: S13034
A;Molecule type: protein
A;Residues: 29-35 <G14>
R;Novotny, W.F.; Girard, T.J.; Miletich, J.P.; Broze Jr., G.J.
J. Biol. Chem. 264, 18832-18837, 1989
A;Title: Purification and characterization of the lipoprotein-associated coagulation inh
A;Reference number: A34315; MUID:90036596; PMID:2553722
A;Accession: A34315
A;Molecule type: protein
A;Residues: 'XX', 31-33, 'L', 35-50 <NOV>
A;Experimental source: plasma
R;Pedersen, A.H.; Nordfang, O.; Norris, F.; Wiberg, F.C.; Christensen, P.M.; Moeller, K.
J. Biol. Chem. 265, 16786-16793, 1990
A;Title: Recombinant human extrinsic pathway inhibitor. Production, isolation, and chara
A;Reference number: A38294; MUID:91009092; PMID:2211593
A;Accession: A38294
A;Molecule type: protein
A;Residues: 29-41 <PED>
R;Girard, T.J.; Warren, L.A.; Novotny, W.F.; Likert, K.M.; Brown, S.G.; Miletich, J.P.;
Nature 338, 518-520, 1989
A;Title: Functional significance of the Kunitz-type inhibitory domains of lipoprotein-as
A;Reference number: S03903; MUID:89181950; PMID:2927510
A;Contents: annotation; site-directed mutagenesis
C;Comment: The first Kunitz-type domain binds the factor VIIa/tissue factor complex; the
C;Genetics:
A;Gene: GDB:TFPI
A;Cross-references: GDB:127364; OMIM:152310

A;Map position: 2q32-2q32
A;Intons: 41/1; 107/1; 120/1; 179/1; 210/1; 270/1
C;Function:
A;Description: regulates clotting by factor Xa-dependent inhibition of the coagulation f
A;Pathway: blood coagulation
C;Superfamily: tissue factor pathway inhibitor; animal Kunitz-type proteinase inhibitor
C;Keywords: anticoagulant; blood coagulation; duplication; glycoprotein; heparin binding
F;1-28/Domain: signal sequence #status predicted <SIG>
F;29-304/Product: tissue factor pathway inhibitor #status experimental <MAT>
F;54-104/Domain: animal Kunitz-type proteinase inhibitor homology <BP1>
F;125-175/Domain: animal Kunitz-type proteinase inhibitor homology <BP2>
F;217-267/Domain: animal Kunitz-type proteinase inhibitor homology <BP2>
F;284-289/Region: heparin binding #status predicted
F;30/Binding site: phosphate (Ser) (covalent) #status experimental
F;54-104,63-87,79-100,125-175,134-158,150-171,217-267,226-250,242-263/Disulfide bonds: #
F;64/Inhibitory site: Lys (coagulation factor VII/tissue factor complex) #status experim
F;135/Inhibitory site: Arg (coagulation factor X) #status experimental
F;145,195,256/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;227/Inhibitory site: Arg (unidentified proteinase) #status predicted

Query Match 5.3%; Score 7; DB 1; Length 304;
Best Local Similarity 100.0%; Pred. No. 15;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 104 EFVYGGC 110
|||||
Db 81 EFVYGGC 87
|||||

RESULT 19
TIQB1
A;Title: 1-microglobulin/inter-alpha-trypsin inhibitor precursor - pig (fragment)
N;Alternate names: bikunin; ITI; PI-14 (inhibitory fragment of ITI)
C;Species: Sus scrofa domestica (domestic pig)
C;Date: 30-Jun-1987 #sequence_revision 04-Feb-2000 #text_change 09-Jul-2004
C;Accession: S11066; S13493; A01208
R;Gebhard, W.; Schreitmüller, T.; Vetr, H.; Wachter, E.; Hochstrasser, K.
FEBS Lett. 269, 32-36, 1990

A;Title: Complementary DNA and deduced amino acid sequences of porcine alpha1-microglobu
A;Reference number: S11066; MUID:90353595; PMID:1696914
A;Accession: S11066
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-337 <GB>
A;Cross-references: UNIPROT:P04366; EMBL:X53685; NID:g1877; PIDN:CAA37725.1; PID:g1878
R;Tavakkol, A.

Biochim. Biophys. Acta 1088, 47-56, 1991

A;Title: Molecular cloning of porcine alpha(1)-microglobulin/HI-30 reveals developmental
A;Reference number: S13493; MUID:91113729; PMID:1703444
A;Accession: S13493
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 'M', 3-48, 'M', 50-337 <TAV>
A;Cross-references: GB:X52087; NID:g1881; PIDN:CAA36306.1; PID:g1882
A;Note: the authors translated the codon GTG for residue 2 as a Met initiation codon
R;Hochtrasser, K.; Wachter, E.; Albrecht, G.J.; Reisinger, P.
Biol. Chem. Hoppe-Seyler 366, 473-478, 1985

A;Title: Kunitz-type proteinase inhibitors derived by limited proteolysis of the inter-a
A;Reference number: A90685; MUID:85225967; PMID:2408637
A;Accession: A01208
A;Molecule type: protein
A;Residues: 212-258, 'Q', 260-269, 'S', 271-277, 'Q', 279-282, 'A', 284, 'IR', 287-292, 'A', 294-310
C;Comment: This inhibitory fragment, released from native ITI after limited proteolysis
First domain interacts weakly with PMN-granulocytic elastase and not at all with pancrea
C;Comment: The amino acid at position P2' (228-Met) appears to determine the specificity
nd elastase; those with leucine interact strongly.

C;Superfamily: alpha1-microglobulin and inter-alpha-trypsin inhibitor light chain precu
C;Keywords: duplication; glycoprotein; plasma; serine proteinase inhibitor
F;20-173/Domain: lipocalin homology <LIP>
F;216-266/Domain: animal Kunitz-type proteinase inhibitor homology <BP1>
F;272-322/Domain: animal Kunitz-type proteinase inhibitor homology <BP2>
F;216-266,225-249,241-262,272-322,281-305,297-318/Disulfide bonds: #status predicted
F;226/Inhibitory site: Leu (chymotrypsin, elastase) #status predicted

F;235/Binding site: carbohydrate (Asn) (covalent) #status experimental
F;282/Inhibitory site: Arg (trypsin) #status predicted

Query Match 5.3%; Score 7; DB 1; Length 337;
Best Local Similarity 100.0%; Pred. No. 16;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 107 YGCGQGN 113
|||||
Db 302 YGCGQGN 308
|||||

RESULT 20

F83839

hypothetical protein BHI518 [imported] - Bacillus halodurans (strain C-125)

C;Species: Bacillus halodurans

C;Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 09-Jul-2004

C;Accession: F83839

R;Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fujii, F.; Hiran

Nucleic Acids Res. 28, 4317-4331, 2000

A;Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and s

A;Reference number: A83650; MUID:20512582; PMID:11058132

A;Accession: F83839

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-337 <STO>

A;Cross-references: UNIPROT:Q9KCQ1; GB:AP001512; GB:BA000004; NID:g10174030; PIDN:BA8052;

A;Experimental source: strain C-125

C;Genetics:

A;Gene: BHI518

Query Match

5.3%; Score 7; DB 2; Length 337;

Best Local Similarity 100.0%; Pred. No. 16;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 11 VPFIILG 17
|||||

Db 56 VPFIILG 62
|||||

RESULT 21

A72042

conserved hypothetical protein CP0006 [imported] - Chlamydophila pneumoniae (strains CWL0

N;Alternate names: ct 368 hypothetical protein

C;Species: Chlamydophila pneumoniae, Chlamydia pneumoniae

C;Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 09-Jul-2004

C;Accession: A72042; B81624

R;Kalmán, S.; Mitchell, W.; Marathe, R.; Lammel, C.; Fan, J.; Olinger, L.; Grimwood, J.;

Nature Genet. 21, 385-389, 1999

A;Title: Comparative genomes of Chlamydia pneumoniae and C. trachomatis.

A;Reference number: A72000; MUID:99206606; PMID:10192388

A;Accession: A72042

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-337 <ARN>

A;Cross-references: UNIPROT:Q9Z7G6; GB:AE001655; GB:AE001363; NID:g4377039; PIDN:AAD18878

A;Experimental source: strain CWL029

R;Read, T.D.; Brunham, R.C.; Shen, C.; Gill, S.R.; Heidelberg, J.F.; White, O.; Hickey, I.;

C.; Dodson, R.; Gwinn, M.; Nelson, W.; DeBoy, R.; Kolonay, J.; McClarty, G.; Salzberg,

Nucleic Acids Res. 28, 1397-1406, 2000

A;Title: Genome sequences of Chlamydia trachomatis MoPn and Chlamydia pneumoniae AR39.

A;Reference number: A81500; MUID:20150255; PMID:10684935

A;Accession: B81624

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-337 <REA>

A;Cross-references: GB:AE002164; GB:AE002161; NID:g7188939; PIDN:AAF37902.1; PID:g718894;

A;Experimental source: strain AR39, HL cells

C;Genetics:

A;Gene: CPN0739; CP0006

Query Match

5.3%; Score 7; DB 2; Length 337;

Best Local Similarity 100.0%; Pred. No. 16;

Matches	7;	Conservative	0;	Mismatches	0;	Indels	0;	Gaps	0;
Qy	96	NKTKIC 102							
Db	7	NKTKIC 13							
RESULT 22									
H86582									
CT 368 hypothetical protein [imported] - Chlamydomophila pneumoniae (strain J138)									
C:Species: Chlamydomophila pneumoniae, Chlamydia pneumoniae									
C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004									
C:Accession: H86582									
R:Shirai, M.; Hirakawa, H.; Kimoto, M.; Tabuchi, M.; Kishi, F.; Ouchi, K.; Shiba, T.; Ise									
Nucleic Acids Res. 28, 2311-2314, 2000									
A:Title: Comparison of whole genome sequences of chlamydia pneumoniae J138.									
A:Reference number: A86491; MUID:20330349; PMID:10871362									
A:Accession: H86582									
A:Status: preliminary									
A:Molecule type: DNA									
A:Residues: 1-337 <STO>									
A:Cross-references: UNIPROT:Q9JSB0; GB:BA000008; NID:G8979111; PIDN:BAA98946.1; GSPDB:GN									
A:Experimental source: strain J138									
C:Genetics:									
A:Gene: CPJ0739									
Query Match 5.3%; Score 7; DB 2; Length 337;									
Best Local Similarity 100.0%; Pred. No. 16;									
Matches	7;	Conservative	0;	Mismatches	0;	Indels	0;	Gaps	0;
Qy	96	NKTKIC 102							
Db	7	NKTKIC 13							
RESULT 23									
T19885									
hypothetical protein C41G6.6 - Caenorhabditis elegans									
C:Species: Caenorhabditis elegans									
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004									
C:Accession: T19885									
R:Cummings, P.									
submitted to the EMBL Data Library, October 1996									
A:Reference number: Z19191									
A:Accession: T19885									
A:Status: preliminary; translated from GB/EMBL/DBJ									
A:Molecule type: DNA									
A:Residues: 1-348 <WIL>									
A:Cross-references: UNIPROT:O17659; EMBL:Z81047; PIDN:CAB02831.1; GSPDB:GN00023; CESP:C4									
A:Experimental source: clone C41G6									
C:Genetics:									
A:Gene: CESP:C41G6.6									
A:Map position: 5									
A:Introns: 131/1; 321/1									
Query Match 5.3%; Score 7; DB 2; Length 348;									
Best Local Similarity 100.0%; Pred. No. 17;									
Matches	7;	Conservative	0;	Mismatches	0;	Indels	0;	Gaps	0;
Qy	113	NNNNFQT 119							
Db	189	NNNNFQT 195							
RESULT 24									
HCHU									
alpha-1-microglobulin/inter-alpha-trypsin inhibitor precursor [validated] - human									
N:Alternate names: bikunin; complex-forming glycoprotein heterogeneous in charge (HC) pr									
rich protein									
N:Contains: alpha-1-microglobulin (protein HC); inter-alpha-trypsin inhibitor									
C:Species: Homo sapiens (man)									
C:Date: 15-Oct-1982 #sequence_revision 30-Jun-1987 #text change 09-Jul-2004									
C:Accession: S13433; S10778; A93642; A90074; A90225; A90686; PNO450; B39079; A61580; B25									

3217
R:Vetr, H.; Gebhard, W.
Biol. Chem. Hoppe-Seyler 371, 1185-1196, 1990
A:Title: Structure of the human alpha(1)-microglobulin-bikunin gene.
A:Reference number: S13433; MUID:91214554; PMID:1708673
A:Accession: S13433
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-352 <VET1>
A:Cross-references: UNIPROT:P02760; EMBL:X54816; NID:G24475; PIDN:CAA38585.1; PID:982561
R:Diarra-Mahropour, M.; Bourquignon, J.; Seabouee, R.; Salier, J.P.; Leveillard, T.; Mart
Eur. J. Biochem. 191, 131-139, 1990
A:Title: Structural analysis of the human inter-alpha-trypsin inhibitor light-chain gene
A:Reference number: S10778; MUID:90336621; PMID:1696200
A:Accession: S10778
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-202 <DIA>
R:Kaumeyer, J.F.; Polazzi, J.O.; Kotick, M.P.
Nucleic Acids Res. 14, 7839-7850, 1986
A:Title: The mRNA for a proteinase inhibitor related to the HI-30 domain of inter-alpha-
A:Reference number: A93642; MUID:87040757; PMID:2430261
A:Accession: A93642
A:Molecule type: mRNA
A:Residues: 1-352 <KAU>
A:Cross-references: GB:X0494; NID:G24478; PIDN:CAA28182.1; PID:924479
R:Lopez Otin, C.; Grubb, A.O.; Mendez, E.
Arch. Biochem. Biophys. 228, 544-554, 1984
A:Title: The complete amino acid sequence of human complex-forming glycoprotein heteroge
A:Reference number: A90074; MUID:84126849; PMID:6198962
A:Accession: A90074
A:Molecule type: protein
A:Residues: 20-56.58-202 <LOP>
A:Experimental source: individual with tubular proteinuria
A:Note: no evidence of sequence heterogeneity could be found, in spite of persistent het
R:Takagi, T.; Takagi, K.; Kawai, T.
Biochem. Biophys. Res. Commun. 98, 997-1001, 1981
A:Title: Complete amino acid sequence of human alpha-1-microglobulin.
A:Reference number: A90225; MUID:81184038; PMID:6164372
A:Accession: A90225
A:Molecule type: protein
A:Residues: 20-47.58-136.138-141.'T'.143-144.146-198 <TAK>
A:Experimental source: pooled urine of patients with tubular proteinuria
R:Reisinger, P.; Hochstrasser, K.; Albrecht, G.J.; Lempert, K.; Salier, J.P.
Biol. Chem. Hoppe-Seyler 366, 479-483, 1985
A:Title: Human inter-alpha-trypsin inhibitor: localization of the kunitz-type domains in
A:Reference number: A90686; MUID:85225968; PMID:2408638
A:Accession: A90686
A:Molecule type: protein
A:Residues: 206-290.'VI'.293-342.'E'.344-350 <REI>
R:Atmani, F.; Lacour, B.; Strecker, G.; Parvy, P.; Drueeke, T.; Daudon, M.
Biochem. Biophys. Res. Commun. 191, 1158-1165, 1993
A:Title: Molecular characteristics of uronic-acid-rich protein, a strong inhibitor of cr
A:Reference number: PNO450; MUID:93221481; PMID:8466493
A:Accession: PNO450
A:Molecule type: protein
A:Residues: 206-214.'X'. <ATM1>
R:Engchild, J.J.; Salvesen, G.; Hefta, S.A.; Thogersen, I.B.; Rutherford, S.; Pizzo, S.V
J. Biol. Chem. 266, 747-751, 1991
A:Title: Chondroitin 4-sulfate covalently cross-links the chains of the human blood prot
A:Reference number: A39079; MUID:91093267; PMID:1898736
A:Accession: B39079
A:Molecule type: protein
A:Residues: 206-225 <ENGI>
R:Chirat, F.; Balduyck, M.; Mizon, C.; Laroui, S.; Sautiere, P.; Mizon, J.
Int. J. Biochem. 23, 1201-1203, 1991
A:Title: A chondroitin-sulfate chain is located on serine-10 of the urinary trypsin inh
A:Reference number: A61580; MUID:92175157; PMID:1794445
A:Accession: A61580
A:Molecule type: protein
A:Residues: 214.'X'.216-222.'X'. <CHI>
R:McKeehan, W.L.; Sakagami, Y.; Hoshi, H.; McKeehan, K.A.
J. Biol. Chem. 261, 5378-5383, 1986

A;Title: Two apparent human endothelial cell growth factors from human hepatoma cells and
A;Reference number: A92583; MUID:86168278; PMID:3007499
A;Accession: B25604
A;Molecule type: protein
A;Residues: 206-214, 'X', 216-230, 'X', 232-239, 'X', 241-248, 'XX', 251-252, 'X', 254 <MCK>
R;Engchild, J.J.; Thogersten, I.B.; Pizzo, S.V.; Salvesen, G.
J. Biol. Chem. 264, 15975-15981, 1989
A;Title: Analysis of inter-alpha-trypsin inhibitor and a novel trypsin inhibitor, pre-al
A;Reference number: A92736; MUID:89380192; PMID:2476436
A;Accession: C34245
A;Molecule type: protein
A;Residues: 206-225 <ENG2>
R;Traboni, C.; Cortese, R.
Nucleic Acids Res. 14, 6340, 1986
A;Title: Sequence of a full length cDNA coding for human protein HC (alpha-1-microglobul
A;Reference number: A25303; MUID:86312901; PMID:2428011
A;Accession: A25303
A;Molecule type: mRNA
A;Residues: 1-218, 'HW' <TRA>
A;Note: this mRNA sequence appears to contain errors after residue 218
R;Calero, M.; Escibano, J.; Grubb, A.; Mendez, E.
J. Biol. Chem. 269, 384-389, 1994
A;Title: Location of a novel type of interpolypeptide chain linkage in the human protein
A;Reference number: A53110; MUID:94103241; PMID:7506257
A;Accession: A53110
A;Molecule type: protein
A;Residues: 45-57 <CAL1>
R;Vetr, H.; Koegler, M.; Gebhard, W.
FEBS Lett. 245, 137-140, 1989
A;Title: The domain structure of the inhibitor subunit of human inter-alpha-trypsin inh
A;Reference number: S03552; MUID:89171290; PMID:2466696
A;Accession: S03552
A;Status: nucleic acid sequence not shown
A;Molecule type: DNA
A;Residues: 206-352 <VET2>
R;Malki, N.; Balduyck, M.; Maes, P.; Capon, C.; Mizon, C.; Han, K.K.; Tartar, A.; Fourn
Biol. Chem. Hoppe-Seyler 373, 1009-1018, 1992
A;Title: The heavy chains of human plasma inter-alpha-trypsin inhibitor: their isolation
A;Reference number: S28928; MUID:93033735; PMID:1384548
A;Accession: S28930
A;Status: preliminary
A;Molecule type: protein
A;Residues: 206-215 <MAL>
R;Morelle, W.; Capon, C.; Balduyck, M.; Sautiere, P.; Kouach, M.; Michalski, C.; Fourn
Eur. J. Biochem. 221, 861-888, 1994
A;Title: Chondroitin sulphate covalently cross-links the three polypeptide chains of int
A;Reference number: S43466; MUID:942229087; PMID:7513643
A;Accession: S43466
A;Status: preliminary
A;Molecule type: protein
A;Residues: 206-221 <MOR>
R;Wisniewski, H.G.; Burgess, W.H.; Oppenheim, J.D.; Vilcek, J.
Biochemistry 33, 7423-7429, 1994
A;Title: TSG-6, an arthritis-associated hyaluronan binding protein, forms a stable comp
A;Reference number: A53642; MUID:94271799; PMID:7516184
A;Accession: A53642
A;Status: preliminary
A;Molecule type: protein
A;Residues: 206-217 <WIS>
R;Calero, M.; Mendez, E.; Garcia, E.
Biochim. Biophys. Acta 1249, 91-99, 1995
A;Title: Expression of the human complex-forming glycoprotein HC (alpha-1-microglobulin)
A;Reference number: S55688; MUID:95284116; PMID:7539295
A;Accession: S55688
A;Molecule type: protein
A;Residues: 20-24 <CAL2>
R;Bourguignon, J.; Diarra-Mehrpor, M.; Sesboue, R.; Frain, M.; Sala-Trepas, J.M.; Marti
Biochem. Biophys. Res. Commun. 131, 1146-1153, 1985
A;Title: Human inter-alpha-trypsin-inhibitor: characterization and partial nucleotide se
A;Reference number: 152208; MUID:86025577; PMID:2413856
A;Accession: 152208
A;Status: translated from GB/EMBL/DBJ
A;Molecule type: mRNA

A;Residues: 302-352 <BOU>
A;Cross-references: GB:M11562; NID:g186587; PIDN:AAAS9194.1; PID:g307077
R;Wojcik, E.G.C.; van den Berg, M.; van der Linden, I.K.; Poort, S.R.; Cupers, R.; Bertin
Biochem. J. 311, 753-759, 1995
A;Title: Factor IX Zuthphen: a Cys(18) -> Arg mutation results in formation of a heterodit
A;Reference number: S59509; MUID:96067589; PMID:7487929
A;Accession: S59509
A;Molecule type: protein
A;Residues: 27-35, 'Y', 37 <WOJ>
R;Atmani, F.; Mizon, J.; Khan, S.R.
Eur. J. Biochem. 236, 984-990, 1996
A;Title: Identification of uronic-acid-rich protein as urinary bikunin, the light chain (c
A;Reference number: S66434; MUID:96270753; PMID:8665922
A;Accession: S66434
A;Molecule type: protein
A;Residues: 206-214, 'X', 216-230 <ATM2>
R;Akerstroem, B.; Bratt, T.; Engchild, J.J.
FEBS Lett. 362, 50-54, 1995
A;Title: Formation of the alpha(1)-microglobulin chromophore in mammalian and insect cel
A;Reference number: S68728; MUID:95212582; PMID:7535251
A;Accession: S68728
A;Molecule type: protein
A;Residues: 89-100 <AKE>
R;Jessen, T.E.; Faarvang, K.L.; Ploug, M.
FEBS Lett. 230, 195-200, 1988
A;Title: Carbohydrate as covalent crosslink in human inter-alpha-trypsin inhibitor: a nov
A;Reference number: S02431; MUID:88167187; PMID:2450785
A;Accession: S02431
A;Molecule type: protein
A;Residues: 206-214, 'X', 216-217 <JES>
R;Lopez, C.; Grubb, A.; Mendez, E.
FEBS Lett. 144, 349-353, 1982
A;Title: Human protein HC displays variability in its carboxyl-terminal amino acid sequen
A;Reference number: A91304
A;Contents: annotation; variant of alpha-1-microglobulin
A;Note: pooled urine samples contained two forms of this protein, both lacking 57-Lys and
R;Hochtraeger, K.; Schonberger, O.L.; Rossmannith, I.; Wachter, E.
Hoppe-Seyler's Z. Physiol. Chem. 362, 1357-1362, 1981
A;Title: Kunitz-type proteinase inhibitors derived by limited proteolysis of the inter-a-
by affinity chromatography.
A;Reference number: A91698; MUID:82074265; PMID:6171497
A;Contents: annotation; carbohydrate binding sites
R;Morii, M.; Travis, J.
Biol. Chem. Hoppe-Seyler 366, 19-21, 1985
A;Title: The reactive site of human inter-alpha-trypsin inhibitor is in the amino-termi
A;Reference number: A90682; MUID:85225940; PMID:3690890
A;Contents: annotation; inhibitory site
A;Note: in vitro, the first twelve residues of the amino end of the inhibitor appear to l
wn
C;Comment: Alpha-1-microglobulin and inter-alpha-trypsin inhibitor are proteolytically p
C;Comment: Alpha-1-microglobulin occurs in many physiological fluids including plasma, u
. It contains at least one brown-yellow chromophore.
Query Match 5.3%; Score 7; DB 1; Length 352;
Best Local Similarity 100.0%; Pred. No. 17;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 107 YGGCQGN 113
| | | | |
Db 317 YGGCQGN 323
RESULT 25
T05891
myb-related protein homolog FH11.100 - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 16-Aug-2004
C;Accession: T05891
R;Bavan, M.; Brandt, P.; Dose, S.; Jarke, D.; Scharfe, M.; Schon, O.; Bancroft, I.; Mew
submitted to the Protein Sequence Database, April 1998
A;Reference number: Z15456
A;Accession: T05891
A;Molecule type: DNA

A;Residues: 1-374 <BEV>
A;Cross-references: UNIPROT:O49538; EMBL:AL021684; GSPDB:GN00063; ATSP:F6H11.100
A;Experimental source: cultivar Columbia; BAC clone F6H11
C;Genetics:
A;Gene: ATSP:F6H11.100
A;Map position: 5
A;Intons: 46/1; 89/2
C;Superfamily: myb DNA-binding repeat homology
F;9-62/Domain: myb DNA-binding repeat homology <MYB>

Query Match 5.3%; Score 7; DB 2; Length 374;
Best Local Similarity 100.0%; Pred. No. 18;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 116 NFQTEAI 122
|||
Db 294 NFQTEAI 300

RESULT 26
T51673
myb-related transcription factor MYB68 [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 18-Aug-2000 #sequence_revision 18-Aug-2000 #text_change 09-Jul-2004
C;Accession: T51673
R;Kranz, H.D.; Denekamp, M.; Greco, R.; Jin, H.; Kranz, H.D.; Denekamp, M.; Greco, R.; J.
; Paz-Ares, J.; Weisshaar, B.
Plant J. 16, 263-276, 1998
A;Title: Towards functional characterisation of the members of the R2R3-MYB gene from A.
A;Reference number: Z14349; MUID:9839469; PMID:9839469
A;Accession: T51673
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-376 <KRA>
A;Cross-references: UNIPROT:Q9SBF7; EMBL:AF062901; PIDN:AAC83623.1
A;Experimental source: cultivar Columbia
C;Genetics:
A;Map position: V
A;Gene: MYB68
C;Superfamily: Arabidopsis myb-related protein M4; myb DNA-binding repeat homology
C;Keywords: transcription factor

Query Match 5.3%; Score 7; DB 2; Length 376;
Best Local Similarity 100.0%; Pred. No. 18;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 116 NFQTEAI 122
|||
Db 294 NFQTEAI 300

RESULT 27
S53325
tissue factor pathway inhibitor - rabbit
C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Date: 01-Aug-1995 #sequence_revision 01-Sep-1995 #text_change 17-Mar-2003
C;Accession: S53325
R;Girard, T.J.; Gallani, D.; Broze Jr., G.J.
Biochem. J. 303, 923-928, 1994
A;Title: Complementary DNA sequencing of canine tissue factor pathway inhibitor reveals
A;Reference number: S53325; MUID:95071310; PMID:7980463
A;Accession: S53325
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-396 <GIR>
C;Superfamily: tissue factor pathway inhibitor; animal Kunitz-type proteinase inhibitor
C;Keywords: serine proteinase inhibitor
F;53-103/Domain: animal Kunitz-type proteinase inhibitor homology <BPI>
F;125-175/Domain: animal Kunitz-type proteinase inhibitor homology <BP2>
F;309-359/Domain: animal Kunitz-type proteinase inhibitor homology <BP3>

Query Match 5.3%; Score 7; DB 2; Length 396;
Best Local Similarity 100.0%; Pred. No. 18;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 104 EFYGGC 110
|||
Db 80 EFYGGC 86

RESULT 28
F83634
hypothetical protein PA0081 [imported] - Pseudomonas aeruginosa (strain PA01)
C;Species: Pseudomonas aeruginosa
C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 09-Jul-2004
C;Accession: F83634
R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warren, P.; Hickey, M.J.; Br.
adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim,
.; Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A;Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic patho
A;Reference number: A82950; MUID:20437337; PMID:10984043
A;Accession: F83634
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-497 <STO>
A;Cross-references: UNIPROT:Q9I751; GB:AE004447; GB:AE004091; NID:g9945902; PIDN:AAG0347
A;Experimental source: strain PA01
C;Genetics:
A;Gene: PA0081

Query Match 5.3%; Score 7; DB 2; Length 497;
Best Local Similarity 100.0%; Pred. No. 22;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 GLSGLLP 8
|||
Db 443 GLSGLLP 449

RESULT 29
F72268
ABC transporter, ATP-binding protein - Thermotoga maritima (strain MSB8)
C;Species: Thermotoga maritima
C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 16-Aug-2004
C;Accession: F72268
R;Nelson, K.E.; Clayton, R.A.; Gill, S.R.; Gwinn, M.L.; Dodson, R.J.; Haft, D.H.; Hickey
Garrett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson, D.;
C.M.

Nature 399, 323-329, 1999
A;Title: Evidence for lateral gene transfer between Archaea and Bacteria from genome seq
A;Reference number: A72200; MUID:99287316; PMID:10360571
A;Accession: F72268
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-564 <ARN>
A;Cross-references: UNIPROT:Q9X144; GB:AE001786; GB:AE000512; NID:g4981873; PIDN:AAD3639
A;Experimental source: strain MSB8
C;Genetics:
A;Gene: TM1319
C;Superfamily: ATP-binding cassette homology

Query Match 5.3%; Score 7; DB 2; Length 564;
Best Local Similarity 100.0%; Pred. No. 24;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 GLLPILV 11
|||
Db 250 GLLPILV 256

RESULT 30
D90557
hypothetical protein MYPV_3640 [imported] - Mycoplasma pulmonis (strain UAB CTTP)
C;Species: Mycoplasma pulmonis
C;Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 09-Jul-2004

C;Accession: D90557
R;Chambaud, I.; Heilig, R.; Ferris, S.; Barbe, V.; Samson, D.; Galisson, F.; Moszer, I.;
Nucleic Acids Res 29, 2145-2153, 2001
A;Title: The complete genome sequence of the murine respiratory pathogen Mycoplasma pulmonis
A;Reference number: A99512; MUID:21267165; PMID:11353084
A;Accession: D90557
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-602 <KUR>
A;Cross-references: UNIPROT:Q90J7; GB:AL445566; PID:g14089778; PIDN:CAC13537.1; GSPDB:G14089778
A;Experimental source: strain UAB CTIP
C;Genetics:
A;Gene: MYPU 3640
A;Genetic code: SGC3

Query Match 5.3%; Score 7; DB 2; Length 602;
Best Local Similarity 100.0%; Pred. No. 26;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 LVPFILL 16
|||||
Db 184 LVPFILL 190

RESULT 31
S74277
Probable membrane protein YCL073c - yeast (Saccharomyces cerevisiae)
A;Alternate names: hypothetical protein YCL070c; hypothetical protein YCL071c
C;Species: Saccharomyces cerevisiae
C;Date: 19-Mar-1997 #sequence revision 25-Apr-1997 #text_change 09-Jul-2004
C;Accession: S74277; S6990; S19402; S19403; S19405
R;Voet, M.; Volckaert, G.
submitted to the Protein Sequence Database, September 1996
A;Reference number: S74277
A;Accession: S74277
A;Molecule type: DNA
A;Residues: 1-615 <VOB>
A;Cross-references: UNIPROT:P25596; EMBL:X59720; NID:G1907116; PIDN:CAA42397.1; PID:g1907116
A;Note: this is a revision to the sequence from reference S19400
R;Gromadka, R.; Gora, M.; Zielenkiewicz, U.; Slonimski, P.P.; Rycka, J.
Yeast 12, 583-591, 1996
A;Title: Subtelomeric duplications in Saccharomyces cerevisiae chromosomes III and XI: b
A;Reference number: S6990; MUID:96367599; PMID:8771713
A;Accession: S6990
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-465, 'I', 467-526, 'N', 528-533, 'S', 535-615 <GRO>
A;Cross-references: EMBL:X59720
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, January 1996
R;van der Aart, Q.J.M.; Steensma, H.Y.
submitted to the Protein Sequence Database, March 1992
A;Reference number: S19400
A;Accession: S19402
A;Molecule type: DNA
A;Residues: 1-214, 'G', 216-270, 'L', 272-326, 'PNLPNLLF', 335-349, 'VLL', 353, 'SI', 354, 'SP', 357-400
A;Cross-references: EMBL:X59720
A;Note: this was assumed to be protein YCL070c
A;Accession: S19403
A;Note: this sequence has been revised in reference S74277
A;Molecule type: DNA
A;Residues: 374-484, 'ALLSVPPFLVPYGYKPKLTNSTRTLETIH', 497, 'QK' <AAW>
A;Cross-references: EMBL:X59720
A;Note: this was assumed to be protein YCL071c
A;Accession: S19405
A;Note: this sequence has been revised in reference S74277
A;Molecule type: DNA
A;Residues: 501-586, 'VG', 589-590, 'T', 592-604, 'R', 606-609, 'N', 611, 'KL', 614-615 <AAF>
A;Cross-references: EMBL:X59720; MIPS:YCL073c
A;Note: this sequence has been revised in reference S74277
A;Note: this was assumed to be the complete sequence of protein YCL073c
C;Genetics:
A;Cross-references: SGD:S0000575
A;Map position: 3L

A;Note: YCL073c
C;Superfamily: conserved probable membrane protein YCL073c
C;Keywords: transmembrane protein
F;60-76/Domain: transmembrane #status predicted <TM1>
F;125-144/Domain: transmembrane #status predicted <TM2>
F;220-236/Domain: transmembrane #status predicted <TM3>
F;276-292/Domain: transmembrane #status predicted <TM4>
F;308-324/Domain: transmembrane #status predicted <TM5>
F;356-372/Domain: transmembrane #status predicted <TM6>
F;411-427/Domain: transmembrane #status predicted <TM7>
F;445-461/Domain: transmembrane #status predicted <TM8>
F;549-565/Domain: transmembrane #status predicted <TM9>

Query Match 5.3%; Score 7; DB 2; Length 615;
Best Local Similarity 100.0%; Pred. No. 26;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MGLSGLL 7
|||||
Db 447 MGLSGLL 453

RESULT 32
S40624
Probable membrane protein YCL073c homolog YKR106w - yeast (Saccharomyces cerevisiae)
C;Species: Saccharomyces cerevisiae
C;Date: 03-May-1994 #sequence revision 03-May-1994 #text_change 09-Jul-2004
C;Accession: S40624
R;Gallion, L.; Dujon, B.
submitted to the Protein Sequence Database, March 1994
A;Reference number: S38175
A;Accession: S40624
A;Molecule type: DNA
A;Residues: 1-615 <GAI>
A;Cross-references: UNIPROT:P36173; EMBL:Z28202; NID:g486616; PIDN:CAA82047.1; PID:g486616
A;Experimental source: strain S288C
C;Genetics:
A;Gene: MIPS:YKR106w
A;Cross-references: SGD:S0001814
A;Map position: 1L
C;Superfamily: conserved probable membrane protein YCL073c
C;Keywords: transmembrane protein

Query Match 5.3%; Score 7; DB 2; Length 615;
Best Local Similarity 100.0%; Pred. No. 26;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MGLSGLL 7
|||||
Db 447 MGLSGLL 453

RESULT 33
E96621
Hypothetical protein F23H11.8 [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence revision 02-Mar-2001 #text_change 09-Jul-2004
C;Accession: E96621
R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, C.; Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.; C.; Li, J.H.; Li, Y.; Lin, X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziani, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, I.; ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A;Reference number: A86141; MUID:21016719; PMID:11130712
A;Accession: E96621
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-988 <STO>

A;Cross-references: UNIPROT:Q9XIF2; GB:AB005173; NID:G5080810; PIDN:AAD39319.1; GSPDB:GN
C;Genetics:
A;Gene: F23H11.8
A;Map position: 1
C;Superfamily: yeast probable SKI2 protein YJL050w

Query Match 5.3%; Score 7; DB 2; Length 988;
Best Local Similarity 100.0%; Pred. No. 38;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 SGLLPIL 10
|||||
391 SGLLPIL 397

Db 391 SGLLPIL 397

RESULT 34
T37868
probable helicase - fission yeast (Schizosaccharomyces pombe)
C;Species: Schizosaccharomyces pombe
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C;Accession: T37868
R;Skellton, J.; Churcher, C.M.; Barrell, B.G.; Rajandream, M.A.; Wood, V.
submitted to the EMBL Data Library, August 1997
A;Reference number: Z21751
A;Accession: T37868
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-1030 <SKE>
A;Cross-references: UNIPROT:O13799; EMBL:Z98597; PIDN:CAB11211.1; GSPDB:GN000066; SPDB:SF
A;Experimental source: strain 972h-; cosmid c17H9
C;Genetics:
A;Gene: SPDB:SPAC17H9.02
A;Map position: 1
C;Superfamily: yeast probable SKI2 protein YJL050w

Query Match 5.3%; Score 7; DB 2; Length 1030;
Best Local Similarity 100.0%; Pred. No. 39;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 SGLLPIL 10
|||||
441 SGLLPIL 447

Db 441 SGLLPIL 447

RESULT 35
S56822
SKI2 protein homolog YJL050w - yeast (Saccharomyces cerevisiae)
N;Alternate names: protein Jil58
C;Species: Saccharomyces cerevisiae
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C;Accession: S56822
R;Pohl, T.M.; Aljinovic, G.
submitted to the Protein Sequence Database, September 1995
A;Reference number: S56793
A;Accession: S56822
A;Molecule type: DNA
A;Residues: 1-1073 <TOV>
A;Cross-references: UNIPROT:P47047; EMBL:Z49325; NID:G1008184; PIDN:CAA89341.1; PID:G100
C;Genetics:
A;Gene: SGD:MTR4; MIPS:YJL050w
A;Cross-references: SGD:S0003586; MIPS:YJL050w
A;Map position: 10L
C;Superfamily: yeast probable SKI2 protein YJL050w
C;Keywords: ATP; nucleotide binding; P-loop
F;171-178/Region: nucleotide-binding motif A (P-loop)
F;258-263/Region: nucleotide-binding motif B
F;262-265/Region: DEXH motif

Query Match 5.3%; Score 7; DB 1; Length 1073;
Best Local Similarity 100.0%; Pred. No. 40;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 SGLLPIL 10

Db 477 SGLLPIL 483
|||||

RESULT 36
T11667
probable RNA helicase - fission yeast (Schizosaccharomyces pombe)
C;Species: Schizosaccharomyces pombe
C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 09-Jul-2004
C;Accession: T11667
R;Barrell, B.G.; Rajandream, M.A.; Wood, V.
submitted to the EMBL Data Library, August 1997
A;Reference number: Z17305
A;Accession: T11667
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-1117 <BAR>
A;Cross-references: UNIPROT:O14232; EMBL:Z98533
C;Genetics:
A;Map position: 1L
A;Note: SPAC6F12.16c
C;Superfamily: yeast probable SKI2 protein YJL050w

Query Match 5.3%; Score 7; DB 2; Length 1117;
Best Local Similarity 100.0%; Pred. No. 42;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 SGLLPIL 10
|||||
525 SGLLPIL 531

Db 525 SGLLPIL 531

RESULT 37
C47447
calcium channel protein alpha-1 chain type 2 - electric ray (Discoptye ommata) (fragment
C;Species: Discoptye ommata
C;Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 11-Jan-2000
C;Accession: C47447
R;Horne, W.A.; Ellinor, P.T.; Inman, I.; Zhou, M.; Tsien, R.W.; Schwarz, T.L.
Proc. Natl. Acad. Sci. U.S.A. 90, 3787-3791, 1993
A;Title: Molecular diversity of Ca(2+) channel alpha 1 subunits from the marine ray Disc
A;Reference number: A47447; MUID:93248175; PMID:7683405
A;Accession: C47447
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 1-43 <HOR>
C;Superfamily: voltage-dependent calcium channel protein alpha-1 chain

Query Match 4.6%; Score 6; DB 2; Length 43;
Best Local Similarity 100.0%; Pred. No. 39;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 114 NNNFOT 119
|||||
20 NNNFOT 25

Db 20 NNNFOT 25

RESULT 38
C90850
fimbrial minor pilin protein precursor [imported] - Escherichia coli (strain O157:H7, an
C;Species: Escherichia coli
C;Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 09-Jul-2004
C;Accession: C90850
R;Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.
gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shingawa, H.
DNA Res. 8, 11-22, 2001
A;Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and gene
A;Reference number: A99629; MUID:21156231; PMID:11258796
A;Accession: C90850
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-53 <HAY>
A;Cross-references: UNIPROT:Q8X2U5; GB:BA000007; PIDN:BA035194.1; PID:G13361236; GSPDB:G

A:Experimental source: strain O157:H7, substrain RIMD 0509952
 C:Genetics:
 A:Gene: ECs1771

Query Match 4.6%; Score 6; DB 2; Length 53;
 Best Local Similarity 100.0%; Pred. No. 46;
 Matches 6; Conservative 0; Mismatches 0; Gaps 0;

Qy 23 GHAEI 28
 Db 20 GHAEI 25

RESULT 39

S30332
 proteinase inhibitor (Kunitz-type) - sea anemone (Stichodactyla helianthus)
 C:Species: Stichodactyla helianthus, Stichodactyla helianthus (Caribbean sea anemone)
 C>Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 09-Jul-2004
 C:Accession: S30332
 R:Antuch, W.; Berndt, K.D.; Chavez, M.A.; Delfin, J.; Wuethrich, K.
 Eur. J. Biochem. 212, 675-684, 1993
 A:Title: The NMR solution structure of a Kunitz-type proteinase inhibitor from the sea anemone Stichodactyla helianthus
 A:Reference number: S30332; MUID:93215644; PMID:8462542
 A:Accession: S30332
 A:Status: preliminary
 A:Molecule type: protein
 A:Residues: 1-55 <ANT>
 A:Cross-references: UNIPROT:P31713
 C:Superfamily: basic proteinase inhibitor; animal Kunitz-type proteinase inhibitor homol
 F:3-53/Domain: animal Kunitz-type proteinase inhibitor homology <BPI>

Query Match 4.6%; Score 6; DB 2; Length 55;
 Best Local Similarity 100.0%; Pred. No. 47;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 105 FIYGGC 110
 Db 31 FIYGGC 36

RESULT 40

JN0380
 trypsin inhibitor IV - sea anemone (Radianthus macrodactylus)
 C:Species: Radianthus macrodactylus
 C>Date: 15-Jan-1993 #sequence_revision 15-Jan-1993 #text_change 09-Jul-2004
 C:Accession: JN0380
 R:Zykova, T.A.; Vinokurov, L.M.; Markova, L.F.; Kozlovskaya, E.P.; Elyakov, G.B.
 Bioorg. Khim. 11, 293-301, 1985
 A:Title: Amino-acid sequence of trypsin inhibitor IV from Radiantis macrodactylus.
 A:Reference number: JN0380
 A:Accession: JN0380
 A:Molecule type: protein
 A:Residues: 1-56 <ZYK>
 A:Cross-references: UNIPROT:P16344
 C:Superfamily: basic proteinase inhibitor; animal Kunitz-type proteinase inhibitor homol
 F:4-54/Domain: animal Kunitz-type proteinase inhibitor homology <BPI>
 F:4-54,13-37,29-50/Disulfide bonds: #status predicted

Query Match 4.6%; Score 6; DB 2; Length 56;
 Best Local Similarity 100.0%; Pred. No. 48;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 105 FIYGGC 110
 Db 32 FIYGGC 37

RESULT 41

TIHABK
 venom basic proteinase inhibitor II - ringhals
 C:Species: Hemachatus haemachatus, Sepedon haemachatus (ringhals)
 C>Date: 30-Nov-1980 #sequence_revision 30-Nov-1980 #text_change 09-Jul-2004

C:Accession: A01216
 R:Hokama, Y.; Iwanaga, S.; Tateuki, T.; Suzuki, T.
 J. Biochem. 79, 559-578, 1976
 A:Title: Snake venom proteinase inhibitors. III. Isolation of five polypeptide inhibitors o acid sequences of two of them.
 A:Reference number: A91942; MUID:76237547; PMID:950337
 A:Accession: A01216
 A:Molecule type: protein
 A:Residues: 1-57 <HOK>
 A:Cross-references: UNIPROT:P00985
 C:Comment: The activity of this inhibitor is similar to that of bovine basic protease inf
 C:Superfamily: basic proteinase inhibitor; animal Kunitz-type proteinase inhibitor homol
 C:Keywords: serine proteinase inhibitor; venom
 F:5-55/Domain: animal Kunitz-type proteinase inhibitor homology <BPI>
 F:5-55,14-38,30-51/Disulfide bonds: #status predicted

Query Match 4.6%; Score 6; DB 1; Length 57;
 Best Local Similarity 100.0%; Pred. No. 49;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 105 FIYGGC 110
 Db 33 FIYGGC 38

RESULT 42

S13846
 venom animal Kunitz-type trypsin inhibitor - Indian cobra
 C:Species: Naja naja naja (Indian cobra)
 C>Date: 18-Feb-1994 #sequence_revision 03-Nov-1995 #text_change 09-Jul-2004
 C:Accession: S13846
 R:Shafqat, J.; Beg, O.U.; Yin, S.J.; Zaidi, Z.H.; Joernvall, H.
 Eur. J. Biochem. 194, 337-341, 1990
 A:Title: Primary structure and functional properties of cobra (Naja naja naja) venom Kunitz-type proteinase inhibitor
 A:Reference number: S13846; MUID:91099304; PMID:1702708
 A:Accession: S13846
 A:Status: preliminary
 A:Molecule type: protein
 A:Residues: 1-57 <SHA>
 A:Cross-references: UNIPROT:P20229
 C:Superfamily: basic proteinase inhibitor; animal Kunitz-type proteinase inhibitor homol
 C:Keywords: serine proteinase inhibitor; venom
 F:5-55/Domain: animal Kunitz-type proteinase inhibitor homology <BPI>

Query Match 4.6%; Score 6; DB 2; Length 57;
 Best Local Similarity 100.0%; Pred. No. 49;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 105 FIYGGC 110
 Db 33 FIYGGC 38

RESULT 43

TIHABK
 isoinhibitor K (BPI type) - Roman snail
 C:Species: Helix pomatia (Roman snail)
 C>Date: 23-Oct-1981 #sequence_revision 23-Oct-1981 #text_change 09-Jul-2004
 C:Accession: A91232; A01225
 R:Tschesche, H.; Dietl, T.
 Eur. J. Biochem. 58, 439-451, 1975
 A:Title: The amino-acid sequence of isoinhibitor K from snails (Helix pomatia). A sequen
 A:Reference number: A91232; MUID:76043680; PMID:1183446
 A:Accession: A91232
 A:Molecule type: protein
 A:Residues: 1-58 <TSC>
 A:Cross-references: UNIPROT:P00994
 R:Dietl, T.; Tschesche, H.
 Hoppe-Seyler's Z. Physiol. Chem. 357, 139-145, 1976
 A:Title: Die Disulfidbruecken des Trypsin-Kallikrein-Inhibitors K aus Weinbergsschnecken
 A:Reference number: A91666; MUID:76141310; PMID:3462
 A:Contents: annotation; disulfide bonds
 C:Comment: This is one of several isoinhibitors of broad specificity that are secreted in

C;Superfamily: basic proteinase inhibitor; animal Kunitz-type proteinase inhibitor homol
C;Keywords: pyroglutamic acid; serine proteinase inhibitor
F;7-57/Domain: animal Kunitz-type proteinase inhibitor homology <BPI>
F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F;7-57,16-40,32-53/Disulfide bonds: #status predicted

Query Match 4.6%; Score 6; DB 1; Length 58;
Best Local Similarity 100.0%; Pred. No. 49;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 105 FIYGGC 110
Db 35 FIYGGC 40
|||||

RESULT 44

TIVIT1
venom basic proteinase inhibitor I - western sand viper
N;Alternate names: venom trypsin inhibitor I
C;Species: Vipera ammodytes ammodytes (western sand viper)
C;Date: 19-Feb-1984 #sequence_revision 19-Feb-1984 #text_change 09-Jul-2004
C;Accession: A01222
R;Rittonja, A.; Meloun, B.; Gubensek, F.
Biochim. Biophys. Acta 748, 429-435, 1983
A;Title: The primary structure of Vipera ammodytes venom trypsin inhibitor I.
A;Reference number: A01222; MUID:84053385; PMID:6639951
A;Accession: A01222
A;Molecule type: protein
A;Residues: 1-61 <RIT>
A;Cross-references: UNIPROT:P00991
C;Comment: This protein inhibits trypsin and kallikrein.
C;Superfamily: basic proteinase inhibitor; animal Kunitz-type proteinase inhibitor homol
C;Keywords: pyroglutamic acid; serine proteinase inhibitor; venom
F;7-57/Domain: animal Kunitz-type proteinase inhibitor homology <BPI>
F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F;7-57,16-40,32-53/Disulfide bonds: #status predicted
F;17/Inhibitory site: Lys (trypsin) #status predicted

Query Match 4.6%; Score 6; DB 1; Length 61;
Best Local Similarity 100.0%; Pred. No. 51;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 105 FIYGGC 110
Db 35 FIYGGC 40
|||||

RESULT 45

S07451
proteinase inhibitor 5.II - snake-locks sea anemone
C;Species: Anemonia sulcata (snake-locks sea anemone)
C;Date: 31-Dec-1990 #sequence_revision 09-May-1997 #text_change 09-Jul-2004
C;Accession: S07451; B27222
R;Wunderer, G.; Machleidt, W.; Fritz, H.
Meth. Enzymol. 80, 816-820, 1981
A;Title: The broad-specificity proteinase inhibitor 5 II from the sea anemone Anemonia s
A;Reference number: S07451
A;Accession: S07451
A;Molecule type: protein
A;Residues: 1-59 <WUN>
A;Cross-references: UNIPROT:P10280
N;Note: 13-Arg, 16-Gly, 17-Gly, 25-Leu, 28-Arg, and 39-Arg were also found
R;Krebs, H.C.; Habermehl, G.G.
Naturwissenschaften 74, 395-396, 1987
A;Title: Isolierung und Strukturauflaerung eines haemolytisch aktiven peptids aus der s
A;Reference number: A94700
A;Accession: B27222
A;Molecule type: protein
A;Residues: 1-38, 'R', 40, 'B', 42, 'BB', 45-48, 'ZZ', 51, 'Z', 53-62 <KRE>
C;Superfamily: basic proteinase inhibitor; animal Kunitz-type proteinase inhibitor homol
C;Keywords: serine proteinase inhibitor
F;5-55/Domain: animal Kunitz-type proteinase inhibitor homology <BPI>

Query Match 4.6%; Score 6; DB 2; Length 62;
Best Local Similarity 100.0%; Pred. No. 52;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 105 FIYGGC 110
Db 33 FIYGGC 38
|||||

RESULT 46

A44180
taicatoxin serine proteinase inhibitor component - Australian taipan
C;Species: Oxyuranus scutellatus scutellatus (Australian taipan)
C;Date: 27-Apr-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
C;Accession: A44180
R;Possani, L.D.; Martin, B.M.; Yatani, A.; Mochca-Morales, J.; Zamudio, F.Z.; Gurrola, G.
Toxicol. 30, 1343-1364, 1992
A;Title: Isolation and physiological characterization of taicatoxin, a complex toxin wit
A;Reference number: A44180; MUID:93134601; PMID:1485334
A;Accession: A44180
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-62 <POS>
A;Cross-references: UNIPROT:Q7LZE4
A;Experimental source: subsp. scutellatus, venom
A;Note: sequence extracted from NCBI backbone (NCBIP:122482)
C;Superfamily: basic proteinase inhibitor; animal Kunitz-type proteinase inhibitor homol
C;Keywords: serine proteinase inhibitor
F;7-57/Domain: animal Kunitz-type proteinase inhibitor homology <BPI>

Query Match 4.6%; Score 6; DB 2; Length 62;
Best Local Similarity 100.0%; Pred. No. 52;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 105 FIYGGC 110
Db 35 FIYGGC 40
|||||

RESULT 47

S19327
venom basic proteinase inhibitor - leaf-nosed viper
N;Alternate names: trypsin inhibitor (Kunitz-type)
C;Species: Eristocophis macmahoni (leaf-nosed viper)
C;Date: 22-Nov-1993 #sequence_revision 03-Nov-1995 #text_change 09-Jul-2004
C;Accession: S19327
R;Siddiqi, A.R.; Zaidi, Z.H.; Joernvall, H.
FEBS Lett. 294, 141-143, 1991
A;Title: Purification and characterization of a Kunitz-type trypsin inhibitor from Leaf-
A;Reference number: S19327; MUID:92077130; PMID:1743283
A;Accession: S19327
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-82 <SID>
A;Cross-references: UNIPROT:P24541
C;Superfamily: basic proteinase inhibitor; animal Kunitz-type proteinase inhibitor homol
C;Keywords: serine proteinase inhibitor; venom
F;2-52/Domain: animal Kunitz-type proteinase inhibitor homology <BPI>

Query Match 4.6%; Score 6; DB 2; Length 62;
Best Local Similarity 100.0%; Pred. No. 52;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 105 FIYGGC 110
Db 30 FIYGGC 35
|||||

RESULT 48

T34799
probable transcription regulator - Streptomyces coelicolor
C;Species: Streptomyces coelicolor
C;Date: 05-Nov-1999 #sequence_revision 05-Nov-1999 #text_change 09-Jul-2004

C;Accession: T34799
R;Murphy, L.; Harris, D.; Parkhill, J.; Barrrell, B.G.; Rajandream, M.A.
submitted to the EMBL Data Library, June 1998
A;Reference number: Z21557
A;Accession: T34799
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-63 <MUR>
A;Cross-references: UNIPROT:O69902; EMBL:AL023797; PIDN:CAA19406.1; GSPDB:GN00070; SCOE
A;Experimental source: strain A3(2)
C;Genetics:
A;Gene: SCOE:SC2E1.31

Query Match 4.6%; Score 6; DB 2; Length 63;
Best Local Similarity 100.0%; Pred. No. 53; Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MGLSGL 6
Db 25 MGLSGL 30
|||||

RESULT 49
TIVIVC
venom basic proteinase inhibitor III - sand viper
N;Alternate names: venom chymotrypsin inhibitor
C;Species: Vipera ammodytes (sand viper)
C;Date: 17-May-1985 #sequence_revision 17-May-1985 #text_change 09-Jul-2004
C;Accession: A01223
R;Ritonja, A.; Meloun, B.; Gubensek, F.
Biochim. Biophys. Acta 746, 138-145, 1983
A;Title: The primary structure Of Vipera ammodytes venom chymotrypsin inhibitor.
A;Reference number: A01223
A;Accession: A01223
A;Molecule type: protein
A;Residues: 1-65 <RIT>
A;Cross-references: UNIPROT:P00992
C;Superfamily: basic proteinase inhibitor; animal Kunitz-type proteinase inhibitor homol
C;Keywords: serine proteinase inhibitor; venom
F;7-57/Domain: animal Kunitz-type proteinase inhibitor homology <BPI>
F;7-57,16-40,32-53/Disulfide bonds: #status predicted
F;17/Inhibitory site: Leu (chymotrypsin) #status predicted

Query Match 4.6%; Score 6; DB 1; Length 65;
Best Local Similarity 100.0%; Pred. No. 54; Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 105 FIYGGC 110
Db 35 FIYGGC 40
|||||

RESULT 50
D42506
F-ORF-E protein - vaccinia virus (strain Copenhagen)
C;Species: vaccinia virus
A;Note: host Homo sapiens (man)
C;Date: 09-Nov-1990 #sequence_revision 09-Nov-1990 #text_change 09-Jul-2004
C;Accession: D42506
R;Johnson, G.P.
submitted to GenBank, June 1990
A;Reference number: A33172
A;Accession: D42506
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-71 <JOH>
A;Cross-references: UNIPROT:P20563

Query Match 4.6%; Score 6; DB 2; Length 71;
Best Local Similarity 100.0%; Pred. No. 58; Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 LSGLLP 8

Db 65 LSGLLP 70
|||||

Search completed: September 21, 2005, 16:50:44
Job time : 34 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 21, 2005, 16:40:19 ; Search time 133 Seconds
(without alignments)
504.379 Million cell updates/sec

Title: US-10-807-204-1

Perfect score: 131

Sequence: 1 MGISGLLPILVPFILLGDIQ.....GNNNNFQTEAICLVTKCKYH 131

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 1612378 seqs, 512079187 residues

Word size : 0

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 50 summaries

Database : UniProt_03:*

1: uniprot_sprot:*

2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	64	48.9	131	1 WFD6 HUMAN	Q9bqy6 homo sapien
2	14	10.7	134	1 EPI MOUSE	Q9da01 mus musculus
3	14	10.7	137	2 Q9BDL0	Q9bd10 oryctolagus
4	12	9.2	133	1 EPI HUMAN	Q95925 homo sapien
5	12	9.2	133	2 Q8HZ45	Q8hz45 papio papio
6	12	9.2	143	2 Q86TP9	Q86tp9 homo sapien
7	11	8.4	133	1 EPI MACMU	Q9bd11 macaca mula
8	10	7.6	62	1 ICSC1_BOMMO	P10831 bombyx mori
9	10	7.6	63	1 ICSC3_BOMMO	P07481 bombyx mori
10	10	7.6	69	1 CRPT_BOOMI	P81162 boophilus m
11	10	7.6	83	2 Q6ITB9	Q6itb9 pseudechis
12	10	7.6	85	2 Q8WPI5	Q8wpi5 bombyx mori
13	10	7.6	86	2 Q86QT1	Q86qt1 bombyx mori
14	9	6.9	77	2 Q8HZ44	Q8hz44 papio hanad
15	9	6.9	107	2 Q81Q07	Q81q07 drosophila
16	9	6.9	151	2 Q6T269	Q6t269 bitis gabon
17	9	6.9	182	2 Q6IE19	Q6ie19 rattus norv
18	8	6.1	55	1 CST1_BOMMO	P81902 bombyx mori
19	8	6.1	67	1 IBPC_BOVIN	P09076 bos taurus
20	8	6.1	76	2 Q87L9	Q87l9 bombyx mori
21	8	6.1	126	1 C11X_HUMAN	Q15332 homo sapien
22	8	6.1	186	2 Q68V31	Q68v31 bos taurus
23	8	6.1	310	2 Q9WUG1	Q9wug1 cavia porce
24	8	6.1	324	2 Q9FVW9	Q9fvv9 arabidopsis
25	8	6.1	449	2 Q92WQ0	Q92wq0 rhizobium m
26	8	6.1	746	1 CLC5_HUMAN	P51795 homo sapien
27	8	6.1	746	2 Q9GKE7	Q9gke7 sus scrofa
28	8	6.1	746	2 Q9TTU3	Q9ttu3 oryctolagus
29	8	6.1	746	2 Q99P66	Q99p66 cavia porce
30	8	6.1	893	2 Q7QH49	Q7qh49 anopheles g
31	8	6.1	900	2 Q8K206	Q8k206 mus musculus

ALIGNMENTS

RESULT 1

ID	WFD6 HUMAN	STANDARD;	PRT;	131 AA.
AC	Q9BQY6; Q8NFV6;			
DT	10-OCT-2003 (Rel. 42, Created)			
DT	10-OCT-2003 (Rel. 42, Last sequence update)			
DT	05-JUN-2004 (Rel. 44, Last annotation update)			
DE	WAP four-disulfide core domain protein 6 precursor (Putative protease inhibitor WAP6).			
GN	Name=WFD6; Synonyms=C20orf171, WAP6;			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A. (ISOFORM 2).			
RX	MEDLINE=22304654; PubMed=12206714; DOI=10.1042/BJ20020865;			
RA	Claus A., Lilja H., Lundwall A.			
RT	"A locus on human chromosome 20 contains several genes expressing protease inhibitor domains with homology to whey acidic protein.";			
RL	Biochem. J. 368:233-242(2002).			
RN	[2]			
RP	SEQUENCE FROM N.A. (ISOFORM 1).			
RX	MEDLINE=21638749; PubMed=11780052; DOI=10.1038/414865a;			
RA	Deloukas P., Matthews L.H., Ashurst J.L., Burton J., Gilbert J.G.R.,			
RA	Jones M., Stavrides G., Almeida J.P., Babbage A.K., Bagguley C.L.,			
RA	Bailey J., Barlow K.F., Bates K.N., Beard L.M., Beare D.M.,			
RA	Beasley O.P., Bird C.P., Blakey S.E., Bridgeman A.M., Brown A.J.,			
RA	Buck D., Burrill W.D., Butler A.P., Carder C., Carter N.P.,			
RA	Chapman J.C., Clamp M., Clark G., Clark L.N., Clark S.Y., Clee C.M.,			
RA	Clegg S., Cobley V.E., Collier R.E., Connor R.E., Corby N.R.,			
RA	Coulson A., Coville G.J., Deadman R., Dhani P.D., Dunn M.,			
RA	Ellington A.G., Frankland J.A., Fraser A., French L., Garner P.,			
RA	Graham D.V., Griffiths C., Griffiths M.N.D., Gwilliam R., Hall R.E.,			
RA	Hammond S., Harley J.L., Heath P.D., Ho S., Holden J.L., Howden P.J.,			
RA	Huckle E., Hunt A.R., Hunt S.E., Jekosch K., Johnson C.M., Johnson D.,			
RA	Kay M.P., Kimberley A.M., King A., Knights A., Laird G.K., Lawlor S.,			
RA	Lehvaeslahti M.H., Leversha M.A., Lloyd C., Lloyd D.M., Lovell J.D.,			
RA	Marsh V.L., Martin S.L., McConachie L.J., McLeay K., McMurray A.,			
RA	Milne S.A., Mistry D., Moore M.J.F., Mullikin J.C., Nickerson T.,			
RA	Oliver K., Parker A., Patel R., Pearce T.A.V., Peck A.I.,			
RA	Phillimore B.J.C.T., Prathalingam S.R., Plumb R.W., Ramsay H.,			
RA	Rice C.M., Ross M.T., Scott C.E., Sehra H.K., Showkneen R., Sims S.,			
RA	Kuce C.D., Smith M.L., Soderlund C., Steward C.A., Sulston J.E.,			
RA	Swann R.M., Sycamore N., Taylor R., Tee L., Thomas D.W., Thorpe A.,			
RA	Tracey A., Tomans A.C., Vaudin M., Wall M., Wallis J.M.,			
RA	Whitehead S.L., Whitaker P., Willey D.L., Williams L., Williams S.A.,			
RA	Wilming L., Wray P.W., Hubbard T., Durbin R.M., Bentley D.R., Beck S.,			
RA	Rogers J.;			

32	8	6.1	1233	2	Q69Z28
33	8	6.1	1514	2	Q9LK64
34	8	6.1	1515	2	O24510
35	7	5.3	51	2	P78492
36	7	5.3	53	1	HTIB MANSE
37	7	5.3	57	1	IVB2_NAJNI
38	7	5.3	62	1	ISC2_BOMMO
39	7	5.3	76	2	Q96858
40	7	5.3	77	1	CVP2_FIMHY
41	7	5.3	80	2	Q8T3S7
42	7	5.3	80	2	Q9VCM3
43	7	5.3	83	2	Q9W96
44	7	5.3	83	2	Q9W97
45	7	5.3	83	2	Q9WAO
46	7	5.3	83	2	Q9WAI
47	7	5.3	83	2	Q6ITB0
48	7	5.3	83	2	Q6ITB1
49	7	5.3	83	2	Q6ITB2
50	7	5.3	83	2	Q6ITB3

Q69Z28	mus musculus
Q9LK64	arabidopsis
O24510	arabidopsis
P78492	homo sapien
P26227	manduca sex
P00986	naja nivea
P10832	bombyx mori
Q96888	galleria me
Q8T0W4	pimpla hypo
Q8T3B7	araneus ven
Q9VCM3	drosophila
Q9W96	pseudonaja
Q9W97	pseudonaja
Q9WAO	pseudonaja
Q9WAI	pseudonaja
Q6ITB0	tropidochis
Q6ITB1	pseudechis
Q6ITB2	notechis sc
Q6ITB3	notechis sc


```
CC CC -!- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.
CC CC -!- SIMILARITY: Contains 1 WAP-type domain.
CC CC -----
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CC CC -----
DR EMBL; AF346413; AAK31335.1; -
DR EMBL; AK006296; BAB24514.1; -
DR EMBL; BC048637; AAH48637.1; -
DR HSSP; P1713; 1SHP.
DR MGP; MGI:1922776; Spinlwl.
DR GO; GO:0001669; C:cytosol; IDA.
DR GO; GO:0005737; C:cytoplasm; IDA.
DR InterPro; IPR002223; Prot_Inh_Kunz-m.
DR InterPro; IPR008197; WAP.
DR Pfam; PF00014; Kunitz_BPTI; 1.
DR Pfam; PF00095; WAP; 1.
DR PRINTS; PR00003; 4DISULPHCORE.
DR PRINTS; PR00759; BASICPTASE.
DR ProDom; PD00222; Prot_Inh_Kunz-m; 1.
DR PROSITE; PS00317; 4 DISULFIDE CORE; 1.
DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
DR PROSITE; PS0279; BPTI_KUNITZ_2; 1.
KW Serine protease inhibitor; Signal.
FT SIGNAL 1 21 Potential.
FT CHAIN 22 134 WAP.
FT DOMAIN 29 73 BPTI/Kunitz inhibitor.
FT DOMAIN 77 127 WAP.
FT DISULFID 33 61 By similarity.
FT DISULFID 40 65 By similarity.
FT DISULFID 48 60 By similarity.
FT DISULFID 54 69 By similarity.
FT DISULFID 77 127 By similarity.
FT DISULFID 86 110 By similarity.
FT DISULFID 102 123 By similarity.
FT DISULFID 134 AA; 15470 MW; DFEB63DD4C427P CRC64;
SQ SEQUENCE 137 AA; 15470 MW; 15773 MW; F397AF4E065D626B CRC64;

Query Match 10.7%; Score 14; DB 1; Length 134;
Best Local Similarity 100.0%; Pred. No. 3.7e-06;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 105 FIYGGCGNNNFQ 118
DB 105 FIYGGCGNNNFQ 118
|||||
RESULT 3
ID Q9BDL0 PRELIMINARY; PRT; 137 AA.
AC Q9BDL0;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Eppin.
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Testis;
RX MEDLINE=22791380; PubMed=12909348; DOI=10.1016/S0378-1119(03)00608-5;
RA Sivashanmugam P., Hall S.H., Hamil K.G., French F.S., O'Rand M.G.,
RA Richardson R.T.;
RA "Characterization of mouse Eppin and a gene cluster of similar
RT protease inhibitors on mouse chromosome 2.";
RL Gene 312:125-134(2003).
CC -!- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.
```

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DR EMBL; AF346415; AAK31337.1; -
DR HSSP; Q16019; IAAP.
DR GO; GO:0004867; F:serine-type endopeptidase inhibitor activity; IEA.
DR InterPro; IPR002223; Prot_Inh_Kunz-m.
DR InterPro; IPR008197; WAP.
DR Pfam; PF00014; Kunitz_BPTI; 1.
DR Pfam; PF00095; WAP; 1.
DR PRINTS; PR00003; 4DISULPHCORE.
DR PRINTS; PR00759; BASICPTASE.
DR ProDom; PD00222; Prot_Inh_Kunz-m; 1.
DR SMART; SM00131; KU; 1.
DR SMART; SM0217; WAP; 1.
DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
DR PROSITE; PS0279; BPTI_KUNITZ_2; 1.
SQ SEQUENCE 137 AA; 15773 MW; F397AF4E065D626B CRC64;

Query Match 10.7%; Score 14; DB 2; Length 137;
Best Local Similarity 100.0%; Pred. No. 3.7e-06;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 112 GNNNNFQTEAICLV 125
DB 112 GNNNNFQTEAICLV 125
|||||
RESULT 4
ID EPPI_HUMAN STANDARD; PRT; 133 AA.
AC Q95925; Q96SD7; Q9HD30;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 44, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Eppin precursor (Epididymal protease inhibitor) (Serine protease
DE inhibitor-like with Kunitz and WAP domains 1) (WAP four-disulfide core
DE domain protein 7) (Protease inhibitor WAP7).
GN Name=SPINW1; Synonyms=WAP7, WFDC7;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
RC TISSUE=Epididymis, and Testis;
RX MEDLINE=21297183; PubMed=11404006; DOI=10.1016/S0378-1119(01)00462-0;
RA Richardson R.T., Sivashanmugam P., Hall S.H., Hamil K.G., Moore P.A.,
RA Ruben S.M., French F.S., O'Rand M.G.;
RA "Cloning and sequencing of human Eppin: a novel family of protease
RT inhibitors expressed in the epididymis and testis.";
RL Gene 270:93-102(2001).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RA Stavrides G.S., Huckle E.J., Deloukas P.;
RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=21638749; PubMed=11780052; DOI=10.1038/414865a;
RA Deloukas P., Matthews L.H., Ashurst J.L., Burton J., Gilbert J.G.R.,
RA Jones M., Stavrides G., Almeida J.P., Babbage A.K., Bagguley C.L.,
RA Bailey J., Barlow K.F., Bates K.N., Beard L.M., Beare D.M.,
RA Beasley O.P., Bird C.P., Blakey S.E., Bridgeman A.M., Brown A.J.,
RA Buck D., Burrill W.D., Butler A.P., Carder C., Carter N.P., Clee C.M.,
RA Chapman J.C., Clamp M., Clark G., Clark L.N., Clark S.Y., Clee C.M.,
RA Clegg S., Cobley V.E., Collier R.E., Connor R.E., Corby N.R.,
RA Coulson A., Coville G.J., Deadman R., Dhani P.D., Dunn M.,
RA Ellington A.G., Griffiths C., Griffiths M.N.D., Gwilliam R., Hall R.E.,
RA Hammond S., Harley J.L., Heath P.D., Ho S., Holden J.L., Howden P.J.,
RA Huckle E., Hunt A.R., Hunt S.E., Jekosch K., Johnson C.M., Johnson D.,
RA Kay M.P., Kimberley A.M., King A., Knights A., Laird G.K., Lawlor S.,
RA Lehaeslaio M.H., Leversha M.A., Lloyd C., Lloyd D.M., Lovell J.D.,
RA Marsh V.L., Martin S.L., McConnachie L.J., McMay K., McMurray A.A.,
RA Milne S.A., Mistry D., Moore M.J.F., Mullikin J.C., Nickerson T.,
RA Oliver K., Parker A., Patel R., Pearce T.A.V., Peck A.I.,
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RA Phillimore B.J.C.T., Prathalingam S.R., Plumb R.W., Rameay H.,
RA Rice C.M., Ross M.T., Scott C.E., Sehra H.K., Showmken R., Sims S.,
RA Skuce C.D., Smith M.L., Soderlund C., Steward C.A., Sulston J.B.,
RA Swann R.M., Sycamore N., Taylor R., Tee L., Thomas D.W., Thorpe A.,
RA Tracey A., Tromans A.C., Vaudin M., Wall M., Wallis J.M.,
RA Whitehead S.L., Whittaker P., Willey D.L., Williams L., Williams S.A.,
RA Wilming L., Wray P.W., Hubbard T., Durbin R.M., Bentley D.R., Beck S.,
RA Rogers J.,
RT "The DNA sequence and comparative analysis of human chromosome 20.";
RL Nature 414:865-871(2001).
RN [4]
RC SEQUENCE FROM N.A. (ISOFORM 1).
RX TISSUE=Brain;
RA MEDLINE=2238257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haieh P.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalls D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC -1- SUBCELLULAR LOCATION: Secreted (Potential).
CC -1- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=2;
CC IsoId=O95925-1; Sequence=Displayed;
CC Name=2;
CC IsoId=O95925-2; Sequence=VSP_006755;
CC -1- TISSUE SPECIFICITY: Expressed in epididymis and testis.
CC -1- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.
CC -1- SIMILARITY: Contains 1 WAP-type domain.
CC -----
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CC -----
DR EMBL; AF286370; AAG00548.1; -
DR EMBL; AF286369; AAG00547.1; -
DR EMBL; AF286368; AAG00546.1; -
DR EMBL; AL118493; CAB56343.1; -
DR EMBL; AL031663; CAB37635.1; -
DR EMBL; AL031663; CAB37635.1; -
DR EMBL; BC053369; AAH53369.1; -
DR HSSP; P00974; 1BPI.
DR Genew; HGNC:15932; SPINLM1.
DR InterPro; IPR002223; Prot_Inh_Kunz-m.
DR InterPro; IPR008197; WAP.
DR Pfam; PF00014; Kunitz_BPTI; 1.
DR Pfam; PF00095; WAP; 1.
DR PRINTS; PR00003; 4DISULPHCORE.
DR PRINTS; PR00759; BASICPTASE.
DR ProDom; PD000222; Prot_Inh_Kunz-m; 1.
DR SMART; SM00131; KU; 1.
DR SMART; SM00217; WAP; 1.
DR PROSITE; PS00317; 4 DISULFIDE CORE; 1.
DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.

DR PROSITE; PS50279; BPTI_KUNITZ_2; 1.
KW Alternative splicing; Serine protease inhibitor; Signal.
FT SIGNAL 1 21 Potential.
FT CHAIN 22 133 Eppin.
FT DOMAIN 29 73 WAP.
FT DOMAIN 77 127 BPTI/Kunitz inhibitor.
FT DISULFID 33 61 By similarity.
FT DISULFID 40 65 By similarity.
FT DISULFID 48 60 By similarity.
FT DISULFID 54 69 By similarity.
FT DISULFID 77 127 By similarity.
FT DISULFID 86 110 By similarity.
FT DISULFID 102 123 By similarity.
FT VARSPIC 1 31 MGSSGLSLVLFLVLLANVQGPGLTDWLFPR -> MLSKAH
FT /FTIG=VSP_006755.
FT /FTIG=VSP_006755.
SQ SEQUENCE 133 AA; 15284 MW; F7831B203366D9DC CRC64;
Query Match 9.2%; Score 12; DB 1; Length 133;
Best Local Similarity 100.0%; Pred. No. 0.00044;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 107 YGGCGQGNNNFQ 118
Db 107 YGGCGQGNNNFQ 118
RESULT 5
Q8HZ45 PRELIMINARY; PRT; 133 AA.
ID Q8HZ45
AC Q8HZ45
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Epididymal protease inhibitor 1.
GN Name=Eppin;
OS Papio papio (Guinea baboon).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
OC Cercopithecinae; Papio.
OX NCBI_TaxID=100937;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Testis;
RA Sivashanmugam P., O'Rand M.G., Richardson R.T.;
RL Submitted (Aug-2002) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.
DR EMBL; AY141973; AAN08507.1; -
DR HSSP; P00974; 1UUA.
DR GO; GO:0008233; F:peptidase activity; IEA.
DR GO; GO:0004867; F:serine-type endopeptidase inhibitor activity; IEA.
DR InterPro; IPR002223; Prot_Inh_Kunz-m.
DR InterPro; IPR008197; WAP.
DR Pfam; PF00014; Kunitz_BPTI; 1.
DR Pfam; PF00095; WAP; 1.
DR PRINTS; PR00759; BASICPTASE.
DR ProDom; PD000222; Prot_Inh_Kunz-m; 1.
DR SMART; SM00131; KU; 1.
DR SMART; SM00217; WAP; 1.
DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
DR PROSITE; PS50279; BPTI_KUNITZ_2; 1.
KW Protease.
SQ SEQUENCE 133 AA; 15277 MW; B33ABE57ECBE884 CRC64;
Query Match 9.2%; Score 12; DB 2; Length 133;
Best Local Similarity 100.0%; Pred. No. 0.00044;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 107 YGGCGQGNNNFQ 118
Db 107 YGGCGQGNNNFQ 118

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RESULT 6
ID Q86TP9 PRELIMINARY; PRT; 143 AA.
AC Q86TP9;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE SPINLWI protein (Fragment).
GN Name=SPINLWI;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullihy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Faney J., Helton E., Kettner M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smalish D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Warr M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RA Strausberg R.;
RL Submitted (JAN-2003) to the EMBL/GenBank/DBSJ databases.
CC -1- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.
DR EMBL; BC044829; AAH44829.1; -.
DR HSSP; P00974; 1UUA.
DR GO; GO:0004867; F:serine-type endopeptidase inhibitor activity; IEA.
DR InterPro; IPR002223; Prot_Inh_Kunz-m.
DR Pfam; PF00095; WAP; 1.
DR PRINTS; PR00003; 4DISULPHCORE.
DR PRINTS; PR00759; BASICPTASE.
DR ProDom; PD000222; Prot_Inh_Kunz-m; 1.
DR SMART; SM00131; KU; 1.
DR SMART; SM00217; WAP; 1.
DR PROSITE; PS00317; 4 DISULFIDE CORE; 1.
DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
DR PROSITE; PS00279; BPTI_KUNITZ_2; 1.
DR NON_TER
FT SEQUENCE 143 AA; 16506 MW; 92BF56C2B7977508 CRC64;
SQ
Query Match 9.4%; Score 12; DB 2; Length 143;
Best Local Similarity 100.0%; Pred. No. 0.00047;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 107 YGCGCGNNNNFQ 118
Db |||||
117 YGCGCGNNNNFQ 128
RESULT 7
ID BPPI_MACMU STANDARD; PRT; 133 AA.
AC BPPI_MACMU
DT 01-JUL-1989 (Rel. 11, Created)

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DT 01-JUL-1989 (Rel. 11, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Chymotrypsin inhibitor SCI-I.
 OS Bombyx mori (Silk moth).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Lepidoptera; Glossata; Bombycoidea;
 OC Bombycidae; Bombyx.
 OX NCBI_TaxID=7091;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Larval hemolymph;
 RX MEDLINE=89228538; PubMed=3072972;
 RA Sasaki T.;
 RT "Amino-acid sequences of two basic chymotrypsin inhibitors from
 RL silkworm larval hemolymph."; 1235-1241(1988).
 CC -1- FUNCTION: Inhibits chymotrypsin and thus avoids the accidental
 CC chymotrypsin-mediated activation of prophenoloxidase. This enzyme
 CC is required by the insect immune system to produce melanin which
 CC is used to engulf foreign objects.
 CC -1- SIMILARITY: Contains 1 BPTi/Kunitz inhibitor domain.
 DR PIR; S01802; S01802.
 DR HSP; P10646; IADZ.
 DR InterPro; IPR002223; Prot_Inh_Kunz-m.
 DR Pfam; PF00014; Kunitz_BPTi_1.
 DR PRINTS; PR00759; BASICPTASE.
 DR ProDom; PD000222; Prot_Inh_Kunz-m; 1.
 DR SMART; SM00131; KU; 1.
 DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
 DR PROSITE; PS0279; BPTI_KUNITZ_2; 1.
 KW Direct protein sequencing; Serine protease inhibitor.
 FT SITE 20 21 Reactive bond (By similarity).
 FT DISULFID 9 60 By similarity.
 FT DISULFID 19 43 By similarity.
 FT DISULFID 35 56 By similarity.
 SQ SEQUENCE 62 AA; 7065 MW; 7E7C11B9B95AC6DA CRC64;

 Query Match 7.6%; Score 10; DB 1; Length 62;
 Best Local Similarity 100.0%; Pred. No. 0.03;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

 Qy 104 EFIYGGCGGN 113
 |||||
 Db 37 EFIYGGCGGN 46

 RESULT 9
 ICS3 BOMMO STANDARD; PRT; 63 AA.
 AC P07481;
 DT 01-APR-1988 (Rel. 07, Created)
 DT 01-APR-1988 (Rel. 07, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Chymotrypsin inhibitor SCI-III.
 OS Bombyx mori (Silk moth).
 OC Eukaryota; Metazoa; Arthropoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Lepidoptera; Glossata; Bombycoidea;
 OC Bombycidae; Bombyx.
 OX NCBI_TaxID=7091;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Larval hemolymph;
 RA Sasaki T.;
 RT "Amino acid sequence of a novel Kunitz-type chymotrypsin inhibitor
 RL from hemolymph of silkworm larvae, Bombyx mori.";
 RL FEBS Lett. 168:227-230(1984).
 CC -1- FUNCTION: Inhibits chymotrypsin and thus avoids the accidental
 CC chymotrypsin-mediated activation of prophenoloxidase. This enzyme
 CC is required by the insect immune system to produce melanin which
 CC is used to engulf foreign objects.
 CC -1- SIMILARITY: Contains 1 BPTi/Kunitz inhibitor domain.
 DR PIR; A25740; TIMTC3.
 DR HSP; P10646; IADZ.

DR InterPro; IPR002223; Prot_Inh_Kunz-m.
 DR Pfam; PF00014; Kunitz_BPTi_1.
 DR PRINTS; PR00759; BASICPTASE.
 DR ProDom; PD000222; Prot_Inh_Kunz-m; 1.
 DR SMART; SM00131; KU; 1.
 DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
 DR PROSITE; PS0279; BPTI_KUNITZ_2; 1.
 KW Direct protein sequencing; Serine protease inhibitor.
 FT SITE 21 22 Reactive bond (By similarity).
 FT DISULFID 10 61 By similarity.
 FT DISULFID 20 44 By similarity.
 FT DISULFID 36 57 By similarity.
 SQ SEQUENCE 63 AA; 7118 MW; 977BD3C822DBA89B CRC64;

 Query Match 7.6%; Score 10; DB 1; Length 63;
 Best Local Similarity 100.0%; Pred. No. 0.03;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

 Qy 104 EFIYGGCGGN 113
 |||||
 Db 38 EFIYGGCGGN 47

 RESULT 10
 CRPT BOOMI STANDARD; PRT; 69 AA.
 AC P8152;
 DT 15-DEC-1998 (Rel. 37, Created)
 DT 15-DEC-1998 (Rel. 37, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Protease inhibitor carrabatin.
 OS Boophilus microplus (Cattle tick).
 OC Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Acari;
 OC Parasitiformes; Ixodida; Ixodidae; Boophilus.
 OX NCBI_TaxID=6941;
 RN [1]
 RP SEQUENCE.
 RA Fuentes-Prior P., Pereira P.J.B., Mentale R., Bode W.;
 RL Submitted (JAN-1998) to Swiss-Prot.
 CC -1- FUNCTION: Serine protease inhibitor.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- SIMILARITY: Contains 1 BPTi/Kunitz inhibitor domain.
 DR HSP; P00980; IDTX.
 DR InterPro; IPR002223; Prot_Inh_Kunz-m.
 DR Pfam; PF00014; Kunitz_BPTi_1.
 DR PRINTS; PR00759; BASICPTASE.
 DR ProDom; PD000222; Prot_Inh_Kunz-m; 1.
 DR SMART; SM00131; KU; 1.
 DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
 DR PROSITE; PS0279; BPTI_KUNITZ_2; 1.
 KW Direct protein sequencing; Serine protease inhibitor.
 FT SITE 18 19 Reactive bond (By similarity).
 FT DISULFID 8 58 By similarity.
 FT DISULFID 17 41 By similarity.
 FT DISULFID 33 54 By similarity.
 SQ SEQUENCE 69 AA; 7842 MW; E0B14312AC1533BB CRC64;

 Query Match 7.6%; Score 10; DB 1; Length 69;
 Best Local Similarity 100.0%; Pred. No. 0.03;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

 Qy 104 EFIYGGCGGN 113
 |||||
 Db 35 EFIYGGCGGN 44

 RESULT 11
 Q6ITB9 PRELIMINARY; PRT; 83 AA.
 ID Q6ITB9
 AC Q6ITB9; 2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)

DE Mulgin-3.
OS Pseudochis australis (Mulga snake) (King brown snake).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauroidea; Squamata; Scleroglossa; Serpentes; Colubroidae;
OC Elapidae; Acanthophinae; Pseudochis.
OX NCBI_TaxID=8670;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Venom gland;
RA Filipovich I.V., Sorokina N.I.;
RL Submitted (MAY-2004) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.
DR EMBL; AY626926; AAT45402.1; -.
DR HSSP; Q16019; 1AAP.
DR GO; GO:0004867; F:serine-type endopeptidase inhibitor activity; IEA.
DR InterPro; IPR002223; Prot_Inh_Kunz-m.
DR Pfam; PF00014; Kunitz_BPTI; 1.
DR PRINTS; PR00759; BASICPTASE.
DR ProDom; PD000222; Prot_Inh_Kunz-m; 1.
DR SMART; SM00131; KU; 1.
DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
DR PROSITE; PS00279; BPTI_KUNITZ_2; 1.
SQ SEQUENCE 83 AA; 9103 MW; 315C361D8EC89221 CRC64;

Query Match 7.6%; Score 10; DB 2; Length 83;
Best Local Similarity 100.0%; Pred. No. 0.038;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 104 EFIYGGCGQN 113
DB 58 EFIYGGCGQN 67

RESULT 12
QWPI5 PRELIMINARY; PRT; 85 AA.
AC QWPI5;
DT 01-MAR-2002 (TRENBLrel. 20, Created)
DT 01-MAR-2002 (TRENBLrel. 20, Last sequence update)
DT 01-JUN-2003 (TRENBLrel. 24, Last annotation update)
DE Chymotrypsin inhibitor precursor.
GN Name=SCI-SB; (Silk moth).
OS Bombyx mori (Silk moth).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia; Bombycoidea;
OC Bombycidae; Bombyx.
OX NCBI_TaxID=7091;
RN [1]
RP SEQUENCE FROM N.A.
RA Tan A., Tanaka H., Sato N., Yaguchi M., Nagata M., Suzuki K.;
RT "Identification of novel tissue-specific proteins in the subesophageal body of the silkworm, Bombyx mori.";
RL J. Insect Biotechnol. Sericulture 72:41-50(2003).
CC -!- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.
DR EMBL; AB062102; BAB83366.1; -.
DR HSSP; P10646; 1ADZ.
DR GO; GO:0004867; F:serine-type endopeptidase inhibitor activity; IEA.
DR Pfam; PF00014; Kunitz_BPTI; 1.
DR PRINTS; PR00759; BASICPTASE.
DR SMART; SM00131; KU; 1.
DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
DR PROSITE; PS00279; BPTI_KUNITZ_2; 1.
FT SIGNAL.
SQ SEQUENCE 85 AA; 9493 MW; F526B81CF75D8EF1 CRC64;

Query Match 7.6%; Score 10; DB 2; Length 85;
Best Local Similarity 100.0%; Pred. No. 0.038;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 104 EFIYGGCGQN 113
DB 60 EFIYGGCGQN 69

RESULT 13
Q86QTL PRELIMINARY; PRT; 86 AA.
AC Q86QTL;
DT 01-JUN-2003 (TRENBLrel. 24, Created)
DT 01-JUN-2003 (TRENBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)
DE Chymotrypsin inhibitor CII3.
OS Bombyx mori (Silk moth).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia; Bombycoidea;
OC Bombycidae; Bombyx.
OX NCBI_TaxID=7091;
RN [1]
RP SEQUENCE FROM N.A.
RA He N., Fujii H., Banno Y.;
RL Submitted (OCT-2002) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.
DR EMBL; AY167664; AA017293.1; -.
DR HSSP; P10646; 1ADZ.
DR GO; GO:0004867; F:serine-type endopeptidase inhibitor activity; IEA.
DR InterPro; IPR002223; Prot_Inh_Kunz-m.
DR Pfam; PF00014; Kunitz_BPTI; 1.
DR PRINTS; PR00759; BASICPTASE.
DR ProDom; PD000222; Prot_Inh_Kunz-m; 1.
DR SMART; SM00131; KU; 1.
DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
DR PROSITE; PS00279; BPTI_KUNITZ_2; 1.
SQ SEQUENCE 86 AA; 9611 MW; E4F22676B8F30B8B CRC64;

Query Match 7.6%; Score 10; DB 2; Length 86;
Best Local Similarity 100.0%; Pred. No. 0.039;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 104 EFIYGGCGQN 113
DB 61 EFIYGGCGQN 70

RESULT 14
Q8HZ44 PRELIMINARY; PRT; 77 AA.
AC Q8HZ44;
DT 01-MAR-2003 (TRENBLrel. 23, Created)
DT 01-MAR-2003 (TRENBLrel. 23, Last sequence update)
DT 01-MAR-2004 (TRENBLrel. 26, Last annotation update)
DE Epididymal protease inhibitor 2.
GN Name=Eppin;
OS Papio hamadryas (Hamadryas baboon).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecinae; Papio.
OX NCBI_TaxID=9557;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Testis;
RA Sivashanmugam P., O'Rand M.G., Richardson R.T.;
RL Submitted (AUG-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY141975; AAN08509.1; -.
DR GO; GO:0008233; F:peptidase activity; IEA.
DR InterPro; IPR008197; WAP.
DR Pfam; PF00095; WAP; 1.
DR PRINTS; PR00003; 4DISULPHCORE.
DR SMART; SM00217; WAP; 1.
KW Protease.
SQ SEQUENCE 77 AA; 8787 MW; B86E5868C57CEBD0 CRC64;

Query Match 6.9%; Score 9; DB 2; Length 77;
Best Local Similarity 100.0%; Pred. No. 0.39;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 63 FSCGKKCLD 71
 Db 63 FSCGKKCLD 71

RESULT 15
 Q81Q07 PRELIMINARY; PRT; 107 AA.
 AC Q81Q07;
 DT 01-MAR-2003 (TrEMBLrel. 23, Created)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE CG31779-PA.
 GN ORFNames=CG31779;
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Peerygota;
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 OX NCBI_TaxID=7227;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20196006; PubMed=10731132; DOI=10.1126/science.287.5461.2185;
 RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Amanatides P.G., Scher S.E., Li P.W., Hoskins R.A., Galle R.F.,
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
 RA Brandon R.C., Rogers Y.H., Blazej R.G., Champe M., Pfeiffer B.D.,
 RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Gabor G.L.,
 RA Abril J.F., Agbayani A., An H.J., Andrews-Frankoch C., Baldwin D.,
 RA Balow R.M., Baau A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
 RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
 RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brothier P.,
 RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
 RA de Pablo B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleitschmann W.,
 RA Foaier C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glaeser K.,
 RA Glodok A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 RA Harrie N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
 RA Hostin D., Houston K.A., Howland T.J., Wei M.H., Ibegwan C.,
 RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 RA Laoko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Reinert K., Remington K., Saunders R.D., Scheeler F., Shen H.,
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
 RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.Y., Wassarman D.A., Weinstein G.M., Weissenbach J.,
 RA Williams S.M., Woodage, Worley K.C., Wu D., Yang S., Yao Q.A., Ye J.,
 RA Yeh R.F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 RT "The genome sequence of Drosophila melanogaster."
 RL Science 287:2185-2195(2000).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22426065; PubMed=12537568;
 RA Celniker S.E., Wheeler D.A., Kronmiller B., Carlson J.W., Halpern A.,
 RA Patel S., Adams M., Champe M., Dugan S.P., Frise E., Hodgson A.,
 RA George R.A., Hoskins R.A., Lavery T., Muzny D.M., Nelson C.R.,
 RA Pacleb J.M., Park S., Pfeiffer B.D., Richards S., Sodergren E.J.,
 RA Svirskas R., Tabor P.E., Wan K., Stapleton M., Sutton G.G., Venter C.,
 RA Weinstein G., Scher S.E., Myers E.W., Gibbs R.A., Rubin G.M.;
 RT "Finishing a whole-genome shotgun: Release 3 of the Drosophila
 RT melanogaster euchromatic genome sequence."
 RL Genome Biol. 3:RESEARCH0079-RESEARCH0079(2002).
 RN [3]

RP SEQUENCE FROM N.A.
 RX MEDLINE=22426070; PubMed=12537573;
 RA Kaminker J.S., Bergman C.M., Kronmiller B., Carlson J., Svirskas R.,
 RA Patel S., Frise E., Wheeler D.A., Lewis S.E., Rubin G.M.,
 RA Ashburner M., Celniker S.E.;
 RT "The transposable elements of the Drosophila melanogaster euchromatin:
 RT a genomic perspective."
 RL Genome Biol. 3:RESEARCH0084-RESEARCH0084(2002).
 RN [4]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22426069; PubMed=12537572;
 RA Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
 RA Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochnik S.E.,
 RA Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Berman B.P.,
 RA Bettencourt B.R., Celniker S.E., de Grey A.D., Drysdale R.A.,
 RA Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q., M.,
 RA Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
 RA Lewis S.E.;
 RT "Annotation of the Drosophila melanogaster euchromatic genome: a
 RT systematic review."
 RL Genome Biol. 3:RESEARCH0083-RESEARCH0083(2002).
 RN [5]
 RP SEQUENCE FROM N.A.
 RX FlyBase;
 RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
 RN [6]
 RP SEQUENCE FROM N.A.
 RX FlyBase;
 RL Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.
 CC -|- SIMILARITY: Contains 2 BPTI/Kunitz inhibitor domains.
 DR EMBL; AE003579; AAN10377.2; -.
 DR HSP; P12111; 1KNT.
 DR FlyBase; FBR0051779; CG31779.
 DR GO; GO:0004867; F:serine-type endopeptidase inhibitor activity; IEA.
 DR InterPro; IPR002223; Prot_Inh_Kunz-m.
 DR Pfam; PF00014; Kunitz_BPTI; 2.
 DR PRINTS; PR00759; BASICPTASE.
 DR ProDom; PD000222; Prot_Inh_Kunz-m; 2.
 DR SMART; SM00131; KU_2.
 DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
 DR PROSITE; PS02079; BPTI_KUNITZ_2; 2.
 SQ SEQUENCE 107 AA; 13029 MW; 98F3423A59C9E744 CRC64;
 Query Match 6.9%; Score 9; DB 2; Length 107;
 Best Local Similarity 100.0%; Pred No. 0.5;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 105 FLYGCGQN 113
 Db 35 FLYGCGQN 43
 RESULT 16
 Q6T269 PRELIMINARY; PRT; 151 AA.
 ID Q6T269
 AC Q6T269
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE Two-Kunitz protease inhibitor (Fragment).
 OS Bitis gabonica (Gaboon adder) (Gaboon viper).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
 OC Viperidae; Viperinae; Bitis.
 OX NCBI_TaxID=8694;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX PubMed=15276202; DOI=10.1016/j.j-gene.2004.03.024;
 RA Francischetti I.M., My-Pham V., Harrison J., Garfield M.K.,
 RA Ribeiro J.M.;
 RA "Bitis gabonica (Gaboon viper) snake venom gland: toward a catalog for
 RT the full-length transcripts (cDNA) and proteins."
 RL Gene 337:55-69(2004).


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RN  SEQUENCE FROM N.A.
RP  Francischetti I.M.B., Pham V.M., Garfield M.K., Ribeiro J.M.C.;
RA  Submitted (OCT-2003) to the EMBL/GenBank/DBJ databases.
RL  -1- SIMILARITY: Contains 2 BPTI/Kunitz inhibitor domains.
CC  EMBL; AY442289; AAR1925.1; -.
DR  HSSP; Q16019; 1AAP.
DR  GO; GO:0008233; F:peptidase activity; IEA.
DR  GO; GO:0004867; F:serine-type endopeptidase inhibitor activity; IEA.
DR  InterPro; IPR002223; F:serine-type endopeptidase inhibitor (CSTI).
DR  GO; GO:0004867; F:serine-type endopeptidase inhibitor activity; IEA.
DR  Pfam; PF00014; Kunitz_BPTI_2.
DR  PRINTS; PR00759; BASICPTASE.
DR  ProDom; PD000222; Prot_Inh_Kunz-m; 2.
DR  SMART; SM00131; KU; 2.
DR  PROSITE; PS00280; BPTI_KUNITZ_1; 2.
DR  PROSITE; PS50279; BPTI_KUNITZ_2; 2.
KW  Protease.
FT  NON TER 1.
SQ  SEQUENCE 151 AA; 16976 MW; 13E34ACE8DE581ED CRC64;

Query Match 6.9%; Score 9; DB 2; Length 151;
Best Local Similarity 100.0%; Pred.No. 0.64;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 105 FIYGCCQGN 113
Db 100 FIYGCCQGN 108
|||||

RESULT 17
Q6IE19 PRELIMINARY; PRT; 182 AA.
AC Q6IE19;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE WAP four-disulfide core 6-like 1.
GN Name=wfd6c11;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Sprague-Dawley;
RX PubMed=15660002; DOI=10.1101/gr.1946304;
RA Puente X.S., Lopez-Otin C.;
RT "A genomic analysis of rat proteases and protease inhibitors.";
RL Genome Res. 14:609-622(2004).
CC -1- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.
CC -1- MISCCELLANEOUS: The sequence shown here is derived from an
EMBL/GenBank/DBJ third party annotation (TPA) entry.
CC EMBL; BN000374; CAE51900.1; -.
DR HSSP; P00974; 1K6U.
DR GO; GO:0004867; F:serine-type endopeptidase inhibitor activity; IEA.
DR InterPro; IPR002223; Prot_Inh_Kunz-m.
DR InterPro; IPR008197; WAP_Inh_Kunz-m.
DR Pfam; PF00014; Kunitz_BPTI; 1.
DR Pfam; PF00095; WAP; 1.
DR PRINTS; PR00003; 4DISULPHCORE.
DR PRINTS; PR00759; BASICPTASE.
DR ProDom; PD000222; Prot_Inh_Kunz-m; 1.
DR SMART; SM00131; KU; 1.
DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
DR PROSITE; PS50279; BPTI_KUNITZ_2; 1.
SQ SEQUENCE 182 AA; 21018 MW; EB12D7BFF756707E CRC64;

Query Match 6.9%; Score 9; DB 2; Length 182;
Best Local Similarity 100.0%; Pred.No. 0.74;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 105 FIYGCCQGN 113
Db 100 FIYGCCQGN 108
|||||

us-10-807-204-1.oli.rup
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Db 105 FIYGCCQGN 113
RESULT 18
CSTI_BOMMO STANDARD; PRT; 55 AA.
AC B1902;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Trypsin inhibitor (Cocoon shell-associated trypsin inhibitor) (CSTI).
OS Bombyx mori (Silk moth).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Lepidoptera; Glossata; Bombycoidea;
OC Bombycidae; Bombyx.
OX NCBI_TaxID=7091;
RN [1]
RP SEQUENCE, CHARACTERIZATION, AND MASS SPECTROMETRY.
RC STRAIN=Asahi;
RX MEDLINE=99115431; PubMed=9914483;
RA Kurioka A., Yamazaki M., Hirano H.;
RT "Primary structure and possible functions of a trypsin inhibitor of
Bombyx mori.";
RL Eur. J. Biochem. 259:120-126(1999).
CC -1- FUNCTION: This cocoon shell-associated protein inhibits trypsin
Activity by forming a low-dissociation complex with trypsin. May
play an important part in regulating proteolytic activity in the
silk gland or protecting silk proteins from degradation during
histolysis.
CC -1- SUBUNIT: Monomer.
CC -1- TISSUE SPECIFICITY: Expressed exclusively in the middle silk
gland.
CC -1- DEVELOPMENTAL STAGE: Expression differentially regulated in the
middle silk glands during the final stage of larval growth with
highest expression before the onset of spinning.
CC -1- MASS SPECTROMETRY: MW=6658; METHOD=Electrospray; RANGE=1-55;
NOTE=Ref.1.
CC -1- MISCCELLANEOUS: Has an isoelectric point of 4.3.
CC -1- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.
DR HSSP; P31713; 1SHP.
DR InterPro; IPR002223; Prot_Inh_Kunz-m.
DR Pfam; PF00014; Kunitz_BPTI; 1.
DR PRINTS; PR00759; BASICPTASE.
DR ProDom; PD000222; Prot_Inh_Kunz-m; 1.
DR SMART; SM00131; KU; 1.
DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
DR PROSITE; PS50279; BPTI_KUNITZ_2; 1.
KW Developmental protein; Direct protein sequencing;
Serine protease inhibitor.
FT SITE 14 15 Reactive bond for trypsin (By
similarity).
FT DISULFD 4 54 By similarity.
FT DISULFD 13 37 By similarity.
FT DISULFD 29 50 By similarity.
SQ SEQUENCE 55 AA; 6027 MW; C2739BB8F2B86E59 CRC64;

Query Match 6.1%; Score 8; DB 1; Length 55;
Best Local Similarity 100.0%; Pred.No. 3.4;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 104 BFYGGCQ 111
Db 31 BFYGGCQ 38
|||||

RESULT 19
IBPC_BOVIN STANDARD; PRT; 67 AA.
ID IBPC_BOVIN
AC P00976;
DT 21-JUL-1986 (Rel. 01, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Colostrum trypsin inhibitor (Colostrum BPI).
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OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovinae; Bos.
 ON NCBI_TaxID=9913;
 RN [1]
 RP SEQUENCE.
 RA Cechova D., Jonakova V., Sorm F.;
 RT "Primary structure of trypsin inhibitor from cow colostrum (component B2).";
 RL Collect. Czech. Chem. Commun. 36:3342-3357(1971).
 RN [2]
 RP DISULFIDE BONDS.
 RA Cechova D., Ber E.;
 RT "Disulfide bonds of trypsin inhibitor from cow colostrum.";
 RL Collect. Czech. Chem. Commun. 39:680-688(1974).
 RN [3]
 RP CHARACTERIZATION.
 RA Cechova D., Muszyńska G.;
 RT "Role of lysine 18 in active center of cow colostrum trypsin inhibitor.";
 RL FEBS Lett. 8:84-86(1970).
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.
 DR PIR: A01207; TIBOC.
 DR HSP: P02760; IBIK.
 DR InterPro: IPR002223; Prot_Inh_Kunz-m.
 DR Pfam: PF00014; Kunitz_BPTI; 1.
 DR PRINTS: PR00759; BASICTPASE.
 DR ProDom: PD000222; Prot_Inh_Kunz-m; 1.
 DR SMART: SM00131; KU; 1.
 DR PROSITE: PS00280; BPTI_KUNITZ_1; 1.
 DR PROSITE: PS0279; BPTI_KUNITZ_2; 1.
 KW Direct protein sequencing; Glycoprotein; Serine protease inhibitor.
 FT SITE 18 19
 FT DISULFID 8 58
 FT DISULFID 17 41
 FT DISULFID 33 54
 FT CARBOHYD 27 27 N-linked (GlcNAc...).
 SQ SEQUENCE 67 AA; 7511 MW; E2B2093B7CD207CD CRC64;
 Query Match 6.1%; Score 8; DB 1; Length 67;
 Best Local Similarity 100.0%; Pred. No. 3.9;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 107 YGGCGQNN 114
 Db 38 YGGCGQNN 45
 RESULT 20
 Q8T7L9 PRELIMINARY; PRT; 76 AA.
 AC Q8T7L9;
 DT 01-JUN-2002 (TrEMBLrel. 21, Created)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Kazal-type serine proteinase inhibitor 1.
 GN Name=SP11;
 OS Bombyx mori (Silk moth).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia; Bombycoidea;
 OC Bombycidae; Bombyx.
 ON NCBI_TaxID=7091;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA MEDLINE=21873253; PubMed=11881808;
 RA Nimala X., Mita K., Vanisree V., Zurovec M., Sehnal F.;
 RT "Identification of four small molecular mass proteins in the silk of Bombyx mori.";
 RL Insect Mol. Biol. 10:437-445(2001).
 CC -1- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.

DR EMBL: AF352583; AAL83944.1; -.
 DR HSP: P31713; 1SHP.
 DR GO: GO:0004867; F:serine-type endopeptidase inhibitor activity; IEA.
 DR InterPro: IPR002223; Prot_Inh_Kunz-m.
 DR Pfam: PF00014; Kunitz_BPTI; 1.
 DR PRINTS: PR00759; BASICTPASE.
 DR SMART: SM00131; KU; 1.
 DR PROSITE: PS00280; BPTI_KUNITZ_1; 1.
 DR PROSITE: PS0279; BPTI_KUNITZ_2; 1.
 SQ SEQUENCE 76 AA; 8445 MW; AA3F97D373535A3B CRC64;
 Query Match 6.1%; Score 8; DB 2; Length 76;
 Best Local Similarity 100.0%; Pred. No. 4.3;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 104 EFTYGGCQ 111
 Db 52 EFTYGGCQ 59
 RESULT 21
 C1IX_HUMAN STANDARD; PRT; 126 AA.
 ID C1IX_HUMAN
 AC Q15332;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE 13.2 kDa protein in chromosome 11.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 ON NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Kidney;
 RA Austruy E., Belley L., Millasot P., Junien C., Jeanpierre C.;
 RT "Characterization of the human cDNA with partial homology with the gamma subunit of sodium potassium ATPase of rat, mouse, rabbit and sheep.";
 RL Submitted (APR-1995) to the EMBL/GenBank/DBJ databases.
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to license@isb-sib.ch).
 DR EMBL: X86400; CAA60152.1; -.
 DR PIR: S54159; S54159.
 SQ SEQUENCE 126 AA; 13206 MW; F159A1BD0B64F11E CRC64;
 Query Match 6.1%; Score 8; DB 1; Length 126;
 Best Local Similarity 100.0%; Pred. No. 6.2;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 82 EAGPCLAS 89
 Db 35 EAGPCLAS 42
 RESULT 22
 Q68V31 PRELIMINARY; PRT; 186 AA.
 ID Q68V31
 AC Q68V31;
 DT 25-OCT-2004 (TrEMBLrel. 28, Created)
 DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
 DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
 DE Chloride channel protein 5 (Fragment).
 GN Name=cicn5;
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC	Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;	OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC	Bovinae; Bos.	OC	Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OX	NCBI_TaxID=9913;	OC	eurosid II; Brassicales; Brassicaceae; Arabidopsis.
RN	[1]	OX	NCBI_TaxID=3702;
RP	SEQUENCE FROM N.A.	RN	[1]
RC	TISSUE=eye endothelium;	RP	SEQUENCE FROM N.A.
RA	Mitra R., Srinivas S.P.;	RA	Lin X., Kaul S., Town C.D., Benito M., Creasy T.H., Haas B.J., Wu D.,
RT	"Expression of chloride channels in the bovine eye endothelial	RA	Maiti R., Ronning C.M., Koo H., Fujii C.Y., Uterback T.R., Fraser C.M.;
RT	cells.";	RA	Barnstead M.E., Bowman C.L., White O., Nierman W.C., Fraser C.M.;
RL	Submitted (AUG-2004) to the EMBL/GenBank/DBJ databases.	RL	Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.
DR	EMBL; AJ810447; CAH17905.1; -.	RN	[2]
DR	InterPro; IPR001807; Cl-channel_volt.	RP	SEQUENCE FROM N.A.
DR	Pfam; PF00654; Voltage_CLC; 1.	RA	Town C.D., Kaul S.;
FT	NON_TER	RL	Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
FT	NON_TER	CC	-1- SIMILARITY: Belongs to the ABC transporter family.
SQ	SEQUENCE 186 AA; 20749 MW; 4264DC7DB8C7C773 CRC64;	DR	EMBL; AC016162; AAG51884.1; -.
		DR	PIR; B96738; B96738.
		DR	HSSP; P26361; 1R0W.
		DR	GO; GO:0016021; C:integral to membrane; IEA.
		DR	GO; GO:0005524; F:ATP binding; IEA.
		DR	GO; GO:0042626; F:ATPase activity, coupled to transmembrane m. . .; IEA.
		DR	GO; GO:0006810; P:transport; IEA.
		DR	InterPro; IPR011527; ABC membrane 1.
		DR	InterPro; IPR003439; ABC_transporter.
		DR	Pfam; PF00005; ABC_tran; 1.
		DR	ProDom; PD000006; ABC_transporter; 1.
		DR	PROSITE; PS00929; ABC_TM1F; 1.
		KW	ATP-binding.
		SQ	SEQUENCE 324 AA; 35810 MW; 1FA9AAE27A276D21 CRC64;
Query Match	6.1%; Score 8; DB 2; Length 186;	Query Match	6.1%; Score 8; DB 2; Length 324;
Best Local Similarity	100.0%; Pred. No. 8.3;	Best Local Similarity	100.0%; Pred. No. 12;
Matches	8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	Matches	8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy	10 LVPFILLG 17	Qy	10 LVPFILLG 17
Db	105 LVPFILLG 112	Db	221 LVPFILLG 228
RESULT 23		RESULT 25	
Q9WUG1	PRELIMINARY; PRT; 310 AA.	Q92W00	PRELIMINARY; PRT; 449 AA.
ID	Q9WUG1	ID	Q92W00
AC	Q9WUG1;	AC	Q92W00;
DT	01-NOV-1999 (TrEMBLrel. 12, Created)	DT	01-DEC-2001 (TrEMBLrel. 19, Created)
DT	01-NOV-1999 (TrEMBLrel. 12, Last sequence update)	DT	01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT	01-JUN-2003 (TrEMBLrel. 24, Last annotation update)	DT	01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE	Chloride channel Clc-5 (Fragment).	DE	Putative permease protein.
OS	Cavia porcellus (Guinea pig).	GN	ORFNames=Sm20289;
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	OS	Rhizobium meliloti (Sinorhizobium meliloti).
OC	Mammalia; Eutheria; Rodentia; Hystricognathi; Caviidae; Cavia.	OG	Plasmid pSymb.
OX	NCBI_TaxID=10141;	OC	Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
RN	[1]	OC	Rhizobiaceae; Sinorhizobium/Ensifer group; Sinorhizobium.
RP	SEQUENCE FROM N.A.	OX	NCBI_TaxID=382;
RC	TISSUE=Small intestine epithelium;	RN	[1]
RA	Cid L.P., Salinas O., Sepulveda F.V.;	RP	SEQUENCE FROM N.A.
RL	Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.	RC	STRAIN=1021;
DR	EMBL; AF133215; RAD33600.1; -.	RX	MEDLINE=21395508; PubMed=11481431; DOI=10.1073/pnas.161294698;
DR	GO; GO:0016020; C:membrane; IEA.	RA	Finan T.M., Weidner S., Wong K., Buhrmester J., Chain P.,
DR	GO; GO:0005247; F:voltage-gated chloride channel activity; IEA.	RA	Vorhoelter F.J., Hernandez-Lucas I., Becker A., Cowie A., Gouzy J.,
DR	GO; GO:0008821; F:chloride transport; IEA.	RA	Golding B., Puehler A.;
DR	InterPro; IPR001807; Cl-channel_volt.	RA	"The complete sequence of the 1,683-kb pSymb megaplasmid from the N2-
DR	Pfam; PF00654; Voltage_CLC; 1.	RT	fixing endosymbiont Sinorhizobium meliloti.,"
DR	PRINTS; PR00762; CLCHANNEL.	RL	Proc. Natl. Acad. Sci. U.S.A. 98:9889-9894 (2001).
FT	NON_TER	DR	EMBL; AL591985; CAC48679.1; -.
FT	NON_TER	DR	PIR; G95876; G95876.
SQ	SEQUENCE 310 AA; 34691 MW; 15419E709DB531EF CRC64;	DR	GO; GO:0016020; C:membrane; IEA.
		DR	GO; GO:0005215; F:transporter activity; IEA.
		DR	GO; GO:0006810; P:transport; IEA.
		DR	InterPro; IPR005829; Sug transporter.
		DR	InterPro; IPR006043; Xant/urac/vitC.
		DR	InterPro; IPR006042; Xan_ur_permease.
		DR	Pfam; PF00860; Xan_ur_permease; 1.
		DR	PROSITE; PS00216; SUGAR_TRANSPORT_1; UNKNOWN_1.
Query Match	6.1%; Score 8; DB 2; Length 310;	Query Match	6.1%; Score 8; DB 2; Length 310;
Best Local Similarity	100.0%; Pred. No. 12;	Best Local Similarity	100.0%; Pred. No. 12;
Matches	8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	Matches	8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy	10 LVPFILLG 17	Qy	10 LVPFILLG 17
Db	264 LVPFILLG 271	Db	264 LVPFILLG 271
RESULT 24		RESULT 24	
Q9FVV9	PRELIMINARY; PRT; 324 AA.	Q9FVV9	PRELIMINARY; PRT; 324 AA.
ID	Q9FVV9;	ID	Q9FVV9;
AC	Q9FVV9;	AC	Q9FVV9;
DT	01-MAR-2001 (TrEMBLrel. 16, Created)	DT	01-MAR-2001 (TrEMBLrel. 16, Created)
DT	01-MAR-2001 (TrEMBLrel. 16, Last sequence update)	DT	01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT	01-OCT-2003 (TrEMBLrel. 25, Last annotation update)	DT	01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE	Putative ABC transporter; 57695-58850.	DE	Putative ABC transporter; 57695-58850.
GN	Names=F3117.2;	GN	Names=F3117.2;
OS	Arabidopsis thaliana (Mouse-ear cress).	OS	Arabidopsis thaliana (Mouse-ear cress).

DR PROSITE; PS01116; XANTH URACIL_PEMASE; UNKNOWN 1.
 KW Complete proteome; Plasmid.
 SQ SEQUENCE 449 AA; 46750 MW; 33E2705E52580D7D CRC64;

Query Match 6.1%; Score 8; DB 2; Length 449;
 Best Local Similarity 100.0%; Pred. No. 16;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 GLLPILVP 12
 |||||
 Db 391 GLLPILVP 398

RESULT 26
 CLC5 HUMAN
 ID _CLC5_HUMAN STANDARD; PRT; 746 AA.
 AC PS1795;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Chloride channel protein 5 (CLC-5).
 GN Name=CLC5; Synonyms=CLCK2;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Kidney;
 RX MEDLINE=96121370; PubMed=8575751;
 RA Fisher S.E., van Bakel I., Lloyd S.E., Pearce S.H.S., Thakker R.V.,
 RA Craig I.W.;
 RA "Cloning and characterization of CLCN5, the human kidney chloride
 channel gene implicated in Dent disease (an X-linked hereditary
 nephrolithiasis).";
 RT Hum. Mol. Genet. 3:2053-2059(1994).
 RN [3]
 RP TISSUE SPECIFICITY.
 RC TISSUE=Aortic endothelium, and Vascular smooth muscle;
 RX MEDLINE=9222497; PubMed=10198195; DOI=10.1006/jmcc.1998.0901;
 RA Lamb F.S., Clayton G.H., Liu B.-X., Smith R.L., Barna T.J.,
 RA Schutte B.C.;
 RT "Expression of CLCN voltage-gated chloride channel genes in human
 blood vessels.";
 RL J. Mol. Cell. Cardiol. 31:657-666(1999).
 RN [4]
 RP VARIANTS NPHL ARG-200; GLU-506 AND PRO-520, AND VARIANT XLRH LEU-244.
 RX MEDLINE=96158876; PubMed=8559248; DOI=10.1038/379445a0;
 RA Lloyd S.E., Pearce S.H.S., Fisher S.E., Steinmeyer K., Schwappach B.,
 RA Scheinman S.J., Harding B., Bolino A., Devoto M., Goodyer P.,
 RA Rigden S.P.A., Wrong O., Jentsch T.J., Craig I.W., Thakker R.V.;
 RT "A common molecular basis for three inherited kidney stone diseases.";
 RL Nature 379:445-449(1996).
 RN [5]
 RP VARIANTS NPHL.
 RX MEDLINE=97402204; PubMed=9259268; DOI=10.1093/hmg/6.8.1233;
 RA Lloyd S.E., Guenther W., Pearce S.H.S., Thomson A., Bianchi M.L.,
 RA Bosio M., Craig I.W., Fisher S.E., Scheinman S.J., Wrong O.,
 RA Jentsch T.J., Thakker R.V.;
 RT "Characterisation of renal chloride channel, CLCN5, mutations in
 hypercalcaemic nephrolithiasis (kidney stones) disorders.";
 RL Hum. Mol. Genet. 6:1233-1239(1997).
 CC -1- FUNCTION: Voltage-gated chloride channel. Chloride channels have

CC several functions including the regulation of cell volume;
 CC membrane potential stabilization, signal transduction and
 CC transepithelial transport. May play an important role in renal
 CC tubular function.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -1- TISSUE SPECIFICITY: Kidney. Moderately expressed in aortic
 CC vascular smooth muscle and endothelial cells, and at a slightly
 CC higher level in the coronary vascular smooth muscle.
 CC -1- DISEASE: Defects in CLCN5 are a cause of X-linked recessive
 CC hypophosphatemic rickets (XLRH) [MIM:300008].
 CC -1- DISEASE: Defects in CLCN5 are the cause of idiopathic low
 CC molecular weight proteinuria of Japanese children (JILP)
 CC [MIM:300008].
 CC -1- DISEASE: Defects in CLCN5 are the cause of X-linked recessive
 CC nephrolithiasis type 2 (NPHL2) [MIM:300009]; also known as Dent
 CC disease. NPHL2 is a renal form of Fanconi syndrome, characterized
 CC by hypercalciuria, nephrocalcinosis, renal stones and progressive
 CC renal failure.
 CC -1- DISEASE: Defects in CLCN5 are the cause of X-linked recessive
 CC nephrolithiasis type 1 (NPHL1) [MIM:310468]; also designated XRN.
 CC NPHL1 is characterized by hypercalciuria, nephrocalcinosis, renal
 CC stones and renal insufficiency, but differs from Dent disease in
 CC that the patients lack urinary acidification defects, rickets, and
 CC osteomalacia.
 CC -1- SIMILARITY: Belongs to the chloride channel (TC 1.A.11) family.
 CC -1- SIMILARITY: Contains 2 CBS domains.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -
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 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL; X91906; CAA63000.1; -;
 CC EMBL; X81836; CAA57430.1; -;
 CC PIR; I37277; I37277.
 CC Genew; HGNC:2023; CLCN5.
 CC H-InvDB; HIX0016806; -;
 CC MIM; 300008; -;
 CC MIM; 300009; -;
 CC MIM; 310468; -;
 CC GO; GO:0005887; C:integral to plasma membrane; TAS.
 CC GO; GO:0005254; F:chloride channel activity; TAS.
 CC GO; GO:0007588; P:excretion; TAS.
 CC GO; GO:0006810; P:transport; TAS.
 CC InterPro; IPR000644; CBS.
 CC InterPro; IPR001807; Cl-channel volt.
 CC InterPro; IPR002247; Cl_channels.
 CC Pfam; PF00571; CBS; 2.
 CC Pfam; PF00654; Voltage_CLC; 1.
 CC PRINTS; PR00762; CLCHANNEL.
 CC CBS domain; Chloride; Chloride channel; Disease mutation;
 CC Ion transport; Ionic channel; Repeat; Transmembrane;
 CC Voltage-gated channel.
 CC TRANSMEM 55 75 Potential.
 CC TRANSMEM 133 153 Potential.
 CC TRANSMEM 189 209 Potential.
 CC TRANSMEM 246 266 Potential.
 CC TRANSMEM 317 337 Potential.
 CC TRANSMEM 352 372 Potential.
 CC TRANSMEM 428 448 Potential.
 CC TRANSMEM 453 473 Potential.
 CC TRANSMEM 494 514 Potential.
 CC TRANSMEM 521 541 Potential.
 CC TRANSMEM 585 645 CBS 1.
 CC DOMAIN 682 733 CBS 2.
 CC VARIANT 30 30 R -> RH (in NPHL2).
 CC VARIANT 57 57 /FTID=VAR_001615.
 CC VARIANT 200 200 G -> V (in NPHL2).
 CC VARIANT 200 200 L -> R (in NPHL2).

FT VARIANT 244 244 /FTid=VAR_001617.
FT S -> L (in XLRH).
FT /FTid=VAR_001618.
FT R -> P (in JILP).
FT /FTid=VAR_001619.
FT G -> E (in NPHL1).
FT /FTid=VAR_001620.
FT G -> R (in NPHL2; abolishes the chloride
FT currents).
FT /FTid=VAR_001621.
FT S -> P (in NPHL2).
FT /FTid=VAR_001622.
FT E -> D (in NPHL2; abolishes the chloride
FT currents; total loss of function).
FT /FTid=VAR_001623.
SQ SEQUENCE 746 AA; 83146 MW; EF913C5BA0C85D8 CRC64;

Query Match 6.1%; Score 8; DB 1; Length 746;
Best Local Similarity 100.0%; Pred. No. 23;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 LVPFILLG 17
Db 319 LVPFILLG 326

RESULT 27
Q9GKE7 PRELIMINARY; PRT; 746 AA.
AC Q9GKE7;
DT 01-MAR-2001 (Tremblrel. 16, Created)
DT 01-MAR-2001 (Tremblrel. 16, Last sequence update)
DT 01-JUN-2003 (Tremblrel. 24, Last annotation update)
DE Outwardly rectifying chloride channel.
GN Name=CIC-5;
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20545523; PubMed=10978325; DOI=10.1074/jbc.M004840200;
RA Dowland L.K., Luyckx V.A., Enck A.H., Leclercq B., Yu A.S.L.;
RT "Molecular cloning and characterization of an intracellular chloride
RT channel in the proximal tubule cell line, LLC-PK1";
RL J. Biol. Chem. 275:37765-37773 (2000).
DR EMBL; AF274055; AAG29104.1; -;
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005247; P:voltage-gated chloride channel activity; IEA.
DR GO; GO:0006821; P:chloride transport; IEA.
DR InterPro; IPR000644; CBS.
DR InterPro; IPR001807; Cl-channel volt.
DR InterPro; IPR002247; Cl_channel15.
DR Pfam; PF00571; CBS; 1.
DR Pfam; PF00654; Voltage_CLC; 1.
DR PRINTS; PR00762; CLCHANNEL.
DR PRINTS; PR01116; CLCHANNELS.
DR SMART; SM00116; CBS; 2.
SQ SEQUENCE 746 AA; 83123 MW; 655E3ED45FC61229 CRC64;

Query Match 6.1%; Score 8; DB 2; Length 746;
Best Local Similarity 100.0%; Pred. No. 23;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 LVPFILLG 17
Db 319 LVPFILLG 326

RESULT 28
Q9TTU3 PRELIMINARY; PRT; 746 AA.
AC Q9TTU3;

DT 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
DT 01-JUN-2003 (Tremblrel. 24, Last annotation update)
DE Chloride channel CLC-5.
GN Name=CLCN5;
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=New Zealand White; TISSUE=Cornea epithelia;
RA Rae J.L.;
RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.
EMBL; AF195523; AAF06018.1; -;
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005247; P:voltage-gated chloride channel activity; IEA.
DR GO; GO:0006821; P:chloride transport; IEA.
DR InterPro; IPR000644; CBS.
DR InterPro; IPR001807; Cl-channel volt.
DR InterPro; IPR002247; Cl_channel15.
DR Pfam; PF00571; CBS; 1.
DR Pfam; PF00654; Voltage_CLC; 1.
DR PRINTS; PR00762; CLCHANNEL.
DR PRINTS; PR01116; CLCHANNELS.
DR SMART; SM00116; CBS; 2.
SQ SEQUENCE 746 AA; 83206 MW; 667F2701C0BF006A CRC64;

Query Match 6.1%; Score 8; DB 2; Length 746;
Best Local Similarity 100.0%; Pred. No. 23;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 LVPFILLG 17
Db 319 LVPFILLG 326

RESULT 29
Q99P66 PRELIMINARY; PRT; 746 AA.
ID Q99P66;
AC Q99P66;
DT 01-JUN-2001 (Tremblrel. 17, Created)
DT 01-JUN-2001 (Tremblrel. 17, Last sequence update)
DT 01-JUN-2003 (Tremblrel. 24, Last annotation update)
DE Chloride channel CLCN5.
OS Cavia porcellus (Guinea pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Hystricognathi; Caviidae; Cavia.
OX NCBI_TaxID=10141;
RN [1]
RP SEQUENCE FROM N.A.
RA Cornejo I., Cid L.P., Sepulveda F.V.;
RL Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF326988; AAG49590.1; -;
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005247; P:voltage-gated chloride channel activity; IEA.
DR GO; GO:0006821; P:chloride transport; IEA.
DR InterPro; IPR000644; CBS.
DR InterPro; IPR001807; Cl-channel volt.
DR InterPro; IPR002247; Cl_channel15.
DR Pfam; PF00571; CBS; 1.
DR Pfam; PF00654; Voltage_CLC; 1.
DR PRINTS; PR00762; CLCHANNEL.
DR PRINTS; PR01116; CLCHANNELS.
DR SMART; SM00116; CBS; 2.
SQ SEQUENCE 746 AA; 83093 MW; 92FC8AFDC7D8D4A5 CRC64;

Query Match 6.1%; Score 8; DB 2; Length 746;
Best Local Similarity 100.0%; Pred. No. 23;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 LVPFILLG 17
Db 319 LVPFILLG 326

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Db      319 LVPEILLG 326

RESULT 30
Q7QH49          PRELIMINARY;      PRT;      893 AA.
AC Q7QH49;
DT 01-MAR-2004 (TrEMBLrel. 26, Created)
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Eb1P4085 (Fragment).
GN Name=ebiG4085; ORFNames=ENSANG00000003243;
OS Anopheles gambiae str. PEST.
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Anopheles.
OX NCBI_TaxID=180454;
[1]
RP SEQUENCE FROM N.A.
RC STRAIN=PEST;
RA Anopheles Genome Sequencing Consortium;
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
CC -! CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
CC EMBL; AAB0100817; EAA05380.1; -.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0004527; F:exonuclease activity; IEA.
DR InterPro; IPR004859; Put_S3exo.
DR Pfam; PF03159; XRN_N; 1.
FT NON TER      893      893
SQ SEQUENCE      893 AA; 101361 MW; B14EB646182083C8 CRC64;

Query Match      6.1%; Score 8; DB 2; Length 893;
Best Local Similarity 100.0%; Pred. No. 26;
Matches      8; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

Qy      111 QGNNNFQ 118
Db      800 QGNNNFQ 807
|||||||

RESULT 31
Q8K206          PRELIMINARY;      PRT;      900 AA.
AC Q8K206;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE A disintegrin-like and metalloprotease (Repolysin type) with
DE thrombospondin type 1 motif, 16.
GN Name=Adams16;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
[1]
RP SEQUENCE FROM N.A.
RC STRAIN=FVB/N; TISSUE=Mammary tumor. C3;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.2426038999;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,
RA Diatchenko L., Maruina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bobak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny K.C., Hulse S., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A.C., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

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RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Kzywinski M.I., Skaleka U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
[2]
RN SEQUENCE FROM N.A.
RP STRAIN=FVB/N; TISSUE=Mammary tumor. C3;
RC Strausberg R.;
RA Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
RL EMBL; BC034739; AAH34739.1; -.
DR HSP; P07996; ILSL.
DR MEROPS; M12.026; -.
DR MGD; MGI:2439637; Adams16.
DR GO; GO:0004222; F:metalloendopeptidase activity; IEA.
DR GO; GO:0007229; P:integrin-mediated signaling pathway; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR010294; ADAM spacer1.
DR InterPro; IPR001590; Peptidase_M12B.
DR InterPro; IPR002870; Peptidase_M12B_N.
DR InterPro; IPR000884; TSP1.
DR InterPro; IPR008085; TSP 1.
DR Pfam; PF05986; ADAM spacer1; 1.
DR Pfam; PF01421; Repolysin; 1.
DR Pfam; PF00090; TSP_1; 1.
DR PRINTS; PR01705; TSP1REPEAT.
DR SMART; SM00209; TSP1; 1.
DR PROSITE; PS00215; ADAM MBPRO; 1.
DR PROSITE; PS00092; TSP1; 1.
KW Integrin; Metalloprotease; Protease.
SQ SEQUENCE      900 AA; 100679 MW; 590BE2B0E73740FF CRC64;

Query Match      6.1%; Score 8; DB 2; Length 900;
Best Local Similarity 100.0%; Pred. No. 26;
Matches      8; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

Qy      70 LDFRKDIC 77
Db      529 LDFRKDIC 536
|||||||

RESULT 32
Q69Z28          PRELIMINARY;      PRT;      1233 AA.
AC Q69Z28;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE MKIAA2029 protein (Fragment).
GN Name=mKIAA2029;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
[1]
RP SEQUENCE FROM N.A.
RC TISSUE=Embryonic intestinal tract;
RA Okazaki N., Kikuno R.F., Ohara R., Inamoto S., Koseki H., Hiraoka S.,
RA Saga Y., Seino S., Nishimura M., Kaisho T., Hoshino K., Kitamura H.,
RA Nagase T., Ohara O., Koga H.;
RT "Prediction of the Coding Sequences of Mouse Homologues of KIAA Gene:
RT cDNAs Identified by Screening of Terminal Sequences of cDNA Clones
RT Randomly Sampled from Size-Fractionated Libraries.";
RL DNA Res. 11:205-218(2004).
DR EMBL; AK173338; BAD32616.1; -.
DR GO; GO:0004222; F:metalloendopeptidase activity; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR010294; ADAM spacer1.
DR InterPro; IPR001590; Peptidase_M12B.
DR InterPro; IPR002870; Peptidase_M12B_N.

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OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A. PubMed=2413856;
 RX MEDLINE=86025577; Diarra-Mehrpour M., Sesboue R., Frain M.,
 RA Bourguignon J., Diarra-Mehrpour M., Martin J.P., Salier J.P.;
 RA Sala-Trepat J.M., Martin J.P., Salier J.P.;
 RT "Human inter-alpha-trypsin-inhibitor: characterization and partial
 RT nucleotide sequencing of a light chain-encoding cDNA.";
 RL Biochem. Biophys. Res. Commun. 131:1146-1153(1985).
 CC -1- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.
 DR EMBL: M11562; AAA59194.1; -;
 DR HSSP: P02760; 1BIK.
 DR GO: GO:0004867; F:serine-type endopeptidase inhibitor activity; IEA.
 DR InterPro: IPR002223; Prot_Inh_Kunz-m.
 DR Pfam: PF00014; Kunitz BPTI; 1.
 DR PRINTS: PR00759; BASICTPASE.
 DR PRODOM: PD000222; Prot_Inh_Kunz-m; 1.
 DR SMART: SM00131; KU; 1.
 DR PROSITE: PS00280; BPTI_KUNITZ_1; 1.
 DR PROSITE: PS50279; BPTI_KUNITZ_2; 1.
 FT NON_TER 1
 SQ SEQUENCE 51 AA; 5698 MW; C13D74054D45EED2 CRC64;

 Query Match 5.3%; Score 7; DB 2; Length 51;
 Best Local Similarity 100.0%; Pred. No. 35;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

 Qy 107 YGGCQGN 113
 Db 16 YGGCQGN 22
 |||||

 RESULT 36
 HTIB MANSE STANDARD; PRT; 53 AA.
 AC P26227;
 DT 01-MAY-1992 (Rel. 22, Created)
 DT 01-MAY-1992 (Rel. 22, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Hemolymph trypsin inhibitor B (BPI-type) (Fragment).
 OS Manduca sexta (Tobacco hawkmoth) (Tobacco hornworm).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia; Sphingioidea;
 OC Sphingidae; Sphinginae; Manduca.
 OX NCBI_TaxID=7130;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Larval hemolymph;
 RX MEDLINE=88298810; PubMed=3165377;
 RA Ramesh N., Sugumaran M., Mole J.E.;
 RT "Purification and characterization of two trypsin inhibitors from the
 RT hemolymph of Manduca sexta larvae.";
 RL J. Biol. Chem. 263:11523-11527(1988).
 CC -1- FUNCTION: Inhibits trypsin.
 CC -1- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.
 DR PIR: B29235; B29235.
 DR HSSP: P31713; 1SHP.
 DR InterPro: IPR002223; Prot_Inh_Kunz-m.
 DR Pfam: PF00014; Kunitz BPTI; 1.
 DR PRINTS: PR00759; BASICTPASE.
 DR PRODOM: PD000222; Prot_Inh_Kunz-m; 1.
 DR SMART: SM00131; KU; 1.
 DR PROSITE: PS00280; BPTI_KUNITZ_1; 1.
 DR PROSITE: PS50279; BPTI_KUNITZ_2; 1.
 KW Direct protein sequencing; Serine protease inhibitor.
 FT SITE 14 15
 FT DISULFID 4 ?
 FT DISULFID 13 37
 FT DISULFID 29 50
 FT NON_TER 53
 SQ SEQUENCE 53 AA; 5880 MW; 3C34CFD98C6BB329 CRC64;

Query Match 5.3%; Score 7; DB 1; Length 53;
 Best Local Similarity 100.0%; Pred. No. 36;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

 Qy 107 YGGCQGN 113
 Db 34 YGGCQGN 40
 |||||

 RESULT 37
 IVB2 NAJNI STANDARD; PRT; 57 AA.
 AC P00986;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Venom basic protease inhibitor II.
 OS Naja nivea (Cape cobra).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
 OC Elapidae; Elapinae; Naja.
 OX NCBI_TaxID=8655;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Venom;
 RX MEDLINE=76237547; PubMed=950137;
 RA Hokama Y., Iwanaga S., Tateuki T., Suzuki T.;
 RT "Snake venom proteinase inhibitors. III. Isolation of five polypeptide
 RT inhibitors from the venoms of Hemachatus haemachatus (Ringhals
 RT cobra) and Naja nivea (Cape cobra) and the complete amino acid
 RT sequences of two of them.";
 RL J. Biochem. 79:559-578(1976).
 CC -1- FUNCTION: The activity of this inhibitor is probably similar to
 CC that of bovine basic protease inhibitor.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- TISSUE SPECIFICITY: Expressed by the venom gland.
 CC -1- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.
 DR PIR: A01217; TINJVC.
 DR HSSP: P25660; IJC6.
 DR InterPro: IPR002223; Prot_Inh_Kunz-m.
 DR Pfam: PF00014; Kunitz BPTI; 1.
 DR PRINTS: PR00759; BASICTPASE.
 DR PRODOM: PD000222; Prot_Inh_Kunz-m; 1.
 DR SMART: SM00131; KU; 1.
 DR PROSITE: PS00280; BPTI_KUNITZ_1; 1.
 DR PROSITE: PS50279; BPTI_KUNITZ_2; 1.
 KW Direct protein sequencing; Serine protease inhibitor.
 FT SITE 15 16
 FT DISULFID 5 55
 FT DISULFID 14 38
 FT DISULFID 30 51
 FT DISULFID 30 51
 SQ SEQUENCE 57 AA; 6466 MW; 7CA69230A02887D1 CRC64;

 Query Match 5.3%; Score 7; DB 1; Length 57;
 Best Local Similarity 100.0%; Pred. No. 38;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

 Qy 104 EPIYGGC 110
 Db 32 EPIYGGC 38
 |||||

 RESULT 38
 ISC2_BOMMO STANDARD; PRT; 62 AA.
 AC P10832;
 DT 01-JUL-1989 (Rel. 11, Created)
 DT 01-JUL-1989 (Rel. 11, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Chymotrypsin inhibitor SCI-II.
 OS Bombyx mori (Silk moth).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Lepidoptera; Glossata; Bombycoidea;

Bombycidae; Bombyx.
 KW NCBI_TaxID=7091;
 FT SIGNAL 1 20 Potential.
 SQ SEQUENCE 76 AA; 8419 MW; 0C6ED52550632B79 CRC64;
 AC Q870M4;
 DT 25-OCT-2004 (Rel. 45, Created)
 DT 25-OCT-2004 (Rel. 45, Last sequence update)
 DT 25-OCT-2004 (Rel. 45, Last annotation update)
 DE Protease inhibitor cvp2 precursor (Cysteine-rich venom protein 2).
 GN Name=cvp2;
 OS Pimpla hypochondriaca (Parasitoid wasp).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Hymenoptera; Apocrita; Ichneumonidae;
 OC Ichneumonidae; Pimplinae; Pimplini; Pimpla.
 OC NCBI_TaxID=135724;
 RN [1]
 RP SEQUENCE FROM N.A., AND SEQUENCE OF 24-29.
 RC TISSUE=Venom, and Venom gland;
 RX PubMed=15147757; DOI=10.1016/j.jlmb.2004.03.003;
 RA Parkinson N.M., Conyers C., Keen J., MacNicoll A., Smith I.,
 RA Audsley N., Weaver R.;
 RT "Towards a comprehensive view of the primary structure of venom
 proteins from the parasitoid wasp Pimpla hypochondriaca.";
 RL Insect Biochem. Mol. Biol. 34:565-571(2004).
 CC -!- FUNCTION: Probable serine protease inhibitor (By similarity).
 CC -!- TISSUE SPECIFICITY: Expressed by the venom gland.
 CC -!- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.
 CC
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 CC
 CC EMBL; AJ438993; CAD27738.1; -.
 DR HSSP; P31713; LSHP.
 DR InterPro; IPR002223; Prot_Inh_Kunz-m.
 DR Pfam; PF00014; Kunitz_BPTI_1.
 DR PRINTS; PR00759; BASICPTASE.
 DR ProDom; PD000222; Prot_Inh_Kunz-m; 1.
 DR SMART; SM00131; KU; 1.
 DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
 DR PROSITE; PS0279; BPTI_KUNITZ_2; 1.
 KW Direct protein sequencing; Serine protease inhibitor; Signal.
 FT SIGNAL 1 23
 FT CHAIN 24 77 Protease inhibitor cvp2.
 FT DOMAIN 28 76 BPTI/Kunitz inhibitor.
 FT DISULFID 28 76 By similarity.
 FT DISULFID 37 59 By similarity.
 FT DISULFID 51 72 By similarity.
 SQ SEQUENCE 77 AA; 7873 MW; FF40C07F3C7E0D75 CRC64;
 Query Match 5.3%; Score 7; DB 1; Length 77;
 Best Local Similarity 100.0%; Pred. No. 47;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 104 EPIYGC 110
 DB 37 EPIYGC 43
 RESULT 39
 Q968S8 PRELIMINARY; PRT; 76 AA.
 AC Q968S8;
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Silk protease inhibitor 1 precursor.
 OS Galleria mellonella (Wax moth).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia; Pyraloidea;
 OC Pyralidae; Galleriinae; Galleria.
 OC NCBI_TaxID=71137;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21175824; PubMed=11277929;
 RA Nirmla X., Kodrik D., Zurovec M., Sehnal F.;
 RT "Insect silk contains both a Kunitz-type and a unique Kazal-type
 RT proteinase inhibitor.";
 RL Eur. J. Biochem. 268:2064-2073(2001).
 CC -!- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.
 DR EMBL; AF292098; AAK40037.1; -.
 DR HSSP; P10646; IADZ.
 DR GO; GO:008233; F:peptidase activity; IEA.
 DR GO; GO:0004867; F:serine-type endopeptidase inhibitor activity; IEA.
 DR InterPro; IPR002223; Prot_Inh_Kunz-m.
 DR Pfam; PF00014; Kunitz_BPTI_1.
 DR PRINTS; PR00759; BASICPTASE.
 DR SMART; SM00131; KU; 1.
 DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
 DR PROSITE; PS0279; BPTI_KUNITZ_2; 1.

KW Protease; Signal.
 FT SIGNAL 1 20 Potential.
 SQ SEQUENCE 76 AA; 8419 MW; 0C6ED52550632B79 CRC64;
 AC Q870M4;
 DT 25-OCT-2004 (Rel. 45, Created)
 DT 25-OCT-2004 (Rel. 45, Last sequence update)
 DT 25-OCT-2004 (Rel. 45, Last annotation update)
 DE Protease inhibitor cvp2 precursor (Cysteine-rich venom protein 2).
 GN Name=cvp2;
 OS Pimpla hypochondriaca (Parasitoid wasp).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Hymenoptera; Apocrita; Ichneumonidae;
 OC Ichneumonidae; Pimplinae; Pimplini; Pimpla.
 OC NCBI_TaxID=135724;
 RN [1]
 RP SEQUENCE FROM N.A., AND SEQUENCE OF 24-29.
 RC TISSUE=Venom, and Venom gland;
 RX PubMed=15147757; DOI=10.1016/j.jlmb.2004.03.003;
 RA Parkinson N.M., Conyers C., Keen J., MacNicoll A., Smith I.,
 RA Audsley N., Weaver R.;
 RT "Towards a comprehensive view of the primary structure of venom
 proteins from the parasitoid wasp Pimpla hypochondriaca.";
 RL Insect Biochem. Mol. Biol. 34:565-571(2004).
 CC -!- FUNCTION: Probable serine protease inhibitor (By similarity).
 CC -!- TISSUE SPECIFICITY: Expressed by the venom gland.
 CC -!- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.
 CC
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 CC or send an email to license@isb-sib.ch).
 CC
 CC EMBL; AJ438993; CAD27738.1; -.
 DR HSSP; P31713; LSHP.
 DR InterPro; IPR002223; Prot_Inh_Kunz-m.
 DR Pfam; PF00014; Kunitz_BPTI_1.
 DR PRINTS; PR00759; BASICPTASE.
 DR ProDom; PD000222; Prot_Inh_Kunz-m; 1.
 DR SMART; SM00131; KU; 1.
 DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
 DR PROSITE; PS0279; BPTI_KUNITZ_2; 1.
 KW Direct protein sequencing; Serine protease inhibitor; Signal.
 FT SIGNAL 1 23
 FT CHAIN 24 77 Protease inhibitor cvp2.
 FT DOMAIN 28 76 BPTI/Kunitz inhibitor.
 FT DISULFID 28 76 By similarity.
 FT DISULFID 37 59 By similarity.
 FT DISULFID 51 72 By similarity.
 SQ SEQUENCE 77 AA; 7873 MW; FF40C07F3C7E0D75 CRC64;
 Query Match 5.3%; Score 7; DB 1; Length 77;
 Best Local Similarity 100.0%; Pred. No. 47;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 104 EPIYGC 110
 DB 37 EPIYGC 43

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Db          53 EFIYGGC 59

RESULT 41
Q9VCM3      PRELIMINARY;      PRT;      80 AA.
ID          Q8T3S7
AC          Q8T3S7;
DT          01-JUN-2002 (TrEMBLrel. 21, Created)
DE          01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT          01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT          01-JUN-2002 (TrEMBLrel. 24, Last annotation update)
DE          Toxin 1.
OS          Araneus ventricosus.
OC          Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Araneae;
OC          Araneomorphae; Entelegynae; Araneioidea; Araneidae; Araneus.
OX          NCBI_TaxID=192803;
RN          [1]
RP          SEQUENCE FROM N.A.
RA          Jung E.H., Lee K.S., Han J.H., Je Y.H., Chang J.H., Roh J.Y.,
RA          Sohn H.D., Jin B.R.;
RT          "Molecular cloning of two cDNAs encoding an insecticidal toxin from
RT          the spider, Araneus ventricosus, and construction of a recombinant
RT          baculovirus expressing a spider toxin.";
RL          Int. J. Ind. Entomol. 4:43-49 (2002).
RN          [2]
RP          SEQUENCE FROM N.A.
RA          Chung E.H., Lee K.S., Han J.H., Sohn H.D., Jin B.R.;
RL          Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
CC          -1- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.
DR          EMBL; AY091482; AAM14403.1; -.
DR          HSSP; P12111; 1KTH.
DR          GO; GO:0004867; F:serine-type endopeptidase inhibitor activity; IEA.
DR          InterPro; IPR02223; Prot Inh Kunz-m.
DR          Pfam; PF000014; Kunitz BPTI; 1.
DR          PRINTS; PR00759; BASICPTASE.
DR          SMART; SM00131; KU; 1.
DR          PROSITE; PS00280; BPTI_KUNITZ_1; 1.
DR          PROSITE; PS02079; BPTI_KUNITZ_2; 1.
SQ          SEQUENCE      80 AA;  9275 MW;  D07F5F9AC6B7BC10 CRC64;

Query Match      5.3%; Score 7; DB 2; Length 80;
Best Local Similarity 100.0%; Pred. No. 49;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy          104 EFIYGGC 110
Db          54 EFIYGGC 60
|||||

RESULT 42
Q9VCM3      PRELIMINARY;      PRT;      80 AA.
ID          Q9VCM3
AC          Q9VCM3;
DT          01-MAY-2000 (TrEMBLrel. 13, Created)
DT          01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT          01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE          CG17360-PA.
GN          ORNames=CG17380;
OS          Drosophila melanogaster (Fruit fly).
OC          Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC          Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC          Ephydroidea; Drosophilidae; Drosophila.
OX          NCBI_TaxID=7227;
RN          [1]
RP          SEQUENCE FROM N.A.
RA          Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA          Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA          George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA          Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA          Brandon R.C., Rogers Y.H., Blazej R.G., Champe M., Pfeiffer B.D.,
RA          Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Gabor G.L.,
RA          Abril J.F., Agbayani A., An H.J., Andrews-Efankoch C., Baldwin D.,
RA          Balow R.M., Bau A., Baxendale J., Bayraktaroglu L., Beasley E.M.,

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Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
Foeller C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,
Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
Hostin D., Houston K.A., Howland T.J., Wei M.H., Ibegwam C.,
Jalali M., Kalush F., Karpén G.H., Ke Z., Kennison J.A., Ketchum K.A.,
Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
Laeko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
Reinert K., Remington K., Saunders R.D., Scheeler F., Shen H.,
Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
Swirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
Wang Z.Y., Wassearman D.A., Weinstein G.M., Weissenbach J.,
Williams S.M., Woodgett, Worley K.C., Wu D., Yang S., Yao Q.A., Ye J.,
Yeh R.F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT          "The genome sequence of Drosophila melanogaster.";
RL          Science 287:2185-2195 (2000).
RN          [2]
RP          SEQUENCE FROM N.A.
RX          MEDLINE=22426065; PubMed=12537568;
RA          Celniker S.E., Wheeler D.A., Kronmiller B., Carlson J.W., Halpern A.,
RA          Patel S., Adams M., Champe M., Dugan S.P., Frise E., Hodgson A.,
RA          George R.A., Hoskins R.A., Laverly T., Muzny D.M., Nelson C.R.,
RA          Pacleb J.M., Park S., Pfeiffer B.D., Richards S., Sodergren E.J.,
RA          Swirskas R., Tabor P.E., Wan K., Stapleton M., Sutton G.G., Venter C.,
RA          Weinstein G., Scherer S.E., Myers E.W., Gibbs R.A., Rubin G.M.;
RT          "Finishing a whole-genome shotgun: Release 3 of the Drosophila
RT          melanogaster euchromatic genome sequence.";
RL          Genome Biol. 3:RESEARCH0079-RESEARCH0079 (2002).
RN          [3]
RP          SEQUENCE FROM N.A.
RX          MEDLINE=22426070; PubMed=12537573;
RA          Kaminker J.S., Bergman C.M., Kronmiller B., Carlson J., Swirskas R.,
RA          Patel S., Frise E., Wheeler D.A., Lewis S.E., Rubin G.M.,
RA          Ashburner M., Celniker S.E.;
RT          "The transposable elements of the Drosophila melanogaster euchromatin:
RT          a genomics perspective.";
RL          Genome Biol. 3:RESEARCH0084-RESEARCH0084 (2002).
RN          [4]
RP          SEQUENCE FROM N.A.
RX          MEDLINE=22426069; PubMed=12537572;
RA          Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
RA          Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochuk S.E.,
RA          Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Berman B.P.,
RA          Bettecourt B.R., Celniker S.E., de Grey A.D., Drysdale R.A.,
RA          Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,
RA          Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
RA          Lewis S.E.;
RT          "Annotation of the Drosophila melanogaster euchromatic genome: a
RT          systematic review";
RL          Genome Biol. 3:RESEARCH0083-RESEARCH0083 (2002).
RN          [5]
RP          SEQUENCE FROM N.A.
RG          FlyBase;
RL          Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
RN          [6]
RP          SEQUENCE FROM N.A.
RG          FlyBase;
RL          Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.
CC          -1- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.

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Query Match      5.3%; Score 7; DB 2; Length 83;
Best Local Similarity 100.0%; Pred.No. 50;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      104 EFYGGC 110
Db      58 EFYGGC 64

RESULT 46
Q90WA1 ID Q90WA1 PRELIMINARY; PRT; 83 AA.
AC Q90WA1
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Textilin.
OS Pseudonaja textilis textilis.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroides;
OC Elapidae; Acanthophiinae; Pseudonaja.
OX NCBI_TaxID=169397;
RN [1]
RN SEQUENCE FROM N.A.
RP SEQUENCE FROM N.A.
RC TISSUE=Venom gland;
RA Masci P.P., Lavin M.F., Gaffney P.J., Sorokina I.N., Filippovich I.V.;
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
[2]
RN SEQUENCE FROM N.A.
RP SEQUENCE FROM N.A.
RC TISSUE=Venom gland;
RA Filippovich I.V., Sorokina N.I., Masci P.P., de Jersey J.,
RA Whitaker A.N., Gaffney P.J., Lavin M.F.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.
DR EMBL; AF402324; AAK95519.1; -.
DR HSSP; P25660; 1JC6.
DR GO; GO:0004867; F:serine-type endopeptidase inhibitor activity; IEA.
DR Pfam; PF00014; Kunitz_BPTI; 1.
DR PRINTS; PR00759; BASICTPASE.
DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
DR PROSITE; PS0279; BPTI_KUNITZ_2; 1.
SQ SEQUENCE 83 AA; 9173 MW; 2043E50657014221 CRC64;

Query Match      5.3%; Score 7; DB 2; Length 83;
Best Local Similarity 100.0%; Pred.No. 50;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      104 EFYGGC 110
Db      58 EFYGGC 64

RESULT 47
Q6ITB0 ID Q6ITB0 PRELIMINARY; PRT; 83 AA.
AC Q6ITB0;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Carinatin.
OS Tropidochelis carinatus (Australian rough-scaled snake).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroides;
OC Elapidae; Notechidinae; Tropidochelis.
OX NCBI_TaxID=100989;
RN [1]
RN SEQUENCE FROM N.A.
RP SEQUENCE FROM N.A.
RC TISSUE=Venom gland;
RA Filippovich I.V., Sorokina N.I.;
RL Submitted (MAY-2004) to the EMBL/GenBank/DBJ databases.

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CC -1- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.
DR EMBL; AY626935; AAT45411.1; -.
DR HSSP; P10646; 1ADZ.
DR GO; GO:0004867; F:serine-type endopeptidase inhibitor activity; IEA.
DR InterPro; IPR002223; Prot_Inh_Kunz-m.
DR Pfam; PF00014; Kunitz_BPTI; 1.
DR PRINTS; PR00759; BASICTPASE.
DR PRODOM; PD000222; Prot_Inh_Kunz-m; 1.
DR SMART; SM00131; KU; 1.
DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
DR PROSITE; PS0279; BPTI_KUNITZ_2; 1.
SQ SEQUENCE 83 AA; 9285 MW; 52EDB4BB68BB3B79 CRC64;

Query Match      5.3%; Score 7; DB 2; Length 83;
Best Local Similarity 100.0%; Pred.No. 50;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      104 EFYGGC 110
Db      58 EFYGGC 64

RESULT 48
Q6ITB1 ID Q6ITB1 PRELIMINARY; PRT; 83 AA.
AC Q6ITB1;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Blackelin.
OS Pseudechis porphyriacus (Red-bellied black snake).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroides;
OC Elapidae; Acanthophiinae; Pseudechis.
OX NCBI_TaxID=8671;
RN [1]
RN SEQUENCE FROM N.A.
RP TISSUE=Venom gland;
RA Filippovich I.V., Sorokina N.I.;
RL Submitted (MAY-2004) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.
DR EMBL; AY626934; AAT45410.1; -.
DR HSSP; P10646; 1ADZ.
DR GO; GO:0004867; F:serine-type endopeptidase inhibitor activity; IEA.
DR InterPro; IPR002223; Prot_Inh_Kunz-m.
DR PRINTS; PR00759; BASICTPASE.
DR PRODOM; PD000222; Prot_Inh_Kunz-m; 1.
DR SMART; SM00131; KU; 1.
DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
DR PROSITE; PS0279; BPTI_KUNITZ_2; 1.
SQ SEQUENCE 83 AA; 9285 MW; 52EDB4BB68BB3B79 CRC64;

Query Match      5.3%; Score 7; DB 2; Length 83;
Best Local Similarity 100.0%; Pred.No. 50;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      104 EFYGGC 110
Db      58 EFYGGC 64

RESULT 49
Q6ITB2 ID Q6ITB2 PRELIMINARY; PRT; 83 AA.
AC Q6ITB2;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Tigerin-2.
OS Notechis scutatus (Mainland tiger snake) (Common tiger snake).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

```

OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC Elapidae; Acanthophiinae; Notechis.

OX NCBI_TaxID=70142;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=venom gland;

RA Filippovich I.V., Sorokina N.I.;

RL Submitted (MAY-2004) to the EMBL/GenBank/DBJ databases.

CC -!- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.

DR EMBL; AY626933; AAT45408.1; -

DR HSSP; Q16019; 1ADP.

DR GO; GO:0004867; F:serine-type endopeptidase inhibitor activity; IEA.

DR InterPro; IPR002223; Prot_Inh_Kunz-m.

DR Pfam; PF00014; Kunitz_BPTI; 1.

DR PRINTS; PR00759; BASICPTASE.

DR ProDom; PD000222; Prot_Inh_Kunz-m; 1.

DR SMART; SM00131; KU; 1.

DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.

DR PROSITE; PS50279; BPTI_KUNITZ_2; 1.

SQ SEQUENCE 83 AA; 9073 MW; AE4D0E8367EED0A2 CRC64;

Query Match

5.3%; Score 7; DB 2; Length 83;

Best Local Similarity 100.0%; Pred. No. 50;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 104 EFIYGGC 110

|||||

DB 58 EFIYGGC 64

RESULT 50

Q6ITB3

ID Q6ITB3 PRELIMINARY; PRT; 83 AA.

AC Q6ITB3;

DT 05-JUL-2004 (TRENBLrel. 27, Created)

DT 05-JUL-2004 (TRENBLrel. 27, Last sequence update)

DT 05-JUL-2004 (TRENBLrel. 27, Last annotation update)

DE Tigerin-1.

OS Notechis scutatus scutatus (Mainland tiger snake) (Common tiger

OS snake).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;

OC Elapidae; Acanthophiinae; Notechis.

OX NCBI_TaxID=70142;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=Venom gland;

RA Filippovich I.V., Sorokina N.I.;

RL Submitted (MAY-2004) to the EMBL/GenBank/DBJ databases.

CC -!- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.

DR EMBL; AY626932; AAT45408.1; -

DR HSSP; P10646; 1ADZ.

DR GO; GO:0004867; F:serine-type endopeptidase inhibitor activity; IEA.

DR InterPro; IPR002223; Prot_Inh_Kunz-m.

DR Pfam; PF00014; Kunitz_BPTI; 1.

DR PRINTS; PR00759; BASICPTASE.

DR ProDom; PD000222; Prot_Inh_Kunz-m; 1.

DR SMART; SM00131; KU; 1.

DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.

DR PROSITE; PS50279; BPTI_KUNITZ_2; 1.

SQ SEQUENCE 83 AA; 9135 MW; AE4D0E85A486F0A2 CRC64;

Query Match

5.3%; Score 7; DB 2; Length 83;

Best Local Similarity 100.0%; Pred. No. 50;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 104 EFIYGGC 110

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DB 58 EFIYGGC 64

Search completed: September 21, 2005, 16:50:12

Job time : 142 secs

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